

gac cgt gcg gcg gag ctt ttg aac gca cat ccc aag ccc gcc atg tac 835
 Asp Arg Ala Ala Glu Leu Leu Asn Ala His Pro Lys Pro Ala Met Tyr
 230 235 240 245

gct aat gcg cat ggc aaa gaa gac taagaagaat gaacagctgc cgg 882
 Ala Asn Ala His Gly Lys Glu Asp
 250

<210> 236

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

Met Lys Val Ile Ala His Arg Gly Leu Ser Ser Arg Phe Pro Glu Leu
 1 5 10 15

Thr Glu Ser Ala Phe Arg Ala Ala Leu Glu Leu Pro Ile His Gly Ile
 20 25 30

Glu Thr Asp Val Arg Leu Thr Lys Cys Gly Glu Val Val Asn Val His
 35 40 45

Asp Pro Ile Val Asp Arg Val Ser Asn Gly Arg Gly Arg Val Ser Arg
 50 55 60

Leu Asp Leu Glu Ser Leu Leu Ser Leu Asn Phe Gly Thr Lys Glu Thr
 65 70 75 80

Pro Glu Lys Val Leu Thr Leu Asn Asn Leu Leu Asp Ile Phe Glu Asp
 85 90 95

Tyr Pro Asp Lys His Leu Tyr Ile Glu Thr Lys His Pro Met Arg Tyr
 100 105 110

Ala Val Met Leu Glu Glu Glu Ile Thr Lys Ile Leu Lys Tyr Arg Gly
 115 120 125

Leu Thr Glu Asp Pro Arg Ile His Ile Ile Ser Phe Ala Leu Pro Ala
 130 135 140

Met Tyr Arg Met Ala Arg Leu Ala Pro Gln Leu Asp Arg Ile His Leu
 145 150 155 160

Arg Arg Ser Trp Glu Arg Trp Gly Asn Pro Arg Asp Val Arg Cys Gly
 165 170 175

Val Pro Thr Gly Leu Gly Leu Ser Leu Glu Arg Ala Lys Met Asp Pro
 180 185 190

Arg Met Ile Gly Ala Lys Gly Leu Pro Thr Tyr Leu Phe Thr Val Asp
 195 200 205

Lys Gln Lys Asp Met Leu Trp Ala Arg Glu Gln Gly Val Asp Met Leu
 210 215 220

Ala Thr Asn Tyr Pro Asp Arg Ala Ala Glu Leu Leu Asn Ala His Pro
 225 230 235 240

Lys Pro Ala Met Tyr Ala Asn Ala His Gly Lys Glu Asp
 245 250

<210> 237

<211> 1428

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1405)

<223> RXS01166

<400> 237

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atgcgcgtaa tcctaaccgg cgcacactaa tgtggccgat atg ggc tac acc aac 115
                                         Met Gly Tyr Thr Asn
                                         1 5

ctc aac gac aca cgg gtc ttg cgc gcc ggg tca tgt gat gcc tgg tgg 163
Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser Cys Asp Ala Trp Trp
                        10 15 20

cgc acg atg tct ccg cta gtg cag cag gga agt gag gca gtc ttt cgg 211
Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser Glu Ala Val Phe Arg
                        25 30 35

cgc atc atg ggt ctc tcg cgg cgt cct gat cgg aaa cct ggc ttt gac 259
Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg Lys Pro Gly Phe Asp
                        40 45 50

gat gtc cca cat ttc ggc gca gct gtt cga gtt ccc ggt cta aaa cac 307
Asp Val Pro His Phe Gly Ala Ala Val Arg Val Pro Gly Leu Lys His
                        55 60 65

ggc acg ttg gtc aat gct gca ccc ttg aaa gtt ttg ggc gca cgg ggc 355
Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val Leu Gly Ala Arg Gly
                        70 75 80 85

gag ccc aac ccc gcg agt tcg tac cgt ttt gaa tac atc acc ggt gat 403
Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu Tyr Ile Thr Gly Asp
                        90 95 100

tcc gca ggt cga gcc atc act gcg acc ggc gct gtc ctc ttt tcc aca 451
Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala Val Leu Phe Ser Thr
                        105 110 115

cgc ccc tgg aca acc ggc ccg cgt ccc gcg atc gcc atg gct cca tcc 499
Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile Ala Met Ala Pro Ser
                        120 125 130

acc caa ggc gtc gca cag cac tgc gat ccc tcc cac acc tgc gcc atc 547
Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser His Thr Cys Ala Ile
                        135 140 145

gga ctc aac gca ttc tat gac aaa ccc ttc gac gca atc att gct tac 595
Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp Ala Ile Ile Ala Tyr
150 155 160 165

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gaa ctc ccc gtc atc ctc tgg ttt cta gct cac gga ctt gac gtt gtg Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His Gly Leu Asp Val Val 170 175 180	643
ttc atc gat tac ccc cgc gac ccc gca acc ggc gtc caa tac tat tgc Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly Val Gln Tyr Tyr Cys 185 190 195	691
gat tcc atc gct gca gct aaa tcg ctt ctc gac gcc gtc ctc gcc tcc Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp Ala Val Leu Ala Ser 200 205 210	739
aga caa ctc ggc ctt tca ccg gaa gca ccg ctt ggc ctg tgg gga ttc Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu Gly Leu Trp Gly Phe 215 220 225	787
tcc caa gga ggc ggc gcc act ggc tgg gct gca caa ttg cag gat tac Ser Gln Gly Gly Gly Ala Thr Gly Trp Ala Ala Gln Leu Gln Asp Tyr 230 235 240 245	835
gca cct gat gtc cgc cca aag gca gcg gtc gtg ggc gct cca cca gtg Ala Pro Asp Val Arg Pro Lys Ala Ala Val Val Gly Ala Pro Pro Val 250 255 260	883
gat ctc ttc cgc gtc ttg gac act gtc gac ggc gga ttg ctc acc gga Asp Leu Phe Arg Val Leu Asp Thr Val Asp Gly Gly Leu Leu Thr Gly 265 270 275	931
gtg att gcc tac gcc atc gcg gga ctt gca gtg aac tct tca gag atg Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser Ser Glu Met 280 285 290	979
ttt gag gaa atc atg tcg gtg tta aat gaa cgc gga gtc agt gat gtg Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val Ser Asp Val 295 300 305	1027
ctg aaa aat atc acc agc tgc gcg gga ggt tcc ttg ttg gcc agt ggc Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu Ala Ser Gly 310 315 320 325	1075
tac tcg tct tcc cgc ggg tgg aca cat cag ggc acg ccg ctg gca gac Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro Leu Ala Asp 330 335 340	1123
att ctg gac gat ctg cca ctt gtt gtc gct gag ttt ggg aag caa aag Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly Lys Gln Lys 345 350 355	1171
ctg ggt cgt gtg gcg cca gaa atc cca gtg ctg ttg tgg ggc tct aaa Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp Gly Ser Lys 360 365 370	1219
aat gat gat gtc att ccc att gat ccc att agg gaa ttg cgt gat agc Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu Arg Asp Ser 375 380 385	1267
tgg gcg gac aag ggt acg cca ttg acc tgg cat gaa tcc caa gcg ccg Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser Gln Ala Pro 390 395 400 405	1315
cgt gtg cca gga cgc aca ggt ctc aac cat ttc ggg ccc tat ttt aga	1363

Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro Tyr Phe Arg
 410 415 420

aac ctg gaa aag tac tcg gga tgg ctc ata gat cat ctt gtc 1405
 Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu Val
 425 430 435

tgagtgccgt tttaaaggct cgg 1428

<210> 238

<211> 435

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Met Gly Tyr Thr Asn Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser
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Cys Asp Ala Trp Trp Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser
 20 25 30

Glu Ala Val Phe Arg Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg
 35 40 45

Lys Pro Gly Phe Asp Asp Val Pro His Phe Gly Ala Ala Val Arg Val
 50 55 60

Pro Gly Leu Lys His Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val
 65 70 75 80

Leu Gly Ala Arg Gly Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu
 85 90 95

Tyr Ile Thr Gly Asp Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala
 100 105 110

Val Leu Phe Ser Thr Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile
 115 120 125

Ala Met Ala Pro Ser Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser
 130 135 140

His Thr Cys Ala Ile Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp
 145 150 155 160

Ala Ile Ile Ala Tyr Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His
 165 170 175

Gly Leu Asp Val Val Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly
 180 185 190

Val Gln Tyr Tyr Cys Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp
 195 200 205

Ala Val Leu Ala Ser Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu
 210 215 220

Gly Leu Trp Gly Phe Ser Gln Gly Gly Gly Ala Thr Gly Trp Ala Ala
 225 230 235 240

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<210> 239
<211> 690
<212> DNA
<213> Corynebacterium glutamicum
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<400> 239
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                                     Met Thr Thr Glu Val
                                     1                               5
gaa ctg gtt gtt tta gct gat tcc gag ggc aat cct att ggt act gcg 163
Glu Leu Val Val Leu Ala Asp Ser Glu Gly Asn Pro Ile Gly Thr Ala
                10                15                20

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ccg aaa gct acg gtg cac act aag gac acg cct ctg cat ttc gcg ttt 211
 Pro Lys Ala Thr Val His Thr Lys Asp Thr Pro Leu His Phe Ala Phe
 25 30 35

tcc acc tat att ttg aac ccg cgt ggg gag ctg ttg gtg acg cgt cgt 259
 Ser Thr Tyr Ile Leu Asn Pro Arg Gly Glu Leu Leu Val Thr Arg Arg
 40 45 50

gca ttg tcg aag aag aca tgg cct ggt gtg tgg acg aac tct atg tgt 307
 Ala Leu Ser Lys Lys Thr Trp Pro Gly Val Trp Thr Asn Ser Met Cys
 55 60 65

ggg cac cct ggt ccg gat gag aca aac gcg gat gcg att cgt cgc agg 355
 Gly His Pro Gly Pro Asp Glu Thr Asn Ala Asp Ala Ile Arg Arg Arg
 70 75 80 85

ggt gtc gat gag ttg ggg ctg gag gta gat tct ttc ttg gat att caa 403
 Gly Val Asp Glu Leu Gly Leu Glu Val Asp Ser Phe Leu Asp Ile Gln
 90 95 100

gag att ctg cct gat tac cag tac cgt gct gtc gac gcg tcc ggc att 451
 Glu Ile Leu Pro Asp Tyr Gln Tyr Arg Ala Val Asp Ala Ser Gly Ile
 105 110 115

gtg gag tgg gag ttg tgc ccg gtc cac ctc gtg cgt tta gcg gtg ggg 499
 Val Glu Trp Glu Leu Cys Pro Val His Leu Val Arg Leu Ala Val Gly
 120 125 130

gaa ttt gtg gag cca ctg gat gat gag gtg gag gag ttc gag tgg gcg 547
 Glu Phe Val Glu Pro Leu Asp Asp Glu Val Glu Glu Phe Glu Trp Ala
 135 140 145

gaa ccg cag aag ctt ttc gac gct gtt gat gcc aca cca ttt gtg ttt 595
 Glu Pro Gln Lys Leu Phe Asp Ala Val Asp Ala Thr Pro Phe Val Phe
 150 155 160 165

tct cca tgg cta gtg gat cag ctt agc gcc cct gag ctg cgc caa gcc 643
 Ser Pro Trp Leu Val Asp Gln Leu Ser Ala Pro Glu Leu Arg Gln Ala
 170 175 180

atc ctg gaa gcg ttt gac gca gag taactaacta gtctagaagc ctt 690
 Ile Leu Glu Ala Phe Asp Ala Glu
 185

<210> 240

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Met Thr Thr Glu Val Glu Leu Val Val Leu Ala Asp Ser Glu Gly Asn
 1 5 10 15

Pro Ile Gly Thr Ala Pro Lys Ala Thr Val His Thr Lys Asp Thr Pro
 20 25 30

Leu His Phe Ala Phe Ser Thr Tyr Ile Leu Asn Pro Arg Gly Glu Leu
 35 40 45

Leu Val Thr Arg Arg Ala Leu Ser Lys Lys Thr Trp Pro Gly Val Trp

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<210> 241
<211> 1308
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(1285)  
<223> RXA01292
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378

Cys 70	Gly	Thr	Ser	Ile	Asp 75	Asp	His	Leu	Asp	Leu 80	Val	Pro	Leu	Glu	Pro 85	
gcc	tac	cgc	gtc	atc	gac	gac	cac	ggc	gaa	ttc	atc	gac	gtc	acc	tcc	403
Ala	Tyr	Arg	Val	Ile	Asp	Asp	His	Gly	Glu	Phe	Ile	Asp	Val	Thr	Ser	
				90					95					100		
gac	atc	gat	gcg	atg	gcc	gag	ctt	ttc	gaa	tcc	cgc	gaa	ccc	ggc	gcc	451
Asp	Ile	Asp	Ala	Met	Ala	Glu	Leu	Phe	Glu	Ser	Arg	Glu	Pro	Gly	Ala	
			105					110					115			
ggc	gcc	aaa	ctg	cgc	acc	tat	atc	gac	tcc	gcc	aca	cag	gtc	tac	aac	499
Gly	Ala	Lys	Leu	Arg	Thr	Tyr	Ile	Asp	Ser	Ala	Thr	Gln	Val	Tyr	Asn	
		120					125					130				
ctg	gcc	atc	gac	ggc	ttc	ctc	tac	acc	aac	ttc	acc	aac	ttc	atc	cca	547
Leu	Ala	Ile	Asp	Gly	Phe	Leu	Tyr	Thr	Asn	Phe	Thr	Asn	Phe	Ile	Pro	
	135					140					145					
tac	tta	agc	ccc	ggc	atg	ctg	cgc	ctt	tta	ccc	aaa	ctt	cta	gca	agc	595
Tyr	Leu	Ser	Pro	Gly	Met	Leu	Arg	Leu	Leu	Pro	Lys	Leu	Leu	Ala	Ser	
150					155					160					165	
ctg	tcg	acc	tcg	cta	aaa	gtc	aag	gtc	aac	acc	caa	ttc	cgc	gat	aca	643
Leu	Ser	Thr	Ser	Leu	Lys	Val	Lys	Val	Asn	Thr	Gln	Phe	Arg	Asp	Thr	
				170					175					180		
aaa	ctg	cgc	caa	atc	tta	agc	tac	ccc	gca	gtt	ttc	ctc	tcc	tca	gac	691
Lys	Leu	Arg	Gln	Ile	Leu	Ser	Tyr	Pro	Ala	Val	Phe	Leu	Ser	Ser	Asp	
			185					190					195			
cct	tcg	cac	acc	ccg	gcg	ctc	tat	cac	ctc	atg	agc	cac	acc	gac	ctc	739
Pro	Ser	His	Thr	Pro	Ala	Leu	Tyr	His	Leu	Met	Ser	His	Thr	Asp	Leu	
			200				205					210				
gtc	caa	ggc	gtc	tcc	tat	ccc	cga	ggc	ggc	ttc	acc	gcc	ttc	atc	aag	787
Val	Gln	Gly	Val	Ser	Tyr	Pro	Arg	Gly	Gly	Phe	Thr	Ala	Phe	Ile	Lys	
	215					220					225					
gca	cta	att	tcg	ctt	atc	gac	gac	gcc	gtc	ctc	cac	ctc	ggc	acc	ccc	835
Ala	Leu	Ile	Ser	Leu	Ile	Asp	Asp	Ala	Val	Leu	His	Leu	Gly	Thr	Pro	
230					235					240					245	
gtc	agc	gca	atc	acc	acc	caa	ggc	cga	aac	gcc	aca	ggc	gtc	caa	gtc	883
Val	Ser	Ala	Ile	Thr	Thr	Gln	Gly	Arg	Asn	Ala	Thr	Gly	Val	Gln	Val	
				250					255					260		
ggc	tca	gag	ttc	atc	gaa	gcc	gat	atc	gtg	atc	agc	tgc	gct	gat	cag	931
Gly	Ser	Glu	Phe	Ile	Glu	Ala	Asp	Ile	Val	Ile	Ser	Cys	Ala	Asp	Gln	
			265					270					275			
cac	cac	acc	gaa	acc	caa	ctc	cta	cct	gct	tcg	ttg	tgc	gcg	aag	ccg	979
His	His	Thr	Glu	Thr	Gln	Leu	Leu	Pro	Ala	Ser	Leu	Cys	Ala	Lys	Pro	
			280				285					290				
gag	acg	agc	tgg	aag	aac	aaa	caa	ccc	ggc	ctc	agt	act	gtg	ctg	gtt	1027
Glu	Thr	Ser	Trp	Lys	Asn	Lys	Gln	Pro	Gly	Leu	Ser	Thr	Val	Leu	Val	
	295					300					305					
ttg	gca	ggc	gtg	aag	ggg	gag	cac	acc	ctg	ctt	ttt	cct	ccg	act	ggg	1075
Leu	Ala	Gly	Val	Lys	Gly	Glu	His	Thr	Leu	Leu	Phe	Pro	Pro	Thr	Gly	

310 315 320 325

acg aag att tcc gca aag ttt tcg acg gct cca ccc cag aat tcc cgg 1123
 Thr Lys Ile Ser Ala Lys Phe Ser Thr Ala Pro Pro Gln Asn Ser Arg
 330 335 340

ctt cag aat cca tct aga tct cca aga oct ccg caa cag att ccg atg 1171
 Leu Gln Asn Pro Ser Arg Ser Pro Arg Pro Pro Gln Gln Ile Pro Met
 345 350 355

ccg cac ccg aag gcc acg aga acc tct tca tcc tgg tcc cag tac ccg 1219
 Pro His Pro Lys Ala Thr Arg Thr Ser Ser Ser Trp Ser Gln Tyr Pro
 360 365 370

ccg atg tct cca ttg gtc acg ggt ccg ctt acg gag aag aat ctg aca 1267
 Pro Met Ser Pro Leu Val Thr Gly Pro Leu Thr Glu Lys Asn Leu Thr
 375 380 385

tgg tgg gcc gga tcg caa tagcagcagt ggctcaaatt ggg 1308
 Trp Trp Ala Gly Ser Gln
 390 395

<210> 242

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met Thr Lys Ala Val Val Ile Gly Gly Gly Leu Ala Gly Leu Ala Thr
 1 5 10 15

Thr Ala Leu Leu Leu Arg Glu Gly Tyr Glu Val His Leu Val Glu Gln
 20 25 30

Asn Glu His Leu Gly Gly Arg Ala Gly Thr Phe Glu Leu Asp Gly Phe
 35 40 45

Arg Trp Asp Thr Gly Pro Ser Trp Tyr Leu Met Pro Asp Ala Met Ser
 50 55 60

His Phe Phe Lys Leu Cys Gly Thr Ser Ile Asp Asp His Leu Asp Leu
 65 70 75 80

Val Pro Leu Glu Pro Ala Tyr Arg Val Ile Asp Asp His Gly Glu Phe
 85 90 95

Ile Asp Val Thr Ser Asp Ile Asp Ala Met Ala Glu Leu Phe Glu Ser
 100 105 110

Arg Glu Pro Gly Ala Gly Ala Lys Leu Arg Thr Tyr Ile Asp Ser Ala
 115 120 125

Thr Gln Val Tyr Asn Leu Ala Ile Asp Gly Phe Leu Tyr Thr Asn Phe
 130 135 140

Thr Asn Phe Ile Pro Tyr Leu Ser Pro Gly Met Leu Arg Leu Leu Pro
 145 150 155 160

Lys Leu Leu Ala Ser Leu Ser Thr Ser Leu Lys Val Lys Val Asn Thr
 165 170 175

Gln Phe Arg Asp Thr Lys Leu Arg Gln Ile Leu Ser Tyr Pro Ala Val
 180 185 190
 Phe Leu Ser Ser Asp Pro Ser His Thr Pro Ala Leu Tyr His Leu Met
 195 200 205
 Ser His Thr Asp Leu Val Gln Gly Val Ser Tyr Pro Arg Gly Gly Phe
 210 215 220
 Thr Ala Phe Ile Lys Ala Leu Ile Ser Leu Ile Asp Asp Ala Val Leu
 225 230 235 240
 His Leu Gly Thr Pro Val Ser Ala Ile Thr Thr Gln Gly Arg Asn Ala
 245 250 255
 Thr Gly Val Gln Val Gly Ser Glu Phe Ile Glu Ala Asp Ile Val Ile
 260 265 270
 Ser Cys Ala Asp Gln His His Thr Glu Thr Gln Leu Leu Pro Ala Ser
 275 280 285
 Leu Cys Ala Lys Pro Glu Thr Ser Trp Lys Asn Lys Gln Pro Gly Leu
 290 295 300
 Ser Thr Val Leu Val Leu Ala Gly Val Lys Gly Glu His Thr Leu Leu
 305 310 315 320
 Phe Pro Pro Thr Gly Thr Lys Ile Ser Ala Lys Phe Ser Thr Ala Pro
 325 330 335
 Pro Gln Asn Ser Arg Leu Gln Asn Pro Ser Arg Ser Pro Arg Pro Pro
 340 345 350
 Gln Gln Ile Pro Met Pro His Pro Lys Ala Thr Arg Thr Ser Ser Ser
 355 360 365
 Trp Ser Gln Tyr Pro Pro Met Ser Pro Leu Val Thr Gly Pro Leu Thr
 370 375 380
 Glu Lys Asn Leu Thr Trp Trp Ala Gly Ser Gln
 385 390 395

<210> 243
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(427)
 <223> RXA01293

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 ctccattggt caccgggtccg cttacggaga agaattctgac atg gtg ggc cgg atc 115
 Met Val Gly Arg Ile
 1 5

gca ata gca gca gtg gct caa att ggg cga tgg gct ggc att gat ggt 163
 Ala Ile Ala Ala Val Ala Gln Ile Gly Arg Trp Ala Gly Ile Asp Gly
 10 15 20

ttg gaa agc cgc att gtt gtg cag cgc acc atc ggc cct gcc gac ttc 211
 Leu Glu Ser Arg Ile Val Val Gln Arg Thr Ile Gly Pro Ala Asp Phe
 25 30 35

gca gac cga tac aac tcc tgg agc ggc ggg tcc att ggc ccc tca cac 259
 Ala Asp Arg Tyr Asn Ser Trp Ser Gly Gly Ser Ile Gly Pro Ser His
 40 45 50

acc ctg gca caa tcg gcg ttc ttt agg ggt tct aac aaa tcc cgc aaa 307
 Thr Leu Ala Gln Ser Ala Phe Phe Arg Gly Ser Asn Lys Ser Arg Lys
 55 60 65

gta gat ggc ctg tat gac gca ggt gac acc aca gtt cca ggg gtg ggc 355
 Val Asp Gly Leu Tyr Asp Ala Gly Asp Thr Thr Val Pro Gly Val Gly
 70 75 80 85

gta tct atg tgt ttg atc tct gca gaa aac gtg ctc aag cgt ctc cgc 403
 Val Ser Met Cys Leu Ile Ser Ala Glu Asn Val Leu Lys Arg Leu Arg
 90 95 100

ggg gac aac agt gtg gat cgg act taacgggact tttttctttt gct 450
 Gly Asp Asn Ser Val Asp Arg Thr
 105

<210> 244

<211> 109

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Met Val Gly Arg Ile Ala Ile Ala Ala Val Ala Gln Ile Gly Arg Trp
 1 5 10 15

Ala Gly Ile Asp Gly Leu Glu Ser Arg Ile Val Val Gln Arg Thr Ile
 20 25 30

Gly Pro Ala Asp Phe Ala Asp Arg Tyr Asn Ser Trp Ser Gly Gly Ser
 35 40 45

Ile Gly Pro Ser His Thr Leu Ala Gln Ser Ala Phe Phe Arg Gly Ser
 50 55 60

Asn Lys Ser Arg Lys Val Asp Gly Leu Tyr Asp Ala Gly Asp Thr Thr
 65 70 75 80

Val Pro Gly Val Gly Val Ser Met Cys Leu Ile Ser Ala Glu Asn Val
 85 90 95

Leu Lys Arg Leu Arg Gly Asp Asn Ser Val Asp Arg Thr
 100 105

<210> 245

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1363)

<223> RXA02310

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                               Val Ser Thr Thr Phe
                               1           5

gat gtg ttg atc atc ggc gcg ggc ccc tca ggt gcc agc gcc gcc gtc 163
Asp Val Leu Ile Ile Gly Ala Gly Pro Ser Gly Ala Ser Ala Ala Val
                10                15                20

cat gcg gcc agg act ggg ctt caa aca ttg ctt atc gac gcc tcc tcc 211
His Ala Ala Arg Thr Gly Leu Gln Thr Leu Leu Ile Asp Ala Ser Ser
                25                30                35

ttc ccg cgg gat aaa acg tgt ggc gat ggc ctt act ccc cgt gcg att 259
Phe Pro Arg Asp Lys Thr Cys Gly Asp Gly Leu Thr Pro Arg Ala Ile
                40                45                50

cac cag cta gaa ctt cta ggt gtt gct gat cag gtt acc ggg gat tat 307
His Gln Leu Glu Leu Leu Gly Val Ala Asp Gln Val Thr Gly Asp Tyr
                55                60                65

ttc aac aag ggc ttg aaa ctg cat ggt ttt ggt ggc tct gtt gag gcg 355
Phe Asn Lys Gly Leu Lys Leu His Gly Phe Gly Gly Ser Val Glu Ala
                70                75                80                85

ccg tgg ccg gag aca tat ttc acg aat aag ggt tcc gcg atg tcg ccg 403
Pro Trp Pro Glu Thr Tyr Phe Thr Asn Lys Gly Ser Ala Met Ser Arg
                90                95                100

atg gag ttc gat gat ttg tta ttc cgc ttg gca aaa tct cat gag gaa 451
Met Glu Phe Asp Asp Leu Leu Phe Arg Leu Ala Lys Ser His Glu Glu
                105                110                115

gta acc acg tgg gag aac gcg agc gcc caa gac ccc att ttg agg ggg 499
Val Thr Thr Trp Glu Asn Ala Ser Ala Gln Asp Pro Ile Leu Arg Gly
                120                125                130

aat ttc ttg gaa ggc gtt gtg att aat cac gca ggg caa gag aaa acc 547
Asn Phe Leu Glu Gly Val Val Ile Asn His Ala Gly Gln Glu Lys Thr
                135                140                145

gtc aag gcg aag cat gtg att att gcc gat ggt gtc cgc tcc cct ttc 595
Val Lys Ala Lys His Val Ile Ile Ala Asp Gly Val Arg Ser Pro Phe
                150                155                160                165

ggg aag aaa ctg ggt agg cag tgg caa cgc gat gag gtg tat ggc att 643
Gly Lys Lys Leu Gly Arg Gln Trp Gln Arg Asp Glu Val Tyr Gly Ile
                170                175                180

gcg gct cgt gct tat tgt gaa act ccg ctg tct gat gaa ccg tgg att 691
Ala Ala Arg Ala Tyr Cys Glu Thr Pro Leu Ser Asp Glu Pro Trp Ile
                185                190                195

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cac tcc cat gtg gaa ctg cgc gat gaa gat ggt gtg gtg cag cca gga	739
His Ser His Val Glu Leu Arg Asp Glu Asp Gly Val Val Gln Pro Gly	
200 205 210	
tat ggg tgg att ttc ccg ctg ggc aac ggc acg gtg aat ttg ggt tgt	787
Tyr Gly Trp Ile Phe Pro Leu Gly Asn Gly Thr Val Asn Leu Gly Cys	
215 220 225	
ggc gcg ctc tcg acg gat acg aga cca gcg aag atc aat acg aag aaa	835
Gly Ala Leu Ser Thr Asp Thr Arg Pro Ala Lys Ile Asn Thr Lys Lys	
230 235 240 245	
ttg ttg agc ttc tat gcg ggt cag cgt cgt aaa gca tgg caa ctc ggg	883
Leu Leu Ser Phe Tyr Ala Gly Gln Arg Arg Lys Ala Trp Gln Leu Gly	
250 255 260	
ccc gag cac gac gtc gcc tct gcc ctg ctg cct atg ggc ggc gcg gtg	931
Pro Glu His Asp Val Ala Ser Ala Leu Leu Pro Met Gly Gly Ala Val	
265 270 275	
tcg aat gtg gct ggc gcg aac tgg atg ctg atc ggc gat tcc gcc gcg	979
Ser Asn Val Ala Gly Ala Asn Trp Met Leu Ile Gly Asp Ser Ala Ala	
280 285 290	
tgt gtg aac ccg ctg aac ggc gaa ggc atc gac tat ggc ctg gaa acc	1027
Cys Val Asn Pro Leu Asn Gly Glu Gly Ile Asp Tyr Gly Leu Glu Thr	
295 300 305	
gcg gcg atg gcc gtc gac acg ctt gtg gaa aac ccc aag cgc gat ttg	1075
Ala Ala Met Ala Val Asp Thr Leu Val Glu Asn Pro Lys Arg Asp Leu	
310 315 320 325	
acc ttg gta tgg cca cat agg ttg cgc gac gcg tac ggc gag acc ttc	1123
Thr Leu Val Trp Pro His Arg Leu Arg Asp Ala Tyr Gly Glu Thr Phe	
330 335 340	
atg ttg gcg cgc acg gct gct cga ctg ctg acg tac ccg cag ttt ttg	1171
Met Leu Ala Arg Thr Ala Ala Arg Leu Leu Thr Tyr Pro Gln Phe Leu	
345 350 355	
ccg atg gct ggg ccg ctc gca ttc cgc ggg ccg ctg caa aag gcc atc	1219
Pro Met Ala Gly Pro Leu Ala Phe Arg Gly Pro Leu Gln Lys Ala Ile	
360 365 370	
atg ccg gcg gct gcg cgt ttg atg ggc aac ctg atc aca gag gag gat	1267
Met Pro Ala Ala Ala Arg Leu Met Gly Asn Leu Ile Thr Glu Glu Asp	
375 380 385	
aaa gac ctg ctc gcc agg ggt tgg cag gcc gcc gga tcc gcg att agt	1315
Lys Asp Leu Leu Ala Arg Gly Trp Gln Ala Ala Gly Ser Ala Ile Ser	
390 395 400 405	
tgg gcg cgg aag ggc tcc cct ctg tgg gac tcg act agt tct ctg gtt	1363
Trp Ala Arg Lys Gly Ser Pro Leu Trp Asp Ser Thr Ser Ser Leu Val	
410 415 420	
taatcgccga gtgcagcgcg acg	1386

<210> 246

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

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 Ala Ser Ala Ala Val His Ala Ala Arg Thr Gly Leu Gln Thr Leu Leu
 20 25 30
 Ile Asp Ala Ser Ser Phe Pro Arg Asp Lys Thr Cys Gly Asp Gly Leu
 35 40 45
 Thr Pro Arg Ala Ile His Gln Leu Glu Leu Leu Gly Val Ala Asp Gln
 50 55 60
 Val Thr Gly Asp Tyr Phe Asn Lys Gly Leu Lys Leu His Gly Phe Gly
 65 70 75 80
 Gly Ser Val Glu Ala Pro Trp Pro Glu Thr Tyr Phe Thr Asn Lys Gly
 85 90 95
 Ser Ala Met Ser Arg Met Glu Phe Asp Asp Leu Leu Phe Arg Leu Ala
 100 105 110
 Lys Ser His Glu Glu Val Thr Thr Trp Glu Asn Ala Ser Ala Gln Asp
 115 120 125
 Pro Ile Leu Arg Gly Asn Phe Leu Glu Gly Val Val Ile Asn His Ala
 130 135 140
 Gly Gln Glu Lys Thr Val Lys Ala Lys His Val Ile Ile Ala Asp Gly
 145 150 155 160
 Val Arg Ser Pro Phe Gly Lys Lys Leu Gly Arg Gln Trp Gln Arg Asp
 165 170 175
 Glu Val Tyr Gly Ile Ala Ala Arg Ala Tyr Cys Glu Thr Pro Leu Ser
 180 185 190
 Asp Glu Pro Trp Ile His Ser His Val Glu Leu Arg Asp Glu Asp Gly
 195 200 205
 Val Val Gln Pro Gly Tyr Gly Trp Ile Phe Pro Leu Gly Asn Gly Thr
 210 215 220
 Val Asn Leu Gly Cys Gly Ala Leu Ser Thr Asp Thr Arg Pro Ala Lys
 225 230 235 240
 Ile Asn Thr Lys Lys Leu Leu Ser Phe Tyr Ala Gly Gln Arg Arg Lys
 245 250 255
 Ala Trp Gln Leu Gly Pro Glu His Asp Val Ala Ser Ala Leu Leu Pro
 260 265 270
 Met Gly Gly Ala Val Ser Asn Val Ala Gly Ala Asn Trp Met Leu Ile
 275 280 285
 Gly Asp Ser Ala Ala Cys Val Asn Pro Leu Asn Gly Glu Gly Ile Asp
 290 295 300

Tyr Gly Leu Glu Thr Ala Ala Met Ala Val Asp Thr Leu Val Glu Asn
 305 310 315 320
 Pro Lys Arg Asp Leu Thr Leu Val Trp Pro His Arg Leu Arg Asp Ala
 325 330 335
 Tyr Gly Glu Thr Phe Met Leu Ala Arg Thr Ala Ala Arg Leu Leu Thr
 340 345 350
 Tyr Pro Gln Phe Leu Pro Met Ala Gly Pro Leu Ala Phe Arg Gly Pro
 355 360 365
 Leu Gln Lys Ala Ile Met Pro Ala Ala Ala Arg Leu Met Gly Asn Leu
 370 375 380
 Ile Thr Glu Glu Asp Lys Asp Leu Leu Ala Arg Gly Trp Gln Ala Ala
 385 390 395 400
 Gly Ser Ala Ile Ser Trp Ala Arg Lys Gly Ser Pro Leu Trp Asp Ser
 405 410 415
 Thr Ser Ser Leu Val
 420

<210> 247
 <211> 1170
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1147)
 <223> RXA02718

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 cgatgcccat gaccttgacc tcgacaaatt tccggagggtc gtg cga gat cgt ttg 115
 Val Arg Asp Arg Leu
 1 5
 acg cag ttc ctc gat gct caa gag cta aca att gct gat atc ggc gct 163
 Thr Gln Phe Leu Asp Ala Gln Glu Leu Thr Ile Ala Asp Ile Gly Ala
 10 15 20
 cct gtc aca gat gct gtg gcc cat ctt cgc agt ttc gtg ctc aat gga 211
 Pro Val Thr Asp Ala Val Ala His Leu Arg Ser Phe Val Leu Asn Gly
 25 30 35
 gga aag cga atc cgt cct ctt tat gcg tgg gct ggt ttc ctg gcg gcg 259
 Gly Lys Arg Ile Arg Pro Leu Tyr Ala Trp Ala Gly Phe Leu Ala Ala
 40 45 50
 caa ggc cat aag aat tct tct gaa aaa ctt gag tcc gtc ctt gac gcc 307
 Gln Gly His Lys Asn Ser Ser Glu Lys Leu Glu Ser Val Leu Asp Ala
 55 60 65
 gca gcg agt ctc gaa ttc atc cag gct tgt gcc ttg att cat gac gat 355
 Ala Ala Ser Leu Glu Phe Ile Gln Ala Cys Ala Leu Ile His Asp Asp
 70 75 80 85

att atc gat tct tct gat acc cgg cgc gga gcc ccc aca gtt cac cgg Ile Ile Asp Ser Ser Asp Thr Arg Arg Gly Ala Pro Thr Val His Arg	403
90 95 100	
gct gtg gaa gct gat cac cgc gcc aat aat ttc gaa ggc gat ccc gag Ala Val Glu Ala Asp His Arg Ala Asn Asn Phe Glu Gly Asp Pro Glu	451
105 110 115	
cac ttt ggc gtt tca gtc tcg att ttg gct ggc gat atg gca ttg gtg His Phe Gly Val Ser Val Ser Ile Leu Ala Gly Asp Met Ala Leu Val	499
120 125 130	
tgg gca gaa gac atg ctg cag gat tcc ggt ttg agt gca gag gca ttg Trp Ala Glu Asp Met Leu Gln Asp Ser Gly Leu Ser Ala Glu Ala Leu	547
135 140 145	
gcc cgc acg agg gat gct tgg cgt ggc atg cgt act gag gtt att ggc Ala Arg Thr Arg Asp Ala Trp Arg Gly Met Arg Thr Glu Val Ile Gly	595
150 155 160 165	
ggc cag ctg ctt gat att tat cta gag tcg cac gcc aac gag tcg gtg Gly Gln Leu Leu Asp Ile Tyr Leu Glu Ser His Ala Asn Glu Ser Val	643
170 175 180	
gag ctt gcg gat tct gtc aac cgc ttc aaa acg gcc gct tac acg att Glu Leu Ala Asp Ser Val Asn Arg Phe Lys Thr Ala Ala Tyr Thr Ile	691
185 190 195	
gcg cgc cca ttg cac ctg ggc gcc tcc att gct ggc ggt tcg ccg cag Ala Arg Pro Leu His Leu Gly Ala Ser Ile Ala Gly Gly Ser Pro Gln	739
200 205 210	
ctt atc gac gcg ctc ctc cac tac ggc cac gac atc ggc att gca ttc Leu Ile Asp Ala Leu Leu His Tyr Gly His Asp Ile Gly Ile Ala Phe	787
215 220 225	
cag ttg agg gat gat ctg ctt ggt gtg ttt ggg gat ccc gct atc acc Gln Leu Arg Asp Asp Leu Leu Gly Val Phe Gly Asp Pro Ala Ile Thr	835
230 235 240 245	
ggc aaa cca gct gga gac gat atc cgt gaa ggc aag cgc act gtt ctt Gly Lys Pro Ala Gly Asp Asp Ile Arg Glu Gly Lys Arg Thr Val Leu	883
250 255 260	
ctt gcg ctc gct cta caa cgc gct gat aag caa tct cct gaa gct gca Leu Ala Leu Ala Leu Gln Arg Ala Asp Lys Gln Ser Pro Glu Ala Ala	931
265 270 275	
acg gcc att cgc gca ggt gtt gga aag gtg act tca cca gaa gat att Thr Ala Ile Arg Ala Gly Val Gly Lys Val Thr Ser Pro Glu Asp Ile	979
280 285 290	
gct gtc att aca gag cat att cga gct act ggt gct gaa gaa gaa gtt Ala Val Ile Thr Glu His Ile Arg Ala Thr Gly Ala Glu Glu Glu Val	1027
295 300 305	
gag cag cga att tcc cag ctg act gaa tcc ggt ttg gct cac ctc gat Glu Gln Arg Ile Ser Gln Leu Thr Glu Ser Gly Leu Ala His Leu Asp	1075
310 315 320 325	

gat gta gac atc ccc gat gag gtg cgc gca cag ttg cgg gca ctg gct 1123
 Asp Val Asp Ile Pro Asp Glu Val Arg Ala Gln Leu Arg Ala Leu Ala
 330 335 340

atc cgc tca acc gaa cgt cgg atg tagtagacgc gtatgacact ttt 1170
 Ile Arg Ser Thr Glu Arg Arg Met
 345

<210> 248

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Val Arg Asp Arg Leu Thr Gln Phe Leu Asp Ala Gln Glu Leu Thr Ile
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Ala Asp Ile Gly Ala Pro Val Thr Asp Ala Val Ala His Leu Arg Ser
 20 25 30

Phe Val Leu Asn Gly Gly Lys Arg Ile Arg Pro Leu Tyr Ala Trp Ala
 35 40 45

Gly Phe Leu Ala Ala Gln Gly His Lys Asn Ser Ser Glu Lys Leu Glu
 50 55 60

Ser Val Leu Asp Ala Ala Ala Ser Leu Glu Phe Ile Gln Ala Cys Ala
 65 70 75 80

Leu Ile His Asp Asp Ile Ile Asp Ser Ser Asp Thr Arg Arg Gly Ala
 85 90 95

Pro Thr Val His Arg Ala Val Glu Ala Asp His Arg Ala Asn Asn Phe
 100 105 110

Glu Gly Asp Pro Glu His Phe Gly Val Ser Val Ser Ile Leu Ala Gly
 115 120 125

Asp Met Ala Leu Val Trp Ala Glu Asp Met Leu Gln Asp Ser Gly Leu
 130 135 140

Ser Ala Glu Ala Leu Ala Arg Thr Arg Asp Ala Trp Arg Gly Met Arg
 145 150 155 160

Thr Glu Val Ile Gly Gly Gln Leu Leu Asp Ile Tyr Leu Glu Ser His
 165 170 175

Ala Asn Glu Ser Val Glu Leu Ala Asp Ser Val Asn Arg Phe Lys Thr
 180 185 190

Ala Ala Tyr Thr Ile Ala Arg Pro Leu His Leu Gly Ala Ser Ile Ala
 195 200 205

Gly Gly Ser Pro Gln Leu Ile Asp Ala Leu Leu His Tyr Gly His Asp
 210 215 220

Ile Gly Ile Ala Phe Gln Leu Arg Asp Asp Leu Leu Gly Val Phe Gly
 225 230 235 240

Asp Pro Ala Ile Thr Gly Lys Pro Ala Gly Asp Asp Ile Arg Glu Gly

				245					250					255			
Lys	Arg	Thr	Val	Leu	Leu	Ala	Leu	Ala	Leu	Gln	Arg	Ala	Asp	Lys	Gln		
			260					265					270				
Ser	Pro	Glu	Ala	Ala	Thr	Ala	Ile	Arg	Ala	Gly	Val	Gly	Lys	Val	Thr		
		275					280					285					
Ser	Pro	Glu	Asp	Ile	Ala	Val	Ile	Thr	Glu	His	Ile	Arg	Ala	Thr	Gly		
	290					295					300						
Ala	Glu	Glu	Glu	Val	Glu	Gln	Arg	Ile	Ser	Gln	Leu	Thr	Glu	Ser	Gly		
305					310					315					320		
Leu	Ala	His	Leu	Asp	Asp	Val	Asp	Ile	Pro	Asp	Glu	Val	Arg	Ala	Gln		
				325					330					335			
Leu	Arg	Ala	Leu	Ala	Ile	Arg	Ser	Thr	Glu	Arg	Arg	Met					
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<210> 249
<211> 852
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>  
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<222> (101)..(829)  
<223> RXA01067
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<400> 249																		
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aatggcaaac acaaatagtt tgcatggcag aatagcttag						gtg	agt	gaa	ttc	caa					115			
						Val	Ser	Glu	Phe	Gln								
						1					5							
gta	ccc	gaa	atc	cct	gcc	caa	ttc	cta	ccc	aag	cat	att	gcg	ctt	gtc	163		
Val	Pro	Glu	Ile	Pro	Ala	Gln	Phe	Leu	Pro	Lys	His	Ile	Ala	Leu	Val			
				10					15					20				
atg	gat	gga	aat	gga	cgc	tgg	gct	acc	gag	cgt	ggc	atg	aag	cgc	acc	211		
Met	Asp	Gly	Asn	Gly	Arg	Trp	Ala	Thr	Glu	Arg	Gly	Met	Lys	Arg	Thr			
				25					30					35				
gaa	ggc	cat	aag	cgt	ggc	gag	gca	gtc	ctg	ctt	gat	gtt	gtt	gat	gca	259		
Glu	Gly	His	Lys	Arg	Gly	Glu	Ala	Val	Leu	Leu	Asp	Val	Val	Asp	Ala			
			40					45					50					
tgc	att	gaa	ctt	ggt	gtt	ccg	tac	ctt	tct	gct	tat	gcc	ttc	tct	act	307		
Cys	Ile	Glu	Leu	Gly	Val	Pro	Tyr	Leu	Ser	Ala	Tyr	Ala	Phe	Ser	Thr			
			55					60					65					
gaa	aac	tgg	cgt	cgt	tcc	acc	gat	gag	gtc	cgt	ttc	ctc	atg	gga	ttc	355		
Glu	Asn	Trp	Arg	Arg	Ser	Thr	Asp	Glu	Val	Arg	Phe	Leu	Met	Gly	Phe			
		70					75					80					85	
aac	cga	gat	gtg	ctg	cga	cga	caa	cgc	gat	gac	cta	cat	gaa	aag	ggc	403		
Asn	Arg	Asp	Val	Leu	Arg	Arg	Gln	Arg	Asp	Asp	Leu	His	Glu	Lys	Gly			
				90					95					100				

gtt cgt gtg cgt tgg gtt ggc cgt cgt ccc cgc ctg tgg cgt tcg gtt 451
 Val Arg Val Arg Trp Val Gly Arg Arg Pro Arg Leu Trp Arg Ser Val
 105 110 115

atc cgt gag ctg gaa act gcg gaa gag cta acc aaa gac aac acc acc 499
 Ile Arg Glu Leu Glu Thr Ala Glu Glu Leu Thr Lys Asp Asn Thr Thr
 120 125 130

atg acc ttg gcc atg tgt gtg aac tat ggt gga cgc gcc gaa atc atc 547
 Met Thr Leu Ala Met Cys Val Asn Tyr Gly Gly Arg Ala Glu Ile Ile
 135 140 145

gac gca gcc cgc gac atc gcc cgc ctt gca gct gaa ggc aaa ctg cgc 595
 Asp Ala Ala Arg Asp Ile Ala Arg Leu Ala Ala Glu Gly Lys Leu Arg
 150 155 160 165

ccg gaa caa atc act gag aag acc ttc ccg aac ttc ctc gac gaa cct 643
 Pro Glu Gln Ile Thr Glu Lys Thr Phe Pro Asn Phe Leu Asp Glu Pro
 170 175 180

gac atg cca gac gtc gac ctg ttc ctg cgc cca tcc ggt gag aag cgc 691
 Asp Met Pro Asp Val Asp Leu Phe Leu Arg Pro Ser Gly Glu Lys Arg
 185 190 195

acg tca aac ttc ctg ctg tgg cag tct gcc tac gcg gaa atg gtc tac 739
 Thr Ser Asn Phe Leu Leu Trp Gln Ser Ala Tyr Ala Glu Met Val Tyr
 200 205 210

caa gac aag ctg ttc cct gat ttc acg cag caa gat ctg tac gac gcg 787
 Gln Asp Lys Leu Phe Pro Asp Phe Thr Gln Gln Asp Leu Tyr Asp Ala
 215 220 225

gtc ctg gaa tac gcc aag cgg gat cgc aga ttc gga agc gca 829
 Val Leu Glu Tyr Ala Lys Arg Asp Arg Arg Phe Gly Ser Ala
 230 235 240

taatgcccac caaccagccg acg 852

<210> 250

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Val Ser Glu Phe Gln Val Pro Glu Ile Pro Ala Gln Phe Leu Pro Lys
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His Ile Ala Leu Val Met Asp Gly Asn Gly Arg Trp Ala Thr Glu Arg
 20 25 30

Gly Met Lys Arg Thr Glu Gly His Lys Arg Gly Glu Ala Val Leu Leu
 35 40 45

Asp Val Val Asp Ala Cys Ile Glu Leu Gly Val Pro Tyr Leu Ser Ala
 50 55 60

Tyr Ala Phe Ser Thr Glu Asn Trp Arg Arg Ser Thr Asp Glu Val Arg
 65 70 75 80

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<210> 251
<211> 564
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(541)  
<223> RXA01269
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Val Val Phe Glu Met 5																	
1																	
att aag ttt cga acc atg ctt gaa cca gat gaa aaa cat gta act gat 163																	
Ile Lys Phe Arg Thr Met Leu Glu Pro Asp Glu Lys His Val Thr Asp 20																	
10 15																	
gaa cag cgt cta act aaa gtt gga aag ctt ctg cgg gaa acg agt tta 211																	
Glu Gln Arg Leu Thr Lys Val Gly Lys Leu Leu Arg Glu Thr Ser Leu 35																	
25 30																	
gat gag tta cct aca ctc tgg aat gta ttt aaa ggt gat atg agc ctt 259																	
Asp Glu Leu Pro Thr Leu Trp Asn Val Phe Lys Gly Asp Met Ser Leu																	

40	45	50	
gta ggg cct cga cct ttg ctt gtt agc tat ctg gaa cat tac tct tct			307
Val Gly Pro Arg Pro Leu Leu Val Ser Tyr Leu Glu His Tyr Ser Ser			
55	60	65	
gaa caa gct cga cgc cat gaa gtt cgt cct ggg att act ggt ttg gct			355
Glu Gln Ala Arg Arg His Glu Val Arg Pro Gly Ile Thr Gly Leu Ala			
70	75	80	85
cag gtg aat ggc cgt aat caa act act tgg gat gaa cga ctt aag ttg			403
Gln Val Asn Gly Arg Asn Gln Thr Thr Trp Asp Glu Arg Leu Lys Leu			
90	95	100	
gat gtc gaa tat gtg gat cgc tgt agt ttg aaa cta gat ttc aaa ata			451
Asp Val Glu Tyr Val Asp Arg Cys Ser Leu Lys Leu Asp Phe Lys Ile			
105	110	115	
tta atc gcc act gta aaa aca gtt ctt tct aaa aag ggc att agt aat			499
Leu Ile Ala Thr Val Lys Thr Val Leu Ser Lys Lys Gly Ile Ser Asn			
120	125	130	
gaa ggt cat gtc acg atg cca tcc ttc att gaa gaa aga aaa			541
Glu Gly His Val Thr Met Pro Ser Phe Ile Glu Glu Arg Lys			
135	140	145	
tagcaggtaa aaattttact ttc			564

<210> 252

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Val Val Phe Glu Met Ile Lys Phe Arg Thr Met Leu Glu Pro Asp Glu	
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Lys His Val Thr Asp Glu Gln Arg Leu Thr Lys Val Gly Lys Leu Leu	
20	30

Arg Glu Thr Ser Leu Asp Glu Leu Pro Thr Leu Trp Asn Val Phe Lys	
35	45

Gly Asp Met Ser Leu Val Gly Pro Arg Pro Leu Leu Val Ser Tyr Leu	
50	60

Glu His Tyr Ser Ser Glu Gln Ala Arg Arg His Glu Val Arg Pro Gly	
65	80

Ile Thr Gly Leu Ala Gln Val Asn Gly Arg Asn Gln Thr Thr Trp Asp	
85	95

Glu Arg Leu Lys Leu Asp Val Glu Tyr Val Asp Arg Cys Ser Leu Lys	
100	110

Leu Asp Phe Lys Ile Leu Ile Ala Thr Val Lys Thr Val Leu Ser Lys	
115	125

Lys Gly Ile Ser Asn Glu Gly His Val Thr Met Pro Ser Phe Ile Glu	
130	140

Glu Arg Lys
145

<210> 253

<211> 554

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(531)

<223> RXA01205

<400> 253

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tgc gcg gga gtt ttg ccc cat aat ttt gaa ccc tcg cga ata ttt atg	96
Cys Ala Gly Val Leu Pro His Asn Phe Glu Pro Ser Arg Ile Phe Met	
20 25 30	
ggc gat tcc ggc tcc atg ctc atc ggc ctg ctg ttg gct gca gca tcg	144
Gly Asp Ser Gly Ser Met Leu Ile Gly Leu Leu Leu Ala Ala Ser	
35 40 45	
acc tca gcg tca gga aaa atc aac atg agc ctg tat ggc gca gct gat	192
Thr Ser Ala Ser Gly Lys Ile Asn Met Ser Leu Tyr Gly Ala Ala Asp	
50 55 60	
ttt atc gca ttg atc tca ccc atc atc gtt gtt ctc gcc gcc gtg gcc	240
Phe Ile Ala Leu Ile Ser Pro Ile Ile Val Val Leu Ala Ala Val Ala	
65 70 75 80	
atc cca ctg ctc gac ctc gtg atg gca gtg gtt agg cgc gtg ggc agg	288
Ile Pro Leu Leu Asp Leu Val Met Ala Val Val Arg Arg Val Gly Arg	
85 90 95	
gga gca tca ccc ttt tcc ccg gac aaa atg cat ctg cac cac cga ctg	336
Gly Ala Ser Pro Phe Ser Pro Asp Lys Met His Leu His His Arg Leu	
100 105 110	
ctg tcc atc gga cac acc cat agg cgc gtg gtc cta gtg ctc tac acc	384
Leu Ser Ile Gly His Thr His Arg Arg Val Val Leu Val Leu Tyr Thr	
115 120 125	
tgg gcg agc gcc gtg gca ttc ggc gca gtg agc ttc tcc gtc gtt ccg	432
Trp Ala Ser Ala Val Ala Phe Gly Ala Val Ser Phe Ser Val Val Pro	
130 135 140	
cca ctg ttt gcc acc gga tcg agc atc tgt ggc atc ctc atc gcc gtc	480
Pro Leu Phe Ala Thr Gly Ser Ser Ile Cys Gly Ile Leu Ile Ala Val	
145 150 155 160	
gct gtc aca gcc gtg cca gtg atg aaa agc cgg cga gcc gcc aaa ctt	528
Ala Val Thr Ala Val Pro Val Met Lys Ser Arg Arg Ala Ala Lys Leu	
165 170 175	
gat taagtgattg tcactttgga ttg	554

Asp

<210> 254
 <211> 177
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 254
 Val Ser Ala Tyr Pro Pro Ala Ile Ile Ala Ala Ala Leu Val Gly Ile
 1 5 10 15
 Cys Ala Gly Val Leu Pro His Asn Phe Glu Pro Ser Arg Ile Phe Met
 20 25 30
 Gly Asp Ser Gly Ser Met Leu Ile Gly Leu Leu Leu Ala Ala Ala Ser
 35 40 45
 Thr Ser Ala Ser Gly Lys Ile Asn Met Ser Leu Tyr Gly Ala Ala Asp
 50 55 60
 Phe Ile Ala Leu Ile Ser Pro Ile Ile Val Val Leu Ala Ala Val Ala
 65 70 75 80
 Ile Pro Leu Leu Asp Leu Val Met Ala Val Val Arg Arg Val Gly Arg
 85 90 95
 Gly Ala Ser Pro Phe Ser Pro Asp Lys Met His Leu His His Arg Leu
 100 105 110
 Leu Ser Ile Gly His Thr His Arg Arg Val Val Leu Val Leu Tyr Thr
 115 120 125
 Trp Ala Ser Ala Val Ala Phe Gly Ala Val Ser Phe Ser Val Val Pro
 130 135 140
 Pro Leu Phe Ala Thr Gly Ser Ser Ile Cys Gly Ile Leu Ile Ala Val
 145 150 155 160
 Ala Val Thr Ala Val Pro Val Met Lys Ser Arg Arg Ala Ala Lys Leu
 165 170 175

Asp

<210> 255
 <211> 882
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(859)
 <223> RXA01576

<400> 255
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 aatggatttc atgacaatca agttatcatc actgggggtcg gtg gca cct aac agg 115

	Val	Ala	Pro	Asn	Arg	
	1				5	
aaa atc agc cat cat gca cta ggc tct att cct atc atg gat gca tca						163
Lys Ile Ser His His Ala Leu Gly Ser Ile Pro Ile Met Asp Ala Ser						
	10			15	20	
aaa aac agc gac ttt aaa gac acc tgg cta gtc gta cct tgt tat aac						211
Lys Asn Ser Asp Phe Lys Asp Thr Trp Leu Val Val Pro Cys Tyr Asn						
	25			30	35	
gag gca aca gtt atc cgg gaa gtt tta gag aac gca ctc aaa aca ttc						259
Glu Ala Thr Val Ile Arg Glu Val Leu Glu Asn Ala Leu Lys Thr Phe						
	40			45	50	
cct aat att gtt gcg gtc aac gat ggc tcc ccg gac aac tcc gcg gaa						307
Pro Asn Ile Val Ala Val Asn Asp Gly Ser Pro Asp Asn Ser Ala Glu						
	55			60	65	
gaa atc cat gcg gcc ggc gca cac ctg gtc aac cac ccc gtg aac ctc						355
Glu Ile His Ala Ala Gly Ala His Leu Val Asn His Pro Val Asn Leu						
	70			75	80	85
gga caa ggt gcc gcg atc caa acc ggc atc gaa tac gcc cgc aag caa						403
Gly Gln Gly Ala Ala Ile Gln Thr Gly Ile Glu Tyr Ala Arg Lys Gln						
	90			95	100	
ccc ggt gca aaa tac ttt gta act ttc gac gcc gac ggc caa cac caa						451
Pro Gly Ala Lys Tyr Phe Val Thr Phe Asp Ala Asp Gly Gln His Gln						
	105			110	115	
gtg aaa gac gtt atc cgc atg gtg gag cga ctg cgt gcc gag gac gtg						499
Val Lys Asp Val Ile Arg Met Val Glu Arg Leu Arg Ala Glu Asp Val						
	120			125	130	
gac att atc gtc ggc acg cgt ttt gga cgc cca cgc caa gcc gat gac						547
Asp Ile Ile Val Gly Thr Arg Phe Gly Arg Pro Arg Gln Ala Asp Asp						
	135			140	145	
cag gtg cca cta atc aag cgc ctt gtg ctg cgc acc gtg gtc ctg ctg						595
Gln Val Pro Leu Ile Lys Arg Leu Val Leu Arg Thr Val Val Leu Leu						
	150			155	160	165
tca ccg aaa acc cgc cga ctt ggg ctc acc gac gcc cac aac ggc ctg						643
Ser Pro Lys Thr Arg Arg Leu Gly Leu Thr Asp Ala His Asn Gly Leu						
	170			175	180	
cgc gta ttc aac caa aaa gtg gcg cag gaa atg aac atc cgc atg aac						691
Arg Val Phe Asn Gln Lys Val Ala Gln Glu Met Asn Ile Arg Met Asn						
	185			190	195	
ggc atg tcg cat gca tcc gaa atc gtc gac caa atc gat gaa cgc ggc						739
Gly Met Ser His Ala Ser Glu Ile Val Asp Gln Ile Asp Glu Arg Gly						
	200			205	210	
tgg cgc att tca gaa gaa ccc gta gac atc ctc tac acc gaa tac tcc						787
Trp Arg Ile Ser Glu Glu Pro Val Asp Ile Leu Tyr Thr Glu Tyr Ser						
	215			220	225	
atg agc aag ggg caa tcc ctg ctc aac ggc gta aac atc ctg gcc gac						835
Met Ser Lys Gly Gln Ser Leu Leu Asn Gly Val Asn Ile Leu Ala Asp						

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<210> 256
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<212> PRT
<213> Corynebacterium glutamicum
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396

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<220>
<221> CDS
<222> (101)..(1150)
<223> RXN02309
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397

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 Arg Asp Thr Asp Pro Ile Glu His Tyr Thr Asn Val Ile Arg Glu Lys
 185 190 195

act ggt gtc ctc atc gcc tcc gca ggc tat ttg gga gcc atg cac gca 739
 Thr Gly Val Leu Ile Ala Ser Ala Gly Tyr Leu Gly Ala Met His Ala
 200 205 210

ggc gcc gca cct gaa cac atc gac gcc ctg aag aac ttc ggc gca gcc 787
 Gly Ala Ala Pro Glu His Ile Asp Ala Leu Lys Asn Phe Gly Ala Ala
 215 220 225

gtc ggc atg atc ttc caa atc gtc gac gac atc atc gac atc ttc tcg 835
 Val Gly Met Ile Phe Gln Ile Val Asp Asp Ile Ile Asp Ile Phe Ser
 230 235 240 245

gaa acc cac gaa tcc gga aaa acg ccc ggc acc gac ctc cgc gaa ggt 883
 Glu Thr His Glu Ser Gly Lys Thr Pro Gly Thr Asp Leu Arg Glu Gly
 250 255 260

gta ttc acc ctc cca gtg ctc tac gca ctc cgt gaa gac acc ccc gtc 931
 Val Phe Thr Leu Pro Val Leu Tyr Ala Leu Arg Glu Asp Thr Pro Val
 265 270 275

ggc gca gaa ctc cgc gac atc ctc acc ggc cct cta gaa gac gac gag 979
 Gly Ala Glu Leu Arg Asp Ile Leu Thr Gly Pro Leu Glu Asp Asp Glu
 280 285 290

acc gtc aac cac gtc ctc gag ctc ctc tcc caa tcc ggc gga cgc caa 1027
 Thr Val Asn His Val Leu Glu Leu Leu Ser Gln Ser Gly Gly Arg Gln
 295 300 305

gca gcc ctc gac gag gtc tac cgc tac atg gac atc gcc aac gca gaa 1075
 Ala Ala Leu Asp Glu Val Tyr Arg Tyr Met Asp Ile Ala Asn Ala Glu
 310 315 320 325

ctc gac cgc ctc cca gac agc acc gtc aag gaa gcc ctc cgc aac ctt 1123
 Leu Asp Arg Leu Pro Asp Ser Thr Val Lys Glu Ala Leu Arg Asn Leu
 330 335 340

gca acc ttc aca gtc aag cgc gtc gga taaccccgta atccaccact 1170
 Ala Thr Phe Thr Val Lys Arg Val Gly
 345 350

taa 1173

<210> 258

<211> 350

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

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 20 25 30

Glu Leu Thr Ala Arg Ile Asn Asp Ala Met Val Gln Val Glu Glu Leu

<211> 1075
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1075)
 <223> FRXA02309

<400> 259

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                                         Met Ser Ser Gly Arg
                                         1 5
acc gtt cca acc cgt tcc cac ggg ctc gga aaa gaa ggt gta tcc acc 163
Thr Val Pro Thr Arg Ser His Gly Leu Gly Lys Glu Gly Val Ser Thr
                        10 15 20
aca gga gca tct cag gtc gag ttt ggt gat ccc gag cta acg gcc agg 211
Thr Gly Ala Ser Gln Val Glu Phe Gly Asp Pro Glu Leu Thr Ala Arg
                        25 30 35
atc aat gac gcc atg gtg cag gta gaa gaa ctc ctg cac act gaa cta 259
Ile Asn Asp Ala Met Val Gln Val Glu Glu Leu Leu His Thr Glu Leu
                        40 45 50
tcg tcc ggg gaa gac ttc ctc gtc gat atc gtc atg cac cta aca cga 307
Ser Ser Gly Glu Asp Phe Leu Val Asp Ile Val Met His Leu Thr Arg
                        55 60 65
gcc ggc ggc aaa cga ttc cgc ccc atg ttt gca ctg ctg gcc tcc gag 355
Ala Gly Gly Lys Arg Phe Arg Pro Met Phe Ala Leu Leu Ala Ser Glu
                        70 75 80 85
ttc ggt gaa aaa cca ctc tcc gaa aac gtc atc aaa gcc gcc gtt gtc 403
Phe Gly Glu Lys Pro Leu Ser Glu Asn Val Ile Lys Ala Ala Val Val
                        90 95 100
gta gag atc acc cac ctg gcc acc ctg tac cac gac gat gtc atg gac 451
Val Glu Ile Thr His Leu Ala Thr Leu Tyr His Asp Asp Val Met Asp
                        105 110 115
gag gca tcc atg cgc cgc ggc gtc cca agt gct aac gcg cga tgg gac 499
Glu Ala Ser Met Arg Arg Gly Val Pro Ser Ala Asn Ala Arg Trp Asp
                        120 125 130
aac tcc gta gcc atc ctc gca ggc gac atc ctc cta gca cat gca tca 547
Asn Ser Val Ala Ile Leu Ala Gly Asp Ile Leu Leu Ala His Ala Ser
                        135 140 145
ggg ctg atg agt cag ctg ggt acc gac aca gtc gcc cac ttt gcc gaa 595
Gly Leu Met Ser Gln Leu Gly Thr Asp Thr Val Ala His Phe Ala Glu
                        150 155 160 165
aca ttc ggc gaa cta gtc acc ggc caa atg cgc gaa aca gtc ggg cca 643
Thr Phe Gly Glu Leu Val Thr Gly Gln Met Arg Glu Thr Val Gly Pro
                        170 175 180
cgc gac acc gac ccg atc gag cac tac acc aac gta atc cgt gaa aaa 691

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Arg Asp Thr Asp Pro Ile Glu His Tyr Thr Asn Val Ile Arg Glu Lys
 185 190 195
 act ggt gtc ctc atc gcc tcc gca ggc tat ttg gga gcc atg cac gca 739
 Thr Gly Val Leu Ile Ala Ser Ala Gly Tyr Leu Gly Ala Met His Ala
 200 205 210
 ggc gcc gca cct gaa cac atc gac gcc ctg aag aac ttc ggc gca gcc 787
 Gly Ala Ala Pro Glu His Ile Asp Ala Leu Lys Asn Phe Gly Ala Ala
 215 220 225
 gtc ggc atg atc ttc caa atc gtc gac gac atc atc gac atc ttc tcg 835
 Val Gly Met Ile Phe Gln Ile Val Asp Asp Ile Ile Asp Ile Phe Ser
 230 235 240 245
 gaa acc cac gaa tcc gga aaa acg ccc ggc acc gac ctc cgc gaa ggt 883
 Glu Thr His Glu Ser Gly Lys Thr Pro Gly Thr Asp Leu Arg Glu Gly
 250 255 260
 gta ttc acc ctc cca gtg ctc tac gca ctc cgt gaa gac acc ccc gtc 931
 Val Phe Thr Leu Pro Val Leu Tyr Ala Leu Arg Glu Asp Thr Pro Val
 265 270 275
 ggc gca gaa ctc cgc gac atc ctc acc ggc cct cta gaa gac gac gag 979
 Gly Ala Glu Leu Arg Asp Ile Leu Thr Gly Pro Leu Glu Asp Asp Glu
 280 285 290
 acc gtc aac cac gtc ctc gag ctc ctc tcc caa tcc ggc gga cgc caa 1027
 Thr Val Asn His Val Leu Glu Leu Leu Ser Gln Ser Gly Gly Arg Gln
 295 300 305
 gca gcc ctc gac gag gtc tac cgc tac atg gac atc gcc aac gca gaa 1075
 Ala Ala Leu Asp Glu Val Tyr Arg Tyr Met Asp Ile Ala Asn Ala Glu
 310 315 320 325
 <210> 260
 <211> 325
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 260
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 20 25 30
 Glu Leu Thr Ala Arg Ile Asn Asp Ala Met Val Gln Val Glu Glu Leu
 35 40 45
 Leu His Thr Glu Leu Ser Ser Gly Glu Asp Phe Leu Val Asp Ile Val
 50 55 60
 Met His Leu Thr Arg Ala Gly Gly Lys Arg Phe Arg Pro Met Phe Ala
 65 70 75 80
 Leu Leu Ala Ser Glu Phe Gly Glu Lys Pro Leu Ser Glu Asn Val Ile
 85 90 95
 Lys Ala Ala Val Val Val Glu Ile Thr His Leu Ala Thr Leu Tyr His

100					105					110						
Asp	Asp	Val	Met	Asp	Glu	Ala	Ser	Met	Arg	Arg	Gly	Val	Pro	Ser	Ala	
115					120					125						
Asn	Ala	Arg	Trp	Asp	Asn	Ser	Val	Ala	Ile	Leu	Ala	Gly	Asp	Ile	Leu	
130					135					140						
Leu	Ala	His	Ala	Ser	Gly	Leu	Met	Ser	Gln	Leu	Gly	Thr	Asp	Thr	Val	
145					150					155					160	
Ala	His	Phe	Ala	Glu	Thr	Phe	Gly	Glu	Leu	Val	Thr	Gly	Gln	Met	Arg	
165					170					175						
Glu	Thr	Val	Gly	Pro	Arg	Asp	Thr	Asp	Pro	Ile	Glu	His	Tyr	Thr	Asn	
180					185					190						
Val	Ile	Arg	Glu	Lys	Thr	Gly	Val	Leu	Ile	Ala	Ser	Ala	Gly	Tyr	Leu	
195					200					205						
Gly	Ala	Met	His	Ala	Gly	Ala	Ala	Pro	Glu	His	Ile	Asp	Ala	Leu	Lys	
210					215					220						
Asn	Phe	Gly	Ala	Ala	Val	Gly	Met	Ile	Phe	Gln	Ile	Val	Asp	Asp	Ile	
225					230					235					240	
Ile	Asp	Ile	Phe	Ser	Glu	Thr	His	Glu	Ser	Gly	Lys	Thr	Pro	Gly	Thr	
245					250					255						
Asp	Leu	Arg	Glu	Gly	Val	Phe	Thr	Leu	Pro	Val	Leu	Tyr	Ala	Leu	Arg	
260					265					270						
Glu	Asp	Thr	Pro	Val	Gly	Ala	Glu	Leu	Arg	Asp	Ile	Leu	Thr	Gly	Pro	
275					280					285						
Leu	Glu	Asp	Asp	Glu	Thr	Val	Asn	His	Val	Leu	Glu	Leu	Leu	Ser	Gln	
290					295					300						
Ser	Gly	Gly	Arg	Gln	Ala	Ala	Leu	Asp	Glu	Val	Tyr	Arg	Tyr	Met	Asp	
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325																

<210> 261

<211> 1767

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1744)

<223> RXN00477

<400> 261

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				Met	Lys	Val	Ser	Thr	
				1				5	

aaa act cca cgc tcc tca ggt acc gcc gta gtc ata ggc gca ggt gtt	163
Lys Thr Pro Arg Ser Ser Gly Thr Ala Val Val Ile Gly Ala Gly Val	
10 15 20	
gct ggt tta gcc act tct gca ctt tta gca cgt gat ggc tgg caa gta	211
Ala Gly Leu Ala Thr Ser Ala Leu Leu Ala Arg Asp Gly Trp Gln Val	
25 30 35	
act gtt ttg gaa aaa aat act gat gtc ggt ggc cga gct gga tcg ctt	259
Thr Val Leu Glu Lys Asn Thr Asp Val Gly Gly Arg Ala Gly Ser Leu	
40 45 50	
gaa ata tca ggc ttt cct ggc ttt cga tgg gat acc gga cct tct tgg	307
Glu Ile Ser Gly Phe Pro Gly Phe Arg Trp Asp Thr Gly Pro Ser Trp	
55 60 65	
tac ctc atg ccc gag gcc ttt gac cat ttc ttc gca ctt ttt ggt gca	355
Tyr Leu Met Pro Glu Ala Phe Asp His Phe Phe Ala Leu Phe Gly Ala	
70 75 80 85	
tgt act tct gat tat ctc gat ttg gta gaa tta acg cct ggt tat cga	403
Cys Thr Ser Asp Tyr Leu Asp Leu Val Glu Leu Thr Pro Gly Tyr Arg	
90 95 100	
gtt ttt tct ggc aca cat gac gct gtc gat gtc ccc act ggg cgt gaa	451
Val Phe Ser Gly Thr His Asp Ala Val Asp Val Pro Thr Gly Arg Glu	
105 110 115	
gaa gca att gcg cta ttc gaa tcc atc gaa ccc ggc gcg ggt gca aaa	499
Glu Ala Ile Ala Leu Phe Glu Ser Ile Glu Pro Gly Ala Gly Ala Lys	
120 125 130	
cta gga aat tat ctt gat agc gcg gca gac gcc tat gac att gcc att	547
Leu Gly Asn Tyr Leu Asp Ser Ala Ala Asp Ala Tyr Asp Ile Ala Ile	
135 140 145	
gat aga ttc ctt tat aat aat ttc tcc acg tta ggc ccg ctg ctt cac	595
Asp Arg Phe Leu Tyr Asn Asn Phe Ser Thr Leu Gly Pro Leu Leu His	
150 155 160 165	
cgg gat gta ctg acc cga gct ggc cga ctg ttt tct cta ctg acc cgt	643
Arg Asp Val Leu Thr Arg Ala Gly Arg Leu Phe Ser Leu Leu Thr Arg	
170 175 180	
tct tta caa aag tac gta aat agt caa ttc agt agc ccg gtg ttg cgc	691
Ser Leu Gln Lys Tyr Val Asn Ser Gln Phe Ser Ser Pro Val Leu Arg	
185 190 195	
cag atc cta acc tat cca gca gtc ttc ctg tct tcc cga ccc act act	739
Gln Ile Leu Thr Tyr Pro Ala Val Phe Leu Ser Ser Arg Pro Thr Thr	
200 205 210	
acc cca tcg atg tac cac ttg atg agt cat acc gat ttg gtg cag gga	787
Thr Pro Ser Met Tyr His Leu Met Ser His Thr Asp Leu Val Gln Gly	
215 220 225	
gtg aaa tac cct ata ggt ggt ttt act gca gtg gtt aac gct ctg cat	835
Val Lys Tyr Pro Ile Gly Gly Phe Thr Ala Val Val Asn Ala Leu His	
230 235 240 245	

cag tta gcg ctg gaa aac ggg gtt gag ttt caa ctc gat tct gag gtc	883
Gln Leu Ala Leu Glu Asn Gly Val Glu Phe Gln Leu Asp Ser Glu Val	
250 255 260	
att tcc atc aac act gct tca tcg agg ggc aac aca agc gcc aca ggt	931
Ile Ser Ile Asn Thr Ala Ser Ser Arg Gly Asn Thr Ser Ala Thr Gly	
265 270 275	
gtg agc ttg ctt cac aac aga aaa gtg caa aat cta gat gcg gat ctt	979
Val Ser Leu Leu His Asn Arg Lys Val Gln Asn Leu Asp Ala Asp Leu	
280 285 290	
gtg gtt tca gca ggc gac cta cac cat aca gaa aat aat ctg ctt ccc	1027
Val Val Ser Ala Gly Asp Leu His His Thr Glu Asn Asn Leu Leu Pro	
295 300 305	
cgg gaa ctt cga acc tat ccc gaa cga tat tgg tcc aat cgc aat cct	1075
Arg Glu Leu Arg Thr Tyr Pro Glu Arg Tyr Trp Ser Asn Arg Asn Pro	
310 315 320 325	
gga att gga gcg gta tta atc ctc ctg ggc gta aaa gga gag tta ccc	1123
Gly Ile Gly Ala Val Leu Ile Leu Leu Gly Val Lys Gly Glu Leu Pro	
330 335 340	
cag ctc gac cat cac aac ctt ttc ttc agt gaa gat tgg aca gat gat	1171
Gln Leu Asp His His Asn Leu Phe Phe Ser Glu Asp Trp Thr Asp Asp	
345 350 355	
ttt gct gta gtt ttc gac ggg cct caa ctt acc cgc ccc cac aat gca	1219
Phe Ala Val Val Phe Asp Gly Pro Gln Leu Thr Arg Pro His Asn Ala	
360 365 370	
tca aat tcc att tat gtc tcc aag cct tca acg tcc gaa gac ggc gtt	1267
Ser Asn Ser Ile Tyr Val Ser Lys Pro Ser Thr Ser Glu Asp Gly Val	
375 380 385	
gca cct gct gga tac gaa aac ctt ttt gtt tta att ccg acc aag gcc	1315
Ala Pro Ala Gly Tyr Glu Asn Leu Phe Val Leu Ile Pro Thr Lys Ala	
390 395 400 405	
tct agc agc atc ggc cac ggt gat gcg tat atg cag tcg gct tca gca	1363
Ser Ser Ser Ile Gly His Gly Asp Ala Tyr Met Gln Ser Ala Ser Ala	
410 415 420	
tcc gtg gaa aca atc gcg tca cat gca atc aat caa att gct acg caa	1411
Ser Val Glu Thr Ile Ala Ser His Ala Ile Asn Gln Ile Ala Thr Gln	
425 430 435	
gcc ggc atc cct gac ctc act gac cga att gtg gtc aaa cgc acc att	1459
Ala Gly Ile Pro Asp Leu Thr Asp Arg Ile Val Val Lys Arg Thr Ile	
440 445 450	
ggc cct gcg gat ttt gag cac cgc tac cat tca tgg gta ggc agt gcg	1507
Gly Pro Ala Asp Phe Glu His Arg Tyr His Ser Trp Val Gly Ser Ala	
455 460 465	
ctg ggt cca gca cat acc ctc aga cag tcc gct ttc tta aga ggg cgc	1555
Leu Gly Pro Ala His Thr Leu Arg Gln Ser Ala Phe Leu Arg Gly Arg	
470 475 480 485	
aat agc tcc cgc aag gtc aat aac ctc ttc tat tcc ggt gcc acc acc	1603

Asn Ser Ser Arg Lys Val Asn Asn Leu Phe Tyr Ser Gly Ala Thr Thr
 490 495 500

gtc ccg ggt gta gga ata ccc atg tgt tta att tct gcc gag aat att 1651
 Val Pro Gly Val Gly Ile Pro Met Cys Leu Ile Ser Ala Glu Asn Ile
 505 510 515

att aag cgt tta cat gcc gat acc agt gca gga cca ctg ccc gaa cca 1699
 Ile Lys Arg Leu His Ala Asp Thr Ser Ala Gly Pro Leu Pro Glu Pro
 520 525 530

ttg ccg cct aaa acg aca cca tct caa aag acc tca tac gat cat 1744
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 535 540 545

taaattttga tccctatcat cga 1767

<210> 262

<211> 548

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

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Ile Gly Ala Gly Val Ala Gly Leu Ala Thr Ser Ala Leu Leu Ala Arg
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Asp Gly Trp Gln Val Thr Val Leu Glu Lys Asn Thr Asp Val Gly Gly
 35 40 45

Arg Ala Gly Ser Leu Glu Ile Ser Gly Phe Pro Gly Phe Arg Trp Asp
 50 55 60

Thr Gly Pro Ser Trp Tyr Leu Met Pro Glu Ala Phe Asp His Phe Phe
 65 70 75 80

Ala Leu Phe Gly Ala Cys Thr Ser Asp Tyr Leu Asp Leu Val Glu Leu
 85 90 95

Thr Pro Gly Tyr Arg Val Phe Ser Gly Thr His Asp Ala Val Asp Val
 100 105 110

Pro Thr Gly Arg Glu Glu Ala Ile Ala Leu Phe Glu Ser Ile Glu Pro
 115 120 125

Gly Ala Gly Ala Lys Leu Gly Asn Tyr Leu Asp Ser Ala Ala Asp Ala
 130 135 140

Tyr Asp Ile Ala Ile Asp Arg Phe Leu Tyr Asn Asn Phe Ser Thr Leu
 145 150 155 160

Gly Pro Leu Leu His Arg Asp Val Leu Thr Arg Ala Gly Arg Leu Phe
 165 170 175

Ser Leu Leu Thr Arg Ser Leu Gln Lys Tyr Val Asn Ser Gln Phe Ser
 180 185 190

Ser Pro Val Leu Arg Gln Ile Leu Thr Tyr Pro Ala Val Phe Leu Ser

195						200						205					
Ser	Arg	Pro	Thr	Thr	Thr	Pro	Ser	Met	Tyr	His	Leu	Met	Ser	His	Thr		
210						215						220					
Asp	Leu	Val	Gln	Gly	Val	Lys	Tyr	Pro	Ile	Gly	Gly	Phe	Thr	Ala	Val		
225						230						235					
Val	Asn	Ala	Leu	His	Gln	Leu	Ala	Leu	Glu	Asn	Gly	Val	Glu	Phe	Gln		
245						250						255					
Leu	Asp	Ser	Glu	Val	Ile	Ser	Ile	Asn	Thr	Ala	Ser	Ser	Arg	Gly	Asn		
260						265						270					
Thr	Ser	Ala	Thr	Gly	Val	Ser	Leu	Leu	His	Asn	Arg	Lys	Val	Gln	Asn		
275						280						285					
Leu	Asp	Ala	Asp	Leu	Val	Val	Ser	Ala	Gly	Asp	Leu	His	His	Thr	Glu		
290						295						300					
Asn	Asn	Leu	Leu	Pro	Arg	Glu	Leu	Arg	Thr	Tyr	Pro	Glu	Arg	Tyr	Trp		
305						310						315					
Ser	Asn	Arg	Asn	Pro	Gly	Ile	Gly	Ala	Val	Leu	Ile	Leu	Leu	Gly	Val		
325						330						335					
Lys	Gly	Glu	Leu	Pro	Gln	Leu	Asp	His	His	Asn	Leu	Phe	Phe	Ser	Glu		
340						345						350					
Asp	Trp	Thr	Asp	Asp	Phe	Ala	Val	Val	Phe	Asp	Gly	Pro	Gln	Leu	Thr		
355						360						365					
Arg	Pro	His	Asn	Ala	Ser	Asn	Ser	Ile	Tyr	Val	Ser	Lys	Pro	Ser	Thr		
370						375						380					
Ser	Glu	Asp	Gly	Val	Ala	Pro	Ala	Gly	Tyr	Glu	Asn	Leu	Phe	Val	Leu		
385						390						395					
Ile	Pro	Thr	Lys	Ala	Ser	Ser	Ser	Ser	Ile	Gly	His	Gly	Asp	Ala	Tyr		
405						410						415					
Gln	Ser	Ala	Ser	Ala	Ser	Val	Glu	Thr	Ile	Ala	Ser	His	Ala	Ile	Asn		
420						425						430					
Gln	Ile	Ala	Thr	Gln	Ala	Gly	Ile	Pro	Asp	Leu	Thr	Asp	Arg	Ile	Val		
435						440						445					
Val	Lys	Arg	Thr	Ile	Gly	Pro	Ala	Asp	Phe	Glu	His	Arg	Tyr	His	Ser		
450						455						460					
Trp	Val	Gly	Ser	Ala	Leu	Gly	Pro	Ala	His	Thr	Leu	Arg	Gln	Ser	Ala		
465						470						475					
Phe	Leu	Arg	Gly	Arg	Asn	Ser	Ser	Arg	Lys	Val	Asn	Asn	Leu	Phe	Tyr		
485						490						495					
Ser	Gly	Ala	Thr	Thr	Val	Pro	Gly	Val	Gly	Ile	Pro	Met	Cys	Leu	Ile		
500						505						510					
Ser	Ala	Glu	Asn	Ile	Ile	Lys	Arg	Leu	His	Ala	Asp	Thr	Ser	Ala	Gly		
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Ser Tyr Asp His
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<210> 263

<211> 1767

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1744)

<223> FRXA00477

<400> 263

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 Met Lys Val Ser Thr
 1 5

aaa act cca cgc tcc tca ggt acc gcc gta gtc ata ggc gca ggt gtt 163
 Lys Thr Pro Arg Ser Ser Gly Thr Ala Val Val Ile Gly Ala Gly Val
 10 15 20

gct ggt tta gcc act tct gca ctt tta gca cgt gat ggc tgg caa gta 211
 Ala Gly Leu Ala Thr Ser Ala Leu Leu Ala Arg Asp Gly Trp Gln Val
 25 30 35

act gtt ttg gaa aaa aat act gat gtc ggt ggc cga gct gga tcg ctt 259
 Thr Val Leu Glu Lys Asn Thr Asp Val Gly Gly Arg Ala Gly Ser Leu
 40 45 50

gaa ata tca ggc ttt cct ggc ttt cga tgg gat acc gga cct tct tgg 307
 Glu Ile Ser Gly Phe Pro Gly Phe Arg Trp Asp Thr Gly Pro Ser Trp
 55 60 65

tac ctc atg ccc gag gcc ttt gac cat ttc ttc gca ctt ttt ggt gca 355
 Tyr Leu Met Pro Glu Ala Phe Asp His Phe Phe Ala Leu Phe Gly Ala
 70 75 80 85

tgt act tct gat tat ctc gat ttg gta gaa tta acg cct ggt tat cga 403
 Cys Thr Ser Asp Tyr Leu Asp Leu Val Glu Leu Thr Pro Gly Tyr Arg
 90 95 100

gtt ttt tct ggc aca cat gac gct gtc gat gtc ccc act ggg cgt gaa 451
 Val Phe Ser Gly Thr His Asp Ala Val Asp Val Pro Thr Gly Arg Glu
 105 110 115

gaa gca att gcg cta ttc gaa tcc atc gaa ccc ggc gcg ggt gca aaa 499
 Glu Ala Ile Ala Leu Phe Glu Ser Ile Glu, Pro Gly Ala Gly Ala Lys
 120 125 130

cta gga aat tat ctt gat agc gcg gca gac gcc tat gac att gcc att 547
 Leu Gly Asn Tyr Leu Asp Ser Ala Ala Asp Ala Tyr Asp Ile Ala Ile
 135 140 145

gat aga ttc ctt tat aat aat ttc tcc acg tta ggc ccg ctg ctt cac	595
Asp Arg Phe Leu Tyr Asn Asn Phe Ser Thr Leu Gly Pro Leu Leu His	
150 155 160 165	
cgg gat gta ctg acc cga gct ggc cga ctg ttt tct cta ctg acc cgt	643
Arg Asp Val Leu Thr Arg Ala Gly Arg Leu Phe Ser Leu Leu Thr Arg	
170 175 180	
tct tta caa aag tac gta aat agt caa ttc agt agc ccg gtg ttg cgc	691
Ser Leu Gln Lys Tyr Val Asn Ser Gln Phe Ser Ser Pro Val Leu Arg	
185 190 195	
cag atc cta acc tat cca gca gtc ttc ctg tct tcc cga ccc act act	739
Gln Ile Leu Thr Tyr Pro Ala Val Phe Leu Ser Ser Arg Pro Thr Thr	
200 205 210	
acc cca tcg atg tac cac ttg atg agt cat acc gat ttg gtg cag gga	787
Thr Pro Ser Met Tyr His Leu Met Ser His Thr Asp Leu Val Gln Gly	
215 220 225	
gtg aaa tac cct ata ggt ggt ttt act gca gtg gtt aac gct ctg cat	835
Val Lys Tyr Pro Ile Gly Gly Phe Thr Ala Val Val Asn Ala Leu His	
230 235 240 245	
cag tta gcg ctg gaa aac ggg gtt gag ttt caa ctc gat tct gag gtc	883
Gln Leu Ala Leu Glu Asn Gly Val Glu Phe Gln Leu Asp Ser Glu Val	
250 255 260	
att tcc atc aac act gct tca tcg agg ggc aac aca agc gcc aca ggt	931
Ile Ser Ile Asn Thr Ala Ser Ser Arg Gly Asn Thr Ser Ala Thr Gly	
265 270 275	
gtg agc ttg ctt cac aac aga aaa gtg caa aat cta gat gcg gat ctt	979
Val Ser Leu Leu His Asn Arg Lys Val Gln Asn Leu Asp Ala Asp Leu	
280 285 290	
gtg gtt tca gca ggc gac cta cac cat aca gaa aat aat ctg ctt ccc	1027
Val Val Ser Ala Gly Asp Leu His His Thr Glu Asn Asn Leu Leu Pro	
295 300 305	
cgg gaa ctt cga acc tat ccc gaa cga tat tgg tcc aat cgc aat cct	1075
Arg Glu Leu Arg Thr Tyr Pro Glu Arg Tyr Trp Ser Asn Arg Asn Pro	
310 315 320 325	
gga att gga gcg gta tta atc ctc ctg ggc gta aaa gga gag tta ccc	1123
Gly Ile Gly Ala Val Leu Ile Leu Leu Gly Val Lys Gly Glu Leu Pro	
330 335 340	
cag ctc gac cat cac aac ctt ttc ttc agt gaa gat tgg aca gat gat	1171
Gln Leu Asp His His Asn Leu Phe Phe Ser Glu Asp Trp Thr Asp Asp	
345 350 355	
ttt gct gta gtt ttc gac ggg cct caa ctt acc cgc ccc cac aat gca	1219
Phe Ala Val Val Phe Asp Gly Pro Gln Leu Thr Arg Pro His Asn Ala	
360 365 370	
tca aat tcc att tat gtc tcc aag cct tca acg tcc gaa gac ggc gtt	1267
Ser Asn Ser Ile Tyr Val Ser Lys Pro Ser Thr Ser Glu Asp Gly Val	
375 380 385	
gca cct gct gga tac gaa aac ctt ttt gtt tta att ccg acc aag gcc	1315

Ala Pro Ala Gly Tyr Glu Asn Leu Phe Val Leu Ile Pro Thr Lys Ala
 390 395 400 405

tct agc agc atc ggc cac ggt gat gcg tat atg cag tcg gct tca gca 1363
 Ser Ser Ser Ile Gly His Gly Asp Ala Tyr Met Gln Ser Ala Ser Ala
 410 415 420

tcc gtg gaa aca atc gcg tca cat gca atc aat caa att gct acg caa 1411
 Ser Val Glu Thr Ile Ala Ser His Ala Ile Asn Gln Ile Ala Thr Gln
 425 430 435

gcc ggc atc cct gac ctc act gac cga att gtg gtc aaa cgc acc att 1459
 Ala Gly Ile Pro Asp Leu Thr Asp Arg Ile Val Val Lys Arg Thr Ile
 440 445 450

ggc cct gcg gat ttt gag cac cgc tac cat tca tgg gta ggc agt gcg 1507
 Gly Pro Ala Asp Phe Glu His Arg Tyr His Ser Trp Val Gly Ser Ala
 455 460 465

ctg ggt cca gca cat acc ctc aga cag tcc gct ttc tta aga ggg cgc 1555
 Leu Gly Pro Ala His Thr Leu Arg Gln Ser Ala Phe Leu Arg Gly Arg
 470 475 480 485

aat agc tcc cgc aag gtc aat aac ctc ttc tat tcc ggt gcc acc acc 1603
 Asn Ser Ser Arg Lys Val Asn Asn Leu Phe Tyr Ser Gly Ala Thr Thr
 490 495 500

gtc ccg ggt gta gga ata ccc atg tgt tta att tct gcc gag aat att 1651
 Val Pro Gly Val Gly Ile Pro Met Cys Leu Ile Ser Ala Glu Asn Ile
 505 510 515

att aag cgt tta cat gcc gat acc agt gca gga cca ctg ccc gaa cca 1699
 Ile Lys Arg Leu His Ala Asp Thr Ser Ala Gly Pro Leu Pro Glu Pro
 520 525 530

ttg ccg cct aaa acg aca cca tct caa aag acc tca tac gat cat 1744
 Leu Pro Pro Lys Thr Thr Pro Ser Gln Lys Thr Ser Tyr Asp His
 535 540 545

taaattttga tccctatcat cga 1767

<210> 264

<211> 548

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met Lys Val Ser Thr Lys Thr Pro Arg Ser Ser Gly Thr Ala Val Val
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Ile Gly Ala Gly Val Ala Gly Leu Ala Thr Ser Ala Leu Leu Ala Arg
 20 25 30

Asp Gly Trp Gln Val Thr Val Leu Glu Lys Asn Thr Asp Val Gly Gly
 35 40 45

Arg Ala Gly Ser Leu Glu Ile Ser Gly Phe Pro Gly Phe Arg Trp Asp
 50 55 60

Thr Gly Pro Ser Trp Tyr Leu Met Pro Glu Ala Phe Asp His Phe Phe

65	70	75	80
Ala Leu Phe Gly	Ala Cys Thr Ser Asp Tyr	Leu Asp Leu Val Glu Leu	
	85	90	95
Thr Pro Gly Tyr	Arg Val Phe Ser Gly	Thr His Asp Ala Val Asp Val	
	100	105	110
Pro Thr Gly Arg	Glu Glu Ala Ile Ala Leu Phe Glu Ser	Ile Glu Pro	
	115	120	125
Gly Ala Gly Ala	Lys Leu Gly Asn Tyr Leu Asp Ser	Ala Ala Asp Ala	
	130	135	140
Tyr Asp Ile Ala	Ile Asp Arg Phe Leu Tyr Asn Asn Phe Ser Thr	Leu	
	145	150	155
Gly Pro Leu Leu	His Arg Asp Val Leu Thr Arg Ala Gly Arg	Leu Phe	
	165	170	175
Ser Leu Leu Thr	Arg Ser Leu Gln Lys Tyr Val Asn Ser	Gln Phe Ser	
	180	185	190
Ser Pro Val Leu	Arg Gln Ile Leu Thr Tyr Pro Ala Val Phe Leu Ser		
	195	200	205
Ser Arg Pro Thr	Thr Thr Pro Ser Met Tyr His Leu Met Ser His Thr		
	210	215	220
Asp Leu Val Gln	Gly Val Lys Tyr Pro Ile Gly Gly Phe Thr Ala Val		
	225	230	235
Val Asn Ala Leu	His Gln Leu Ala Leu Glu Asn Gly Val Glu Phe Gln		
	245	250	255
Leu Asp Ser Glu	Val Ile Ser Ile Asn Thr Ala Ser Ser Arg Gly Asn		
	260	265	270
Thr Ser Ala Thr	Gly Val Ser Leu Leu His Asn Arg Lys Val Gln Asn		
	275	280	285
Leu Asp Ala Asp	Leu Val Val Ser Ala Gly Asp Leu His His Thr Glu		
	290	295	300
Asn Asn Leu Leu	Pro Arg Glu Leu Arg Thr Tyr Pro Glu Arg Tyr Trp		
	305	310	315
Ser Asn Arg Asn	Pro Gly Ile Gly Ala Val Leu Ile Leu Leu Gly Val		
	325	330	335
Lys Gly Glu Leu	Pro Gln Leu Asp His His Asn Leu Phe Phe Ser Glu		
	340	345	350
Asp Trp Thr Asp	Asp Phe Ala Val Val Phe Asp Gly Pro Gln Leu Thr		
	355	360	365
Arg Pro His Asn	Ala Ser Asn Ser Ile Tyr Val Ser Lys Pro Ser Thr		
	370	375	380
Ser Glu Asp Gly	Val Ala Pro Ala Gly Tyr Glu Asn Leu Phe Val Leu		
	385	390	395
			400

Ile Pro Thr Lys Ala Ser Ser Ser Ile Gly His Gly Asp Ala Tyr Met
 405 410 415

Gln Ser Ala Ser Ala Ser Val Glu Thr Ile Ala Ser His Ala Ile Asn
 420 425 430

Gln Ile Ala Thr Gln Ala Gly Ile Pro Asp Leu Thr Asp Arg Ile Val
 435 440 445

Val Lys Arg Thr Ile Gly Pro Ala Asp Phe Glu His Arg Tyr His Ser
 450 455 460

Trp Val Gly Ser Ala Leu Gly Pro Ala His Thr Leu Arg Gln Ser Ala
 465 470 475 480

Phe Leu Arg Gly Arg Asn Ser Ser Arg Lys Val Asn Asn Leu Phe Tyr
 485 490 495

Ser Gly Ala Thr Thr Val Pro Gly Val Gly Ile Pro Met Cys Leu Ile
 500 505 510

Ser Ala Glu Asn Ile Ile Lys Arg Leu His Ala Asp Thr Ser Ala Gly
 515 520 525

Pro Leu Pro Glu Pro Leu Pro Pro Lys Thr Thr Pro Ser Gln Lys Thr
 530 535 540

Ser Tyr Asp His
 545

<210> 265
 <211> 954
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXA00478

<400> 265

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gagactttac aatcgggcct cattcaaggc ttcacataaa gtg atc gaa gaa tat 115
 Val Ile Glu Glu Tyr
 1 5

tcc acg agc ttc agt ctg tct acg tgg ttg cta tcc cca cgc ata cga 163
 Ser Thr Ser Phe Ser Leu Ser Thr Trp Leu Leu Ser Pro Arg Ile Arg
 10 15 20

aat gac ata cga aat ctc tat gca gta gtt cgt atc gcc gat gag att 211
 Asn Asp Ile Arg Asn Leu Tyr Ala Val Val Arg Ile Ala Asp Glu Ile
 25 30 35

gtc gac ggc act gca cat gcc gct ggt tgc tca act gcc aaa atc gaa 259
 Val Asp Gly Thr Ala His Ala Ala Gly Cys Ser Thr Ala Lys Ile Glu
 40 45 50

gag att ctc gat gcc tat gaa att gcg gtt ctt gca gca cca caa caa	307
Glu Ile Leu Asp Ala Tyr Glu Ile Ala Val Leu Ala Ala Pro Gln Gln	
55 60 65	
cgc ttc aac aca gat ctt gtt tta caa gct tat ggt gaa act gcc cga	355
Arg Phe Asn Thr Asp Leu Val Leu Gln Ala Tyr Gly Glu Thr Ala Arg	
70 75 80 85	
cgc tgt gat ttc gaa caa gag cat gta ata gcc ttc ttt gca tca atg	403
Arg Cys Asp Phe Glu Gln Glu His Val Ile Ala Phe Phe Ala Ser Met	
90 95 100	
cgt aag gac ctc aaa gct aat aca cac gac cca gat agc ttc aca acg	451
Arg Lys Asp Leu Lys Ala Asn Thr His Asp Pro Asp Ser Phe Thr Thr	
105 110 115	
tat gtc tat ggc tcc gcg gaa gtt ata ggc ctg ctt tgt ctc agc gtt	499
Tyr Val Tyr Gly Ser Ala Glu Val Ile Gly Leu Leu Cys Leu Ser Val	
120 125 130	
ttc aac caa ggt aga acg att agc aaa aaa cgg cta gag att atg caa	547
Phe Asn Gln Gly Arg Thr Ile Ser Lys Lys Arg Leu Glu Ile Met Gln	
135 140 145	
aac gga gcc cgc tca ttg gga gcg gca ttc cag aaa att aac ttt ctc	595
Asn Gly Ala Arg Ser Leu Gly Ala Ala Phe Gln Lys Ile Asn Phe Leu	
150 155 160 165	
cgt gac ttg gca gaa gat cag caa aat ttg ggc cga ttt tat ttc ccc	643
Arg Asp Leu Ala Glu Asp Gln Gln Asn Leu Gly Arg Phe Tyr Phe Pro	
170 175 180	
aaa acc agc caa gga act ctt act aaa gaa caa aaa gaa gat ctc atc	691
Lys Thr Ser Gln Gly Thr Leu Thr Lys Glu Gln Lys Glu Asp Leu Ile	
185 190 195	
gct gat atc cgt caa gac cta gca att gcc cac gat gca ttt cca gaa	739
Ala Asp Ile Arg Gln Asp Leu Ala Ile Ala His Asp Ala Phe Pro Glu	
200 205 210	
ata cca gtg cag gct cgc atc gga gtg atc tct gct tat ttg ctc ttt	787
Ile Pro Val Gln Ala Arg Ile Gly Val Ile Ser Ala Tyr Leu Leu Phe	
215 220 225	
caa aaa ctc act gac cga att gag gct act cct acc gcc gat tta ttg	835
Gln Lys Leu Thr Asp Arg Ile Glu Ala Thr Pro Thr Ala Asp Leu Leu	
230 235 240 245	
cgg gag cga atc aga gtt cca ctt cat atc aaa ctc tct aca ctc gct	883
Arg Glu Arg Ile Arg Val Pro Leu His Ile Lys Leu Ser Thr Leu Ala	
250 255 260	
aga gcc acg atg aaa ggt cta tct atg agc atc tac aga aag aat tcg	931
Arg Ala Thr Met Lys Gly Leu Ser Met Ser Ile Tyr Arg Lys Asn Ser	
265 270 275	
tgatgaaggt ctcgactaaa act	954

<210> 266

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Val Ile Glu Glu Tyr Ser Thr Ser Phe Ser Leu Ser Thr Trp Leu Leu
 1 5 10 15
 Ser Pro Arg Ile Arg Asn Asp Ile Arg Asn Leu Tyr Ala Val Val Arg
 20 25 30
 Ile Ala Asp Glu Ile Val Asp Gly Thr Ala His Ala Ala Gly Cys Ser
 35 40 45
 Thr Ala Lys Ile Glu Glu Ile Leu Asp Ala Tyr Glu Ile Ala Val Leu
 50 55 60
 Ala Ala Pro Gln Gln Arg Phe Asn Thr Asp Leu Val Leu Gln Ala Tyr
 65 70 75 80
 Gly Glu Thr Ala Arg Arg Cys Asp Phe Glu Gln Glu His Val Ile Ala
 85 90 95
 Phe Phe Ala Ser Met Arg Lys Asp Leu Lys Ala Asn Thr His Asp Pro
 100 105 110
 Asp Ser Phe Thr Thr Tyr Val Tyr Gly Ser Ala Glu Val Ile Gly Leu
 115 120 125
 Leu Cys Leu Ser Val Phe Asn Gln Gly Arg Thr Ile Ser Lys Lys Arg
 130 135 140
 Leu Glu Ile Met Gln Asn Gly Ala Arg Ser Leu Gly Ala Ala Phe Gln
 145 150 155 160
 Lys Ile Asn Phe Leu Arg Asp Leu Ala Glu Asp Gln Gln Asn Leu Gly
 165 170 175
 Arg Phe Tyr Phe Pro Lys Thr Ser Gln Gly Thr Leu Thr Lys Glu Gln
 180 185 190
 Lys Glu Asp Leu Ile Ala Asp Ile Arg Gln Asp Leu Ala Ile Ala His
 195 200 205
 Asp Ala Phe Pro Glu Ile Pro Val Gln Ala Arg Ile Gly Val Ile Ser
 210 215 220
 Ala Tyr Leu Leu Phe Gln Lys Leu Thr Asp Arg Ile Glu Ala Thr Pro
 225 230 235 240
 Thr Ala Asp Leu Leu Arg Glu Arg Ile Arg Val Pro Leu His Ile Lys
 245 250 255
 Leu Ser Thr Leu Ala Arg Ala Thr Met Lys Gly Leu Ser Met Ser Ile
 260 265 270
 Tyr Arg Lys Asn Ser
 275

<210> 267

<211> 1056

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1033)

<223> RXA01291

<400> 267

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tggatttctc gcggtaaagt ttcctgtgaa ggaggcgagt gtg gct gat cag caa 115
                               Val Ala Asp Gln Gln
                               1                               5

gat ttt ttg ggc cgt ttt gat gcg atg agc tca aag gcg acg gcc acg 163
Asp Phe Leu Gly Arg Phe Asp Ala Met Ser Ser Lys Ala Thr Ala Thr
                               10                               15                               20

gta atc gcc cat tat tcc tcc agt ttt act ctg gca tcg aag ctg ttg 211
Val Ile Ala His Tyr Ser Ser Ser Phe Thr Leu Ala Ser Lys Leu Leu
                               25                               30                               35

tcg ccg aaa att cgt cgc gat att gag gca ttg tac gca atg gtg cga 259
Ser Pro Lys Ile Arg Arg Asp Ile Glu Ala Leu Tyr Ala Met Val Arg
                               40                               45                               50

gtg gcc gat gag gtt gtg gac ggc gct gct gct gcc gcg ggg tgt gcg 307
Val Ala Asp Glu Val Val Asp Gly Ala Ala Ala Ala Ala Gly Cys Ala
                               55                               60                               65

ccg gac gcc gtt gcg gag att ttg gac aat tac gaa cgc cag gtt ctg 355
Pro Asp Ala Val Ala Glu Ile Leu Asp Asn Tyr Glu Arg Gln Val Leu
                               70                               75                               80                               85

ctc agt ttg tcc gtt cct ttt cat acc gat cca gtg atc cat gcg ttt 403
Leu Ser Leu Ser Val Pro Phe His Thr Asp Pro Val Ile His Ala Phe
                               90                               95                               100

ggc aat acc gcc cgc aaa tgt ggt ttt gag cag gct cac atc gtg gcg 451
Gly Asn Thr Ala Arg Lys Cys Gly Phe Glu Gln Ala His Ile Val Ala
                               105                               110                               115

ttt ttt gat tcc atg cgc cgc gat ctc tcc caa acc tcc tat gat ccg 499
Phe Phe Asp Ser Met Arg Arg Asp Leu Ser Gln Thr Ser Tyr Asp Pro
                               120                               125                               130

act cag ttg gat gag tac att tac ggc tcc gct gag gtc atc ggg ttg 547
Thr Gln Leu Asp Glu Tyr Ile Tyr Gly Ser Ala Glu Val Ile Gly Leu
                               135                               140                               145

atg tgt ttg aaa att ttc ctc caa gat tcc act gcc agc ccg cag gat 595
Met Cys Leu Lys Ile Phe Leu Gln Asp Ser Thr Ala Ser Pro Gln Asp
                               150                               155                               160                               165

cgg gcc acg atg gaa cac ggc gcc agg cgt ttg ggt gcg gca ttt caa 643
Arg Ala Thr Met Glu His Gly Ala Arg Arg Leu Gly Ala Ala Phe Gln
                               170                               175                               180

aag gta aat ttc ctg cga gat cta gct gaa gac cgc gaa ggc cta ggc 691
Lys Val Asn Phe Leu Arg Asp Leu Ala Glu Asp Arg Glu Gly Leu Gly

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185	190	195	
cgt tct tat ttg ccg gta ttc acc gaa gaa atg cgc gat gag atc gtt			739
Arg Ser Tyr Leu Pro Val Phe Thr Glu Glu Met Arg Asp Glu Ile Val			
200	205	210	
act gat atc cga gag gat ttg gat gcc gcc cgg ctg agc att ccg ctg			787
Thr Asp Ile Arg Glu Asp Leu Asp Ala Ala Arg Leu Ser Ile Pro Leu			
215	220	225	
ctg cca ttt ggc gcg cga acc ggt gtg cgc gcc gcg acc gat ctc tac			835
Leu Pro Phe Gly Ala Arg Thr Gly Val Arg Ala Ala Thr Asp Leu Tyr			
230	235	240	245
ggt tgc ctc gtg gac aac ctg gaa tcc gcg tcc ctc gaa gac tta aaa			883
Gly Cys Leu Val Asp Asn Leu Glu Ser Ala Ser Leu Glu Asp Leu Lys			
250	255	260	
aac ggg cgg gat ttt gtg ccg tct tta aaa aag cca gcc tgg caa cca			931
Asn Gly Arg Asp Phe Val Pro Ser Leu Lys Lys Pro Ala Trp Gln Pro			
265	270	275	
aag caa tgt gga aag aag tgt ttc aaa aat gac aaa agc agt ggt cat			979
Lys Gln Cys Gly Lys Lys Cys Phe Lys Asn Asp Lys Ser Ser Gly His			
280	285	290	
cgg cgg ggg act agc agg act agc cac cac cgc act gct ctt acg cga			1027
Arg Arg Gly Thr Ser Arg Thr Ser His His Arg Thr Ala Leu Thr Arg			
295	300	305	
agg ata tgaagtccac ctgctcgaac aaa			1056
Arg Ile			
310			

<210> 268

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Val Ala Asp Gln Gln Asp Phe Leu Gly Arg Phe Asp Ala Met Ser Ser	
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Lys Ala Thr Ala Thr Val Ile Ala His Tyr Ser Ser Ser Phe Thr Leu	
20 25 30	
Ala Ser Lys Leu Leu Ser Pro Lys Ile Arg Arg Asp Ile Glu Ala Leu	
35 40 45	
Tyr Ala Met Val Arg Val Ala Asp Glu Val Val Asp Gly Ala Ala Ala	
50 55 60	
Ala Ala Gly Cys Ala Pro Asp Ala Val Ala Glu Ile Leu Asp Asn Tyr	
65 70 75 80	
Glu Arg Gln Val Leu Leu Ser Leu Ser Val Pro Phe His Thr Asp Pro	
85 90 95	
Val Ile His Ala Phe Gly Asn Thr Ala Arg Lys Cys Gly Phe Glu Gln	
100 105 110	

Ala His Ile Val Ala Phe Phe Asp Ser Met Arg Arg Asp Leu Ser Gln
 115 120 125

Thr Ser Tyr Asp Pro Thr Gln Leu Asp Glu Tyr Ile Tyr Gly Ser Ala
 130 135 140

Glu Val Ile Gly Leu Met Cys Leu Lys Ile Phe Leu Gln Asp Ser Thr
 145 150 155 160

Ala Ser Pro Gln Asp Arg Ala Thr Met Glu His Gly Ala Arg Arg Leu
 165 170 175

Gly Ala Ala Phe Gln Lys Val Asn Phe Leu Arg Asp Leu Ala Glu Asp
 180 185 190

Arg Glu Gly Leu Gly Arg Ser Tyr Leu Pro Val Phe Thr Glu Glu Met
 195 200 205

Arg Asp Glu Ile Val Thr Asp Ile Arg Glu Asp Leu Asp Ala Ala Arg
 210 215 220

Leu Ser Ile Pro Leu Leu Pro Phe Gly Ala Arg Thr Gly Val Arg Ala
 225 230 235 240

Ala Thr Asp Leu Tyr Gly Cys Leu Val Asp Asn Leu Glu Ser Ala Ser
 245 250 255

Leu Glu Asp Leu Lys Asn Gly Arg Asp Phe Val Pro Ser Leu Lys Lys
 260 265 270

Pro Ala Trp Gln Pro Lys Gln Cys Gly Lys Lys Cys Phe Lys Asn Asp
 275 280 285

Lys Ser Ser Gly His Arg Arg Gly Thr Ser Arg Thr Ser His His Arg
 290 295 300

Thr Ala Leu Thr Arg Arg Ile
 305 310

<210> 269
 <211> 1239
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1216)
 <223> RXA00480

<400> 269
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ttgggaattt ttgcgagata actggccgtg tgatactcga atg gac aat ggc atg 115
 Met Asp Asn Gly Met
 1 5

aca atc acc aca gaa cat tca act cat cct gat ctt gat ttc aat gat 163
 Thr Ile Thr Thr Glu His Ser Thr His Pro Asp Leu Asp Phe Asn Asp
 10 15 20

gag att tat cgg gaa cta aac cgc atc tgc gct tcg cta tct caa cag	211
Glu Ile Tyr Arg Glu Leu Asn Arg Ile Cys Ala Ser Leu Ser Gln Gln	
25 30 35	
tgc agc aca tat caa cca gag ttc cgt acc tgc cta gat gct gct ttc	259
Cys Ser Thr Tyr Gln Pro Glu Phe Arg Thr Cys Leu Asp Ala Ala Phe	
40 45 50	
caa gct ttg cga ggt ggc aag tta atc cgc cct cga atg cta ctg ggg	307
Gln Ala Leu Arg Gly Gly Lys Leu Ile Arg Pro Arg Met Leu Leu Gly	
55 60 65	
cta tac aac acg ctt gta gac gat gac att gag gtc aaa ctc aac acc	355
Leu Tyr Asn Thr Leu Val Asp Asp Asp Ile Glu Val Lys Leu Asn Thr	
70 75 80 85	
gtt tta cag gta gca gtg gct tta gaa cta ctg cat ttt tcc ctt ttg	403
Val Leu Gln Val Ala Val Ala Leu Glu Leu Leu His Phe Ser Leu Leu	
90 95 100	
gtt cat gac gat gtt att gac gga gac ctc tat cgc cga ggc aaa ctt	451
Val His Asp Asp Val Ile Asp Gly Asp Leu Tyr Arg Arg Gly Lys Leu	
105 110 115	
aat ttt att ggg cag att ctc atg cat cgc aca cct gaa agt ttt gca	499
Asn Phe Ile Gly Gln Ile Leu Met His Arg Thr Pro Glu Ser Phe Ala	
120 125 130	
caa atc cag cgc gat cca gag cat cta gat tgg gca caa tct aat gga	547
Gln Ile Gln Arg Asp Pro Glu His Leu Asp Trp Ala Gln Ser Asn Gly	
135 140 145	
ctg ctt atg gga aat ctt ttt ctt gct gcc acc cat caa atc ttc gcg	595
Leu Leu Met Gly Asn Leu Phe Leu Ala Ala Thr His Gln Ile Phe Ala	
150 155 160 165	
cgc ctt gac ctt cca cat cac caa cgg gtt cga ctt tta gat tta ctc	643
Arg Leu Asp Leu Pro His His Gln Arg Val Arg Leu Leu Asp Leu Leu	
170 175 180	
aac cac acg ata aat gac act att gtg ggt gag ttt ctt gat gtg gga	691
Asn His Thr Ile Asn Asp Thr Ile Val Gly Glu Phe Leu Asp Val Gly	
185 190 195	
tta agc agc aaa gcc atc agc ccc aat atg gac att gct cta gaa atg	739
Leu Ser Ser Lys Ala Ile Ser Pro Asn Met Asp Ile Ala Leu Glu Met	
200 205 210	
agt cgg cta aaa aca gcc aca tac act ttt gaa ctt cca atg aga gca	787
Ser Arg Leu Lys Thr Ala Thr Tyr Thr Phe Glu Leu Pro Met Arg Ala	
215 220 225	
gcg gca att ctc gcg gaa cta cct cag gag att gaa aca aag ata ggt	835
Ala Ala Ile Leu Ala Glu Leu Pro Gln Glu Ile Glu Thr Lys Ile Gly	
230 235 240 245	
gag ata ggc aca aac ttg ggc atc gct tat caa ttg cag gac gat tac	883
Glu Ile Gly Thr Asn Leu Gly Ile Ala Tyr Gln Leu Gln Asp Asp Tyr	
250 255 260	

tta tct act ttt ggt gac gca gcc gaa cac ggc aaa gat gcc ttt tct 931
 Leu Ser Thr Phe Gly Asp Ala Ala Glu His Gly Lys Asp Ala Phe Ser
 265 270 275

gac ctt cga gaa gga aaa gaa act aca att atc gcc ttc gct cga gat 979
 Asp Leu Arg Glu Gly Lys Glu Thr Thr Ile Ile Ala Phe Ala Arg Asp
 280 285 290

act gct aaa tgg act gat att caa gac aac ttc ggc tcc gca gat ctg 1027
 Thr Ala Lys Trp Thr Asp Ile Gln Asp Asn Phe Gly Ser Ala Asp Leu
 295 300 305

agc acc tct cag gca gag cga att caa cat ctt ctc ata cag tgt gga 1075
 Ser Thr Ser Gln Ala Glu Arg Ile Gln His Leu Leu Ile Gln Cys Gly
 310 315 320 325

gca aag aat cac tcc ttg aat gcc atc tcc gac cac tta aat atc tgc 1123
 Ala Lys Asn His Ser Leu Asn Ala Ile Ser Asp His Leu Asn Ile Cys
 330 335 340

cgt tcg atg atc aaa aca cta agc ccc cag gta gat ccc aag gct caa 1171
 Arg Ser Met Ile Lys Thr Leu Ser Pro Gln Val Asp Pro Lys Ala Gln
 345 350 355

aat tta tta ctt aaa caa gtt gag caa cta gcc agc cgc aaa tct 1216
 Asn Leu Leu Leu Lys Gln Val Glu Gln Leu Ala Ser Arg Lys Ser
 360 365 370

tagaactaac ctttacgcct tta 1239

<210> 270

<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

Met Asp Asn Gly Met Thr Ile Thr Thr Glu His Ser Thr His Pro Asp
 1 5 10 15

Leu Asp Phe Asn Asp Glu Ile Tyr Arg Glu Leu Asn Arg Ile Cys Ala
 20 25 30

Ser Leu Ser Gln Gln Cys Ser Thr Tyr Gln Pro Glu Phe Arg Thr Cys
 35 40 45

Leu Asp Ala Ala Phe Gln Ala Leu Arg Gly Gly Lys Leu Ile Arg Pro
 50 55 60

Arg Met Leu Leu Gly Leu Tyr Asn Thr Leu Val Asp Asp Asp Ile Glu
 65 70 75 80

Val Lys Leu Asn Thr Val Leu Gln Val Ala Val Ala Leu Glu Leu Leu
 85 90 95

His Phe Ser Leu Leu Val His Asp Asp Val Ile Asp Gly Asp Leu Tyr
 100 105 110

Arg Arg Gly Lys Leu Asn Phe Ile Gly Gln Ile Leu Met His Arg Thr
 115 120 125

Pro Glu Ser Phe Ala Gln Ile Gln Arg Asp Pro Glu His Leu Asp Trp
 130 135 140
 Ala Gln Ser Asn Gly Leu Leu Met Gly Asn Leu Phe Leu Ala Ala Thr
 145 150 155 160
 His Gln Ile Phe Ala Arg Leu Asp Leu Pro His His Gln Arg Val Arg
 165 170 175
 Leu Leu Asp Leu Leu Asn His Thr Ile Asn Asp Thr Ile Val Gly Glu
 180 185 190
 Phe Leu Asp Val Gly Leu Ser Ser Lys Ala Ile Ser Pro Asn Met Asp
 195 200 205
 Ile Ala Leu Glu Met Ser Arg Leu Lys Thr Ala Thr Tyr Thr Phe Glu
 210 215 220
 Leu Pro Met Arg Ala Ala Ala Ile Leu Ala Glu Leu Pro Gln Glu Ile
 225 230 235 240
 Glu Thr Lys Ile Gly Glu Ile Gly Thr Asn Leu Gly Ile Ala Tyr Gln
 245 250 255
 Leu Gln Asp Asp Tyr Leu Ser Thr Phe Gly Asp Ala Ala Glu His Gly
 260 265 270
 Lys Asp Ala Phe Ser Asp Leu Arg Glu Gly Lys Glu Thr Thr Ile Ile
 275 280 285
 Ala Phe Ala Arg Asp Thr Ala Lys Trp Thr Asp Ile Gln Asp Asn Phe
 290 295 300
 Gly Ser Ala Asp Leu Ser Thr Ser Gln Ala Glu Arg Ile Gln His Leu
 305 310 315 320
 Leu Ile Gln Cys Gly Ala Lys Asn His Ser Leu Asn Ala Ile Ser Asp
 325 330 335
 His Leu Asn Ile Cys Arg Ser Met Ile Lys Thr Leu Ser Pro Gln Val
 340 345 350
 Asp Pro Lys Ala Gln Asn Leu Leu Leu Lys Gln Val Glu Gln Leu Ala
 355 360 365
 Ser Arg Lys Ser
 370

<210> 271

<211> 1056

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1033)

<223> RXS01879

<400> 271

ctttgcgggc cgctgatatt gatccaacgc ttcgtggcga aaagcttgat gtcactgact 60

atgtgcgcct agctgggggtg ttgcagcaaa aggatgagaa	gtg aaa att acc gct	115
	Val Lys Ile Thr Ala	
	1 5	
aag gcg tgg gcg aaa acc aac ctg cat tta ggt gtg gga ccg gct cac	163	
Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly Val Gly Pro Ala His		
	10 15 20	
gac gat gga ttt cac gag ctc atg acg gtg ttt caa acc att gat ctg	211	
Asp Asp Gly Phe His Glu Leu Met Thr Val Phe Gln Thr Ile Asp Leu		
	25 30 35	
ttt gac acc gtc acc tta acc acc ctc gat gag gag ttg gtg gag gag	259	
Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu Glu Leu Val Glu Glu		
	40 45 50	
ggg agc gtc gtc aag caa tta tct gtg acc ggt gcc cgt ggc gtg cct	307	
Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly Ala Arg Gly Val Pro		
	55 60 65	
gag gac gcc agc aat ctt gcg tgg cgc gct gtg gat gcg ttg gtt aag	355	
Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val Asp Ala Leu Val Lys		
	70 75 80 85	
cgg cgc gcg gaa aag acg ccg ctg tct gca gtt tcg ctg cat att tcc	403	
Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val Ser Leu His Ile Ser		
	90 95 100	
aag ggg att ccg gtg gct ggc ggc atg gct ggc ggc tct gcg gat gcg	451	
Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly Gly Ser Ala Asp Ala		
	105 110 115	
gct gcg aca ctg cgc gca gtg gat gcc tgg att ggg cct ttc ggc gag	499	
Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile Gly Pro Phe Gly Glu		
	120 125 130	
gac aca ttg ctg gag gtt gcc gcg gag ctc ggc tca gat gtg ccg ttt	547	
Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly Ser Asp Val Pro Phe		
	135 140 145	
tgc ctg ctt ggt ggc acc atg cgc ggt acc ggt cgc ggc gag cag ctg	595	
Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly Arg Gly Glu Gln Leu		
	150 155 160 165	
gta gat atg ttg acg cgc ggc aag cta cat tgg gtg gtg gcc gcg atg	643	
Val Asp Met Leu Thr Arg Gly Lys Leu His Trp Val Val Ala Ala Met		
	170 175 180	
gcg cat ggc ctg tcc acg cct gag gta ttc aaa aag cat gat gag ctg	691	
Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys Lys His Asp Glu Leu		
	185 190 195	
aat ccg gaa tcg cat atg gat atc agc gac ctc agc gcc gca ctt ctc	739	
Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu Ser Ala Ala Leu Leu		
	200 205 210	
acc ggc aac acc gcc gag gtg ggg cag tgg ctg cac aat gat ctg acc	787	
Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu His Asn Asp Leu Thr		
	215 220 225	

agc gcc gca ctc agt ttg cgc cct gaa ctg cgc agc gtc ctc caa gaa 835
 Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg Ser Val Leu Gln Glu
 230 235 240 245
 ggc atc cgc tcc ggc gcg cat gca gga att gtc tcc ggc tcc ggc ccg 883
 Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val Ser Gly Ser Gly Pro
 250 255 260
 acc acg gta ttc ttg tgc gaa tcg gag cac aaa gcg caa gac gtt aaa 931
 Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys Ala Gln Asp Val Lys
 265 270 275
 gag gcg cta atc gac gcc ggc cag gtg tac gct gct tac acc gcc acc 979
 Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala Ala Tyr Thr Ala Thr
 280 285 290
 ggc cct gcg gcc tca acc gcc gac cag cgc ggc gca cac att ttg act 1027
 Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly Ala His Ile Leu Thr
 295 300 305
 gtt tca taataaagac aaacttaagt atc 1056
 Val Ser
 310

<210> 272

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Val Lys Ile Thr Ala Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly
 1 5 10 15
 Val Gly Pro Ala His Asp Asp Gly Phe His Glu Leu Met Thr Val Phe
 20 25 30
 Gln Thr Ile Asp Leu Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu
 35 40 45
 Glu Leu Val Glu Glu Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly
 50 55 60
 Ala Arg Gly Val Pro Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val
 65 70 75 80
 Asp Ala Leu Val Lys Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val
 85 90 95
 Ser Leu His Ile Ser Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly
 100 105 110
 Gly Ser Ala Asp Ala Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile
 115 120 125
 Gly Pro Phe Gly Glu Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly
 130 135 140
 Ser Asp Val Pro Phe Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly
 145 150 155 160

Arg Gly Glu Gln Leu Val Asp Met Leu Thr Arg Gly Lys Leu His Trp
 165 170 175
 Val Val Ala Ala Met Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys
 180 185 190
 Lys His Asp Glu Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu
 195 200 205
 Ser Ala Ala Leu Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu
 210 215 220
 His Asn Asp Leu Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg
 225 230 235 240
 Ser Val Leu Gln Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val
 245 250 255
 Ser Gly Ser Gly Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys
 260 265 270
 Ala Gln Asp Val Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala
 275 280 285
 Ala Tyr Thr Ala Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly
 290 295 300
 Ala His Ile Leu Thr Val Ser
 305 310

<210> 273
 <211> 891
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(868)
 <223> RXS02023

<400> 273
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 gacttccgaa atgtaactag agactagagg aggaaacacg atg gct cct aaa caa 115
 Met Ala Pro Lys Gln
 1 5
 act ccc agc cca gag aag aat cga aac ctg gtg gga cca gtt ctg caa 163
 Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val Gly Pro Val Leu Gln
 10 15 20
 cgt cgg cag aca gag ggt act ttt gat caa cgc ttg cta gaa atg cgc 211
 Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg Leu Leu Glu Met Arg
 25 30 35
 gct gat cac aat tgg aag cac gcc gat cca tgg cgt gta ctg cgt att 259
 Ala Asp His Asn Trp Lys His Ala Asp Pro Trp Arg Val Leu Arg Ile
 40 45 50
 cag tct gag ttt gtg gcg ggt ttt gat gcc ctc cac gag atg cca aag 307

Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu His Glu Met Pro Lys
 55 60 65
 gcc gta acc gtc ttt ggt tcc gca cgc att aaa gag gat cac ccg tac 355
 Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys Glu Asp His Pro Tyr
 70 75 80 85
 tac aag gcg ggt gta gaa ctt ggt gaa aag ctc gtt gca gcg gac tac 403
 Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu Val Ala Ala Asp Tyr
 90 95 100
 gca gtt gtc acc ggt ggc ggt cca ggt ctg atg gaa gcc ccc aat aag 451
 Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met Glu Ala Pro Asn Lys
 105 110 115
 ggg gca agc gag gcc aat ggt tta tca gtt ggt ctg ggc att gag ttg 499
 Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly Leu Gly Ile Glu Leu
 120 125 130
 cca cat gaa cag cat ctg aac cct tat gtg gat ttg ggt ctg aac ttc 547
 Pro His Glu Gln His Leu Asn Pro Tyr Val Asp Leu Gly Leu Asn Phe
 135 140 145
 cgg tac ttc ttc gca cgc aag acc atg ttc ctg aaa tac tcc cag gct 595
 Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu Lys Tyr Ser Gln Ala
 150 155 160 165
 ttt gtg tgt ctg cct ggt ggt ttc ggc acg ctc gat gag ctt ttc gag 643
 Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu Asp Glu Leu Phe Glu
 170 175 180
 gtc ctc tgc atg gta caa acc ggc aag gta ccc aac ttt ccc atc gtg 691
 Val Leu Cys Met Val Gln Thr Gly Lys Val Pro Asn Phe Pro Ile Val
 185 190 195
 ctg atc ggc act gag ttc tgg gca ggt ttg gtg gat tgg atc cgt cac 739
 Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val Asp Trp Ile Arg His
 200 205 210
 cgc ctg gta gag gaa ggc atg atc gat gag aag gat gtt gac cgg atg 787
 Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys Asp Val Asp Arg Met
 215 220 225
 ttg gtc act gat gac ctg gat cag gcc gtc aaa ttc atc gtc gat gca 835
 Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys Phe Ile Val Asp Ala
 230 235 240 245
 cac gct gga ttg gac gta gcg cgt ctc cac aat taagcagtgg ctacattagg 888
 His Ala Gly Leu Asp Val Ala Arg Leu His Asn
 250 255
 tgt 891

<210> 274

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Ala Pro Lys Gln Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val

1	5	10	15
Gly Pro Val Leu Gln Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg	20	25	30
Leu Leu Glu Met Arg Ala Asp His Asn Trp Lys His Ala Asp Pro Trp	35	40	45
Arg Val Leu Arg Ile Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu	50	55	60
His Glu Met Pro Lys Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys	65	70	75
Glu Asp His Pro Tyr Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu	85	90	95
Val Ala Ala Asp Tyr Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met	100	105	110
Glu Ala Pro Asn Lys Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly	115	120	125
Leu Gly Ile Glu Leu Pro His Glu Gln His Leu Asn Pro Tyr Val Asp	130	135	140
Leu Gly Leu Asn Phe Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu	145	150	155
Lys Tyr Ser Gln Ala Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu	165	170	175
Asp Glu Leu Phe Glu Val Leu Cys Met Val Gln Thr Gly Lys Val Pro	180	185	190
Asn Phe Pro Ile Val Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val	195	200	205
Asp Trp Ile Arg His Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys	210	215	220
Asp Val Asp Arg Met Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys	225	230	235
Phe Ile Val Asp Ala His Ala Gly Leu Asp Val Ala Arg Leu His Asn	245	250	255

<210> 275
 <211> 1242
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1219)
 <223> RXS00948

<400> 275

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tgccctcaag ccaagctagt tgtacgatca aactcgttgt atg gca aac gtc gta 115
Met Ala Asn Val Val
1 5

cta gtc gat cga atg gag cct ttg gtg tcc aag ctg ttt acc cca att 163
Leu Val Asp Arg Met Glu Pro Leu Val Ser Lys Leu Phe Thr Pro Ile
10 15 20

caa atc cgc gac atc acc atc ccc aac cgc gtg tgg atg tca ccg atg 211
Gln Ile Arg Asp Ile Thr Ile Pro Asn Arg Val Trp Met Ser Pro Met
25 30 35

tgc acc tac tct gca gcc acc ggt tca ggt ctt ccc acc gat ttt cac 259
Cys Thr Tyr Ser Ala Ala Thr Gly Ser Gly Leu Pro Thr Asp Phe His
40 45 50

cag gct cat tac gca gct cgc gca gca ggt ggt gtc gga tta gtc atg 307
Gln Ala His Tyr Ala Ala Arg Ala Ala Gly Gly Val Gly Leu Val Met
55 60 65

gtt gaa gca act gga gtg aac ccc gta gct ccc atc tcc cca gtc gac 355
Val Glu Ala Thr Gly Val Asn Pro Val Ala Pro Ile Ser Pro Val Asp
70 75 80 85

ctt gga ctt tgg agc cat gac caa att gaa cca ttc tcc cga gtg aca 403
Leu Gly Leu Trp Ser His Asp Gln Ile Glu Pro Phe Ser Arg Val Thr
90 95 100

gca gct att cgc gcc ggt ggg gca gta ccg gcc gtt caa tta gcc cat 451
Ala Ala Ile Arg Ala Gly Gly Ala Val Pro Ala Val Gln Leu Ala His
105 110 115

gct ggc cgc aag gca tcc acc gat gct ccg tgg aat ggt ggc gga tat 499
Ala Gly Arg Lys Ala Ser Thr Asp Ala Pro Trp Asn Gly Gly Gly Tyr
120 125 130

gtt gga cca gaa acc aat gga tgg gag act gtc ggc ccc agc cct ctg 547
Val Gly Pro Glu Thr Asn Gly Trp Glu Thr Val Gly Pro Ser Pro Leu
135 140 145

gca ttc cca ggt ttg cct gct ccg cgc gag ctg acg gtt tca gaa atc 595
Ala Phe Pro Gly Leu Pro Ala Pro Arg Glu Leu Thr Val Ser Glu Ile
150 155 160 165

caa gag gtt gtg cag cag ttc gct ggc gcc gcc gtt cgt gcc gat cag 643
Gln Glu Val Val Gln Gln Phe Ala Gly Ala Ala Val Arg Ala Asp Gln
170 175 180

gct ggt ttt gat gtc gtg gaa att cac gca gca cac ggc tac ctt ttg 691
Ala Gly Phe Asp Val Val Glu Ile His Ala Ala His Gly Tyr Leu Leu
185 190 195

cat aac ttc ctt tct ccg atc tcc aac aag cgc acc gat tca tac ggc 739
His Asn Phe Leu Ser Pro Ile Ser Asn Lys Arg Thr Asp Ser Tyr Gly
200 205 210

gga tct tta gaa aac cgc gct cgc atc gtg ctc gaa gtc att gat gca 787
Gly Ser Leu Glu Asn Arg Ala Arg Ile Val Leu Glu Val Ile Asp Ala

215	220	225	
atc cgc gca gtg tgg cca gag gaa aag cct gta ttc atg cgc att tcc Ile Arg Ala Val Trp Pro Glu Glu Lys Pro Val Phe Met Arg Ile Ser 230 235 240 245			835
acc acc gac tgg gtg gag gaa aac cca cag gat gat cgc gag tcc tgg Thr Thr Asp Trp Val Glu Glu Asn Pro Gln Asp Asp Arg Glu Ser Trp 250 255 260			883
acg ctg agc caa agc agg cag ctg gct ttg tgg gca tcc gag cac gga Thr Leu Ser Gln Ser Arg Gln Leu Ala Leu Trp Ala Ser Glu His Gly 265 270 275			931
gtt gat ttg atc gat gcc tct tct ggt ggc ctc gac atc gtc ccc att Val Asp Leu Ile Asp Ala Ser Ser Gly Gly Leu Asp Ile Val Pro Ile 280 285 290			979
ccg cat gac cgc gat tac caa acc gcg aag gcc gca gat ctt cac gca Pro His Asp Arg Asp Tyr Gln Thr Ala Lys Ala Ala Asp Leu His Ala 295 300 305			1027
agt acc gga gtg aca gtc gct gct gtg ggg cgc att gat gac gcc caa Ser Thr Gly Val Thr Val Ala Ala Val Gly Arg Ile Asp Asp Ala Gln 310 315 320 325			1075
act gcg cac aat ttg gtt gat tct ggc gat gtc aat gca gtt ttc ctc Thr Ala His Asn Leu Val Asp Ser Gly Asp Val Asn Ala Val Phe Leu 330 335 340			1123
ggc cgt cca ctg ctc aag gat cct tcc tgg gca aac caa gca gcc ctc Gly Arg Pro Leu Leu Lys Asp Pro Ser Trp Ala Asn Gln Ala Ala Leu 345 350 355			1171
gca cta ggt gcg gaa ccc agg tat gtt cac caa tac gac tac gta ctt Ala Leu Gly Ala Glu Pro Arg Tyr Val His Gln Tyr Asp Tyr Val Leu 360 365 370			1219
taaaggagag ttgacatgaa ggt			1242
<210> 276			
<211> 373			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 276			
Met Ala Asn Val Val Leu Val Asp Arg Met Glu Pro Leu Val Ser Lys 1 5 10 15			
Leu Phe Thr Pro Ile Gln Ile Arg Asp Ile Thr Ile Pro Asn Arg Val 20 25 30			
Trp Met Ser Pro Met Cys Thr Tyr Ser Ala Ala Thr Gly Ser Gly Leu 35 40 45			
Pro Thr Asp Phe His Gln Ala His Tyr Ala Ala Arg Ala Ala Gly Gly 50 55 60			
Val Gly Leu Val Met Val Glu Ala Thr Gly Val Asn Pro Val Ala Pro 65 70 75 80			

[illegible]

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<210> 277
<211> 1026
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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1003)

<223> RXS02228

<400> 277

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gttgctcgct ggacttttta acttaaggga gatctagatc gtg gta aca ccg atc 115
                Val Val Thr Pro Ile
                1 5

gca gtg gtt gga ccc act gca tct gga aaa tca gct ttg gga att gct 163
Ala Val Val Gly Pro Thr Ala Ser Gly Lys Ser Ala Leu Gly Ile Ala
                10 15 20

cta gcc cac aag ctt gac ggt gaa gta gtc aat gtg gat tcc atg cag 211
Leu Ala His Lys Leu Asp Gly Glu Val Val Asn Val Asp Ser Met Gln
                25 30 35

ctg tac aaa ggc atg gac atc ggc acg gca aag ctg act gtc gaa gaa 259
Leu Tyr Lys Gly Met Asp Ile Gly Thr Ala Lys Leu Thr Val Glu Glu
                40 45 50

cgc gaa ggc att gcg cat cat cag ctc gat gtc tgg gac gtt acc gaa 307
Arg Glu Gly Ile Ala His His Gln Leu Asp Val Trp Asp Val Thr Glu
                55 60 65

act gcg tca gtg gcg agg ttt caa tcc gac gcc gtt gcc gat gtg gaa 355
Thr Ala Ser Val Ala Arg Phe Gln Ser Asp Ala Val Ala Asp Val Glu
                70 75 80 85

gat att atg tcc cgt ggc aaa acc ccc atc ttg gtt ggc ggc tcc atg 403
Asp Ile Met Ser Arg Gly Lys Thr Pro Ile Leu Val Gly Gly Ser Met
                90 95 100

ttg tac gtc caa tct ttg gtc gat gat tgg caa ttc cca cct acc gac 451
Leu Tyr Val Gln Ser Leu Val Asp Asp Trp Gln Phe Pro Pro Thr Asp
                105 110 115

agc gct gtt cgc gca cgc ttt gag gcc cgc ttg gca gac atc ggt gtc 499
Ser Ala Val Arg Ala Arg Phe Glu Ala Arg Leu Ala Asp Ile Gly Val
                120 125 130

gaa gca cta cac gct gaa ctt act cag ctt gac cca gaa gca gca gcc 547
Glu Ala Leu His Ala Glu Leu Thr Gln Leu Asp Pro Glu Ala Ala Ala
                135 140 145

gtc atc gaa agc aat gat ccc cga cgc acc gtc cga gca tta gaa gtc 595
Val Ile Glu Ser Asn Asp Pro Arg Arg Thr Val Arg Ala Leu Glu Val
                150 155 160 165

att gaa cta acc ggc cag ccc ttc caa gca agc caa ccg ccc aaa gac 643
Ile Glu Leu Thr Gly Gln Pro Phe Gln Ala Ser Gln Pro Pro Lys Asp
                170 175 180

gcg cca cct cgc tgg gga act cga atc att ggc ctg aaa acc act cca 691
Ala Pro Pro Arg Trp Gly Thr Arg Ile Ile Gly Leu Lys Thr Thr Pro

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185	190	195	
gaa tgg cta aat cca cgc atc gag cag cgc acc gcc agg atg ttt gaa			739
Glu Trp Leu Asn Pro Arg Ile Glu Gln Arg Thr Ala Arg Met Phe Glu			
200	205	210	
caa ggc ttt gtc gcc gaa gtg gaa cac ctt gtg cag caa gga ctc atc			787
Gln Gly Phe Val Ala Glu Val Glu His Leu Val Gln Gln Gly Leu Ile			
215	220	225	
gct gac tcc acc gcg gga cga gca atc ggc tac tcc caa gta ctg gca			835
Ala Asp Ser Thr Ala Gly Arg Ala Ile Gly Tyr Ser Gln Val Leu Ala			
230	235	240	245
gcc atg gca ggg gag atg acc tgg gaa gac gcc ttc gaa cgc acg gtc			883
Ala Met Ala Gly Glu Met Thr Trp Glu Asp Ala Phe Glu Arg Thr Val			
250	255	260	
acc gga acc aga cgc tat gtc agg cgc caa cgc agc tgg ttc aac aga			931
Thr Gly Thr Arg Arg Tyr Val Arg Arg Gln Arg Ser Trp Phe Asn Arg			
265	270	275	
gac cac cgc gtg tcc tgg gtc gac gcc tct ggc gat ccc acc gca caa			979
Asp His Arg Val Ser Trp Val Asp Ala Ser Gly Asp Pro Thr Ala Gln			
280	285	290	
gcc ttg gag att ttg ggt cta caa tagcggagggt gaatttgacc atc			1026
Ala Leu Glu Ile Leu Gly Leu Gln			
295	300		

<210> 278

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Val Val Thr Pro Ile Ala Val Val Gly Pro Thr Ala Ser Gly Lys Ser			
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Ala Leu Gly Ile Ala Leu Ala His Lys Leu Asp Gly Glu Val Val Asn			
20	25	30	
Val Asp Ser Met Gln Leu Tyr Lys Gly Met Asp Ile Gly Thr Ala Lys			
35	40	45	
Leu Thr Val Glu Glu Arg Glu Gly Ile Ala His His Gln Leu Asp Val			
50	55	60	
Trp Asp Val Thr Glu Thr Ala Ser Val Ala Arg Phe Gln Ser Asp Ala			
65	70	75	80
Val Ala Asp Val Glu Asp Ile Met Ser Arg Gly Lys Thr Pro Ile Leu			
85	90	95	
Val Gly Gly Ser Met Leu Tyr Val Gln Ser Leu Val Asp Asp Trp Gln			
100	105	110	
Phe Pro Pro Thr Asp Ser Ala Val Arg Ala Arg Phe Glu Ala Arg Leu			
115	120	125	

Ala Asp Ile Gly Val Glu Ala Leu His Ala Glu Leu Thr Gln Leu Asp
 130 135 140

Pro Glu Ala Ala Ala Val Ile Glu Ser Asn Asp Pro Arg Arg Thr Val
 145 150 155 160

Arg Ala Leu Glu Val Ile Glu Leu Thr Gly Gln Pro Phe Gln Ala Ser
 165 170 175

Gln Pro Pro Lys Asp Ala Pro Pro Arg Trp Gly Thr Arg Ile Ile Gly
 180 185 190

Leu Lys Thr Thr Pro Glu Trp Leu Asn Pro Arg Ile Glu Gln Arg Thr
 195 200 205

Ala Arg Met Phe Glu Gln Gly Phe Val Ala Glu Val Glu His Leu Val
 210 215 220

Gln Gln Gly Leu Ile Ala Asp Ser Thr Ala Gly Arg Ala Ile Gly Tyr
 225 230 235 240

Ser Gln Val Leu Ala Ala Met Ala Gly Glu Met Thr Trp Glu Asp Ala
 245 250 255

Phe Glu Arg Thr Val Thr Gly Thr Arg Arg Tyr Val Arg Arg Gln Arg
 260 265 270

Ser Trp Phe Asn Arg Asp His Arg Val Ser Trp Val Asp Ala Ser Gly
 275 280 285

Asp Pro Thr Ala Gln Ala Leu Glu Ile Leu Gly Leu Gln
 290 295 300

<210> 279
 <211> 954
 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXC01971

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 Met Ser Lys Lys Lys
 1 5

cct cgc ccc att ccg gtt cct gcc caa ttt atc cct ggt ctc att gat 163
 Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile Pro Gly Leu Ile Asp
 10 15 20

gcg cat aca cat ttg gca tcg tgt gga gga gat ctt gca ggg ttg gtg 211
 Ala His Thr His Leu Ala Ser Cys Gly Gly Asp Leu Ala Gly Leu Val
 25 30 35

gaa agg gcc aag gag gcg ggc gtc gaa aag ctt tgt acc gtc ggt gat 259
 Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu Cys Thr Val Gly Asp

40	45	50	
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aat gtg ttt gct gcg tgt gcg att cat ccg acg aag gct gat cag ttg Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr Lys Ala Asp Gln Leu 70 75 80 85			355
gat ggg gct gcg cgt gcg cgg ctg acg cag atg gcg gcg gat ccg aat Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met Ala Ala Asp Pro Asn 90 95 100			403
tgt gtg gcc att ggt gag act ggt ttg gat tcg tat tgg atc aag cac Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser Tyr Trp Ile Lys His 105 110 115			451
gat cca gag gac acg gcg gcg ttg gat gtg caa gag gag gcg ctg cgc Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln Glu Glu Ala Leu Arg 120 125 130			499
tgg cat att gat ttg gca att agt gcg gat aag ccg ttg atg att cac Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys Pro Leu Met Ile His 135 140 145			547
aat cgt gag gcg gat gct gat ttg atg cga gtg ttg gcg gat gct cca Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val Leu Ala Asp Ala Pro 150 155 160 165			595
cct cca aaa gat acg att ctg cat tgt ttt tct tcg ccg ttg gac gtg Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser Ser Pro Leu Asp Val 170 175 180			643
gcg aag gaa gcg ttg gat cgt gga tat gtg ttg agt ttt gcg ggc aat Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu Ser Phe Ala Gly Asn 185 190 195			691
gtg acg ttt aag cgt aat gag gag ttg ccg gag gct gct cgt att gcg Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu Ala Ala Arg Ile Ala 200 205 210			739
ccg att tcc cag att ttg att gaa acc gat gcg ccg tat atg acg ccg Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala Pro Tyr Met Thr Pro 215 220 225			787
gag ccg ttt ccg ggg agt agg aat gag ccg tcg ttg att ggt cat acg Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser Leu Ile Gly His Thr 230 235 240 245			835
gcg cta tgc att gcg gag gtt ccg ggg atg gct gtg gag gat gtt gcg Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala Val Glu Asp Val Ala 250 255 260			883
gcg gct ttg aat gag aat ttt gat, cgc gtt tat ggg gtc aca aat cta Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr Gly Val Thr Asn Leu 265 270 275			931
taacgtgagg tagctcacag tca			954

<210> 280

<211> 277

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 280

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Met Ser Lys Lys Lys Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile
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Pro Gly Leu Ile Asp Ala His Thr His Leu Ala Ser Cys Gly Gly Asp
      20           25           30

Leu Ala Gly Leu Val Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu
      35           40           45

Cys Thr Val Gly Asp Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala
      50           55           60

Ala Gln Gln Phe Gly Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr
      65           70           75           80

Lys Ala Asp Gln Leu Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met
      85           90           95

Ala Ala Asp Pro Asn Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser
      100          105          110

Tyr Trp Ile Lys His Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln
      115          120          125

Glu Glu Ala Leu Arg Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys
      130          135          140

Pro Leu Met Ile His Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val
      145          150          155          160

Leu Ala Asp Ala Pro Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser
      165          170          175

Ser Pro Leu Asp Val Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu
      180          185          190

Ser Phe Ala Gly Asn Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu
      195          200          205

Ala Ala Arg Ile Ala Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala
      210          215          220

Pro Tyr Met Thr Pro Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser
      225          230          235          240

Leu Ile Gly His Thr Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala
      245          250          255

Val Glu Asp Val Ala Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr
      260          265          270

Gly Val Thr Asn Leu
      275

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ggc gtc gtc gct tac aag atc ttg tgc atc att ggc ctt gct gtg aca	691
Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile Gly Leu Ala Val Thr	
185 190 195	
ggc tgg agc att gtc cgc att gca caa cat ttt gga gcc aac cca gca	739
Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe Gly Ala Asn Pro Ala	
200 205 210	
att gca ttg tgg att ggt gtg gcc aat cct gtg atg atc atc cac atg	787
Ile Ala Leu Trp Ile Gly Val Ala Asn Pro Val Met Ile Ile His Met	
215 220 225	
atc ggc ggc atg cac aat gaa tcc ctc atg gtg gga ttg gtc agc gtc	835
Ile Gly Gly Met His Asn Glu Ser Leu Met Val Gly Leu Val Ser Val	
230 235 240 245	
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Gly Leu Leu Leu Ala Leu Lys Lys Arg Phe Val Ala Gly Val Ala Leu	
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Ile Ala Val Ala Val Ser Leu Lys Ala Thr Ala Ala Ile Ala Leu Pro	
265 270 275	
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Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala Thr	
280 285 290	
aaa aag ggc aaa gac tcc cct acc ctt aag caa cag gtc ccc gcg ttc	1027
Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala Phe	
295 300 305	
ttt gcc act gga gct gca ggt gtt gct gtc act ggt gtt gtt gtc agt	1075
Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val Ser	
310 315 320 325	
gcg atc act tgg gcg tct ggc gct tgc tgg ggc tgg atc agt gag atc	1123
Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu Ile	
330 335 340	
agt ggc aac agc aag gta atc aac ccg ctg gct ttc cct tct ttg gtg	1171
Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu Val	
345 350 355	
gcc agt gtg atc acc atg gtg gct gaa gtg ttc gtt gac gat ttc gac	1219
Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe Asp	
360 365 370	
tac aac gca gtg gtt aat gtt gtg cgc tca atc tcc atg ctg atc atg	1267
Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile Met	
375 380 385	
ctt ggc ggg ttg gtc gta tgt tgg tgg ctg ttc cgc cag aac gaa cgc	1315
Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu Arg	
390 395 400 405	
agg gcg gtc act ggt aca gca gcg gct tat gcc gtg gct ttt gtg ttc	1363
Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val Phe	
410 415 420	
aat tct gtg acc ttg ccg tgg tac tac gcc agc ttg atc tct ttg ctc	1411

Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu Leu
 425 430 435

ggc aca ttt aaa cca ccg atg tgg ttg att cgc ttc gca gcg ggt gct 1459
 Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly Ala
 440 445 450

tcg gtg ttt atc gcg ctg atg ttt acc gga agt gga aac cac cag ctg 1507
 Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln Leu
 455 460 465

tac aac atc gtt acg gtg atc atc gca gca att atc gcg tgg ctt gcc 1555
 Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu Ala
 470 475 480 485

acc gtg gtg atc ttt gat gac act gac cct gca aca acg gcc acg gag 1603
 Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr Glu
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<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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Tyr Arg Gly Gly Val Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe
 35 40 45

Gly His Ala Gln Gly Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu
 50 55 60

Leu Leu Ile Gly Ala Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys
 65 70 75 80

Lys Val Ala Asp Asp Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys
 85 90 95

Arg Thr Leu Tyr Ala Met Val Val Pro Leu Ile Phe Ala Ala Pro Met
 100 105 110

Met Ser Arg Asp Val Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg
 115 120 125

Asp Gly Phe Asp Pro Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro
 130 135 140

Met Leu Leu Glu Val Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr
 145 150 155 160

Gly Pro Leu His Leu Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly

165										170					175				
Asp	Asn	Val	Thr	Leu	Gly	Val	Val	Ala	Tyr	Lys	Ile	Leu	Ser	Ile	Ile				
			180					185					190						
Gly	Leu	Ala	Val	Thr	Gly	Trp	Ser	Ile	Val	Arg	Ile	Ala	Gln	His	Phe				
		195					200					205							
Gly	Ala	Asn	Pro	Ala	Ile	Ala	Leu	Trp	Ile	Gly	Val	Ala	Asn	Pro	Val				
	210					215					220								
Met	Ile	Ile	His	Met	Ile	Gly	Gly	Met	His	Asn	Glu	Ser	Leu	Met	Val				
225					230					235					240				
Gly	Leu	Val	Ser	Val	Gly	Leu	Leu	Leu	Ala	Leu	Lys	Lys	Arg	Phe	Val				
				245					250					255					
Ala	Gly	Val	Ala	Leu	Ile	Ala	Val	Ala	Val	Ser	Leu	Lys	Ala	Thr	Ala				
			260					265					270						
Ala	Ile	Ala	Leu	Pro	Phe	Val	Val	Trp	Ile	Gly	Met	His	His	Phe	Ala				
		275					280					285							
Gly	Phe	Leu	Ala	Thr	Lys	Lys	Gly	Lys	Asp	Ser	Pro	Thr	Leu	Lys	Gln				
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Gln	Val	Pro	Ala	Phe	Phe	Ala	Thr	Gly	Ala	Ala	Gly	Val	Ala	Val	Thr				
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Trp	Ile	Ser	Glu	Ile	Ser	Gly	Asn	Ser	Lys	Val	Ile	Asn	Pro	Leu	Ala				
			340					345					350						
Phe	Pro	Ser	Leu	Val	Ala	Ser	Val	Ile	Thr	Met	Val	Ala	Glu	Val	Phe				
		355					360					365							
Val	Asp	Asp	Phe	Asp	Tyr	Asn	Ala	Val	Val	Asn	Val	Val	Arg	Ser	Ile				
	370					375					380								
Ser	Met	Leu	Ile	Met	Leu	Gly	Gly	Leu	Val	Val	Cys	Trp	Trp	Leu	Phe				
385					390					395					400				
Arg	Gln	Asn	Glu	Arg	Arg	Ala	Val	Thr	Gly	Thr	Ala	Ala	Ala	Tyr	Ala				
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Val	Ala	Phe	Val	Phe	Asn	Ser	Val	Thr	Leu	Pro	Trp	Tyr	Tyr	Ala	Ser				
			420					425					430						
Leu	Ile	Ser	Leu	Leu	Gly	Thr	Phe	Lys	Pro	Pro	Met	Trp	Leu	Ile	Arg				
		435					440					445							
Phe	Ala	Ala	Gly	Ala	Ser	Val	Phe	Ile	Ala	Leu	Met	Phe	Thr	Gly	Ser				
	450					455					460								
Gly	Asn	His	Gln	Leu	Tyr	Asn	Ile	Val	Thr	Val	Ile	Ile	Ala	Ala	Ile				
465					470					475					480				
Ile	Ala	Trp	Leu	Ala	Thr	Val	Val	Ile	Phe	Asp	Asp	Thr	Asp	Pro	Ala				
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<210> 283
<211> 1298
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(1275)
<223> RXN01946

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tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96
Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu
20 25 30
gag gca cgc atc ctc gac cag cag ctt aaa acc ctg tcc ggc ggc cag 144
Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
35 40 45
cgc cgc cgc gtc gag ttg gcg cag atc ctc ttc gcc gcc acc aac ggc 192
Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
50 55 60
tcc ggc aaa tca aaa acc aca ttg ctt ctc gac gag ccc acc aac cac 240
Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His
65 70 75 80
ttg gac gca gac tcg atc acc tgg ctc cgt gac ttc ctg gcg aag cac 288
Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His
85 90 95
gaa ggt gga ctg atc atg att tcg cac gac gtc gaa ctg ctt ggc gcc 336
Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Gly Ala
100 105 110
gta tgt aac aag att tgg tac ctc gac gca gta cgc agc gaa gcc gat 384
Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp
115 120 125
gtc tac aac atg ggc ttt agc aaa tac gtc gat gca cgt gca ctc gat 432
Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp
130 135 140
gaa gca cgc cga cgc cgt gag cgc gca aac gcc gaa aag aag gcc gga 480
Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly
145 150 155 160
gcc ctc aag gac cag gct gca cgc ctc ggc gcg aaa gca acc aag gct 528
Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala
165 170 175
gcc gca gct aag cag atg atc gcc cgt gcg gaa cga atg atc gac aac 576

Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn	
180 185 190	
ctc gac gaa atc cgc gta gct gac cgc gcc gcc aac atc gtt ttc cca	624
Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro	
195 200 205	
gaa cca gca ccc tgt gga aaa acc cca ctc aac gcc aag ggc ctg acc	672
Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr	
210 215 220	
aag atg tac ggc tcc ctc gaa gtc ttc gcc ggc gtc gac cta gcc atc	720
Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile	
225 230 235 240	
gac aaa ggc tcc cgc gta gtc gtc ctc gga ttc aac ggt gca ggt aaa	768
Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys	
245 250 255	
acc acc ctg ctc aaa ctc ctc gcc ggt gtg gaa cgc acc gac ggc gaa	816
Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu	
260 265 270	
ggc ggc atc gtc acc gga tac ggc ctc aaa atc ggc tac ttc gcc cag	864
Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln	
275 280 285	
gaa cac gac acc atc gac ccc gac aaa tcc gtc tgg caa aac acc atc	912
Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile	
290 295 300	
gaa gcc tgc gcc gac gcc gac caa caa agc ctc cgc agc ctc ctc gga	960
Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly	
305 310 315 320	
tcc ttc atg ttc tcc ggc gaa caa ctc gac caa cca gca gga aca ctc	1008
Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu	
325 330 335	
tcc ggc ggt gaa aaa acc cgc ctc gca ctg gcc acc ctc gtg tcc tcc	1056
Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser	
340 345 350	
cgc gca aac gtc ctg ctt ctc gac gag ccc acc aac aac ctt gac ccg	1104
Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro	
355 360 365	
atc tcc cgc gaa cag gtc ctc gac gca ctg cgc acc tac acc ggc gca	1152
Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala	
370 375 380	
gtc gtc ctg gtt acc cac gac ccg ggt gca gtc aag gcc ctt gag cca	1200
Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro	
385 390 395 400	
gaa cgc gtc atc gtg ctt cct gat ggc acc gag gat ctt tgg aat gat	1248
Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp	
405 410 415	
cag tac atg gaa atc gtg gaa ttg gcg taggttctaa ggctgtttat	1295
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420

425

gct

1298

<210> 284

<211> 425

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

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          20           25           30
Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
          35           40           45
Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
          50           55           60
Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His
          65           70           75           80
Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His
          85           90           95
Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala
          100           105           110
Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp
          115           120           125
Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp
          130           135           140
Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly
          145           150           155           160
Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala
          165           170           175
Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn
          180           185           190
Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro
          195           200           205
Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr
          210           215           220
Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile
          225           230           235           240
Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys
          245           250           255
Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu
          260           265           270

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Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln
275 280 285

Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile
290 295 300

Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly
305 310 315 320

Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu
325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser
340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro
355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala
370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro
385 390 395 400

Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp
405 410 415

Gln Tyr Met Glu Ile Val Glu Leu Ala
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<210> 285

<211> 1298

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1275)

<223> FRXA01946

<400> 285

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tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96
Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu
20 25 30

gag gca cgc atc ctc gac cag cag ctt aaa acc ctg tcc ggc ggc cag 144
Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
35 40 45

cgc cgc cgc gtc gag ttg gcg cag atc ctc ttc gcc gcc acc aac ggc 192
Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
50 55 60

tcc ggc aaa tca aaa acc aca ttg ctt ctc gac gag ccc acc aac cac 240
Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His

65	70	75	80
ttg gac gca gac tcg atc acc tgg ctc cgt gac ttc ctg gcg aag cac Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His	85	90	95
gaa ggt gga ctg atc atg att tcg cac gac gtc gaa ctg ctt ggc gcc Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala	100	105	110
gta tgt aac aag att tgg tac ctc gac gca gta cgc agc gaa gcc gat Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp	115	120	125
gtc tac aac atg ggc ttt agc aaa tac gtc gat gca cgt gca ctc gat Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp	130	135	140
gaa gca cgc cga cgc cgt gag cgc gca aac gcc gaa aag aag gcc gga Glu Ala Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly	145	150	155
gcc ctc aag gac cag gct gca cgc ctc ggc gcg aaa gca acc aag gct Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala	165	170	175
gcc gca gct aag cag atg atc gcc cgt gcg gaa cga atg atc gac aac Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn	180	185	190
ctc gac gaa atc cgc gta gct gac cgc gcc gcc aac atc gtt ttc cca Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro	195	200	205
gaa cca gca ccc tgt gga aaa acc cca ctc aac gcc aag ggc ctg acc Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr	210	215	220
aag atg tac ggc tcc ctc gaa gtc ttc gcc ggc gtc gac cta gcc atc Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile	225	230	235
gac aaa ggc tcc cgc gta gtc gtc ctc gga ttc aac ggt gca ggt aaa Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys	245	250	255
acc acc ctg ctc aaa ctc ctc gcc ggt gtg gaa cgc acc gac ggc gaa Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu	260	265	270
ggc ggc atc gtc acc gga tac ggc ctc aaa atc ggc tac ttc gcc cag Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln	275	280	285
gaa cac gac acc atc gac ccc gac aaa tcc gtc tgg caa aac acc atc Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile	290	295	300
gaa gcc tgc gcc gac gcc gac caa caa agc ctc cgc agc ctc ctc gga Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly	305	310	315
			320

tcc ttc atg ttc tcc ggc gaa caa ctc gac caa cca gca gga aca ctc 1008
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu
 325 330 335

tcc ggc ggt gaa aaa acc cgc ctc gca ctg gcc acc ctc gtg tcc tcc 1056
 Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser
 340 345 350

cgc gca aac gtc ctg ctt ctc gac gag ccc acc aac aac ctt gac ccg 1104
 Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro
 355 360 365

atc tcc cgc gaa cag gtc ctc gac gca ctg cgc acc tac acc ggc gca 1152
 Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala
 370 375 380

gtc gtc ctg gtt acc cac gac ccg ggt gca gtc aag gcc ctt gag cca 1200
 Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro
 385 390 395 400

gaa cgc gtc atc gtg ctt cct gat ggc acc gag gat ctt tgg aat gat 1248
 Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp
 405 410 415

cag tac atg gaa atc gtg gaa ttg gcg taggttctaa ggctgtttat 1295
 Gln Tyr Met Glu Ile Val Glu Leu Ala
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gct 1298

<210> 286

<211> 425

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

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 20 25 30

Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
 35 40 45

Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
 50 55 60

Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His
 65 70 75 80

Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His
 85 90 95

Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala
 100 105 110

Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp
 115 120 125

Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp
 130 135 140
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly
 145 150 155 160
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala
 165 170 175
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn
 180 185 190
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro
 195 200 205
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr
 210 215 220
 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile
 225 230 235 240
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys
 245 250 255
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu
 260 265 270
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln
 275 280 285
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile
 290 295 300
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly
 305 310 315 320
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu
 325 330 335
 Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser
 340 345 350
 Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro
 355 360 365
 Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala
 370 375 380
 Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro
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 405 410 415
 Gln Tyr Met Glu Ile Val Glu Leu Ala
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<210> 287

<211> 1812

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1789)

<223> RXN00164

<400> 287

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                               Val Gly Arg Ile Pro
                               1 5

cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163
Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly
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gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211
Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu Gly Arg Ile Val Asp
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ctg gtg tcc gat ggc gcg cag atg cgt gat ttt gtt gag ctc agt gtg 259
Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe Val Glu Leu Ser Val
                               40 45 50

att ctc att gcg gtg gca att gcc ggc gcg gtg ctc agt gcg tgc ggg 307
Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val Leu Ser Ala Cys Gly
                               55 60 65

ttc tat gtg gtg tcg cgg att tct gag aag att atc gcc aat ttg agg 355
Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile Ile Ala Asn Leu Arg
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Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro Thr His Gln Val Glu
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gat gcg ggc tct ggc gat ttg gtg agc cgc tcc acc gat gat gtc tcc 451
Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser Thr Asp Asp Val Ser
                               105 110 115

gag cta tcc gca gcg gtg aca gag acc gtc ccg att tta agt tcc tca 499
Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro Ile Leu Ser Ser Ser
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ctg ttt acc att gcc gcg acg atc att gcg ctg ttt tct ttg gac tgg 547
Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu Phe Ser Leu Asp Trp
                               135 140 145

caa ttt gtg ctc att cct gtc gtg gtg gcg ccg gtg tac tac ttc gcg 595
Gln Phe Val Leu Ile Pro Val Val Val Ala Pro Val Tyr Tyr Phe Ala
                               150 155 160 165

tcc aag cac tat ttg agc aag gcg ccg gat cgg tat gcg gca gaa cgc 643
Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg Tyr Ala Ala Glu Arg
                               170 175 180

gcg gcg atg gcg gag cgt gcg cga aag gta ctt gag gct att cgc ggg 691
Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu Glu Ala Ile Arg Gly

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185	190	195	
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att gat cag gcg tcg tgg tct gtg gtg gtc aag ggt att cgt gcg cgc Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys Gly Ile Arg Ala Arg 215 220 225			787
acc acc atg ttg att ttg aac atg tgg atg ctg ttt gcg gaa ttc ctc Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu Phe Ala Glu Phe Leu 230 235 240 245			835
atg ctc gcg gtc gcg ttg gtg atc ggc tac aag ctg gtc att gat aat Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys Leu Val Ile Asp Asn 250 255 260			883
gcg ctg acg atc ggc gcg gtt acc ggt gcc gtg ctg atg att att cgt Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val Leu Met Ile Ile Arg 265 270 275			931
ctg cgt ggc ccg atg aat atg ttc atg cgc gtg ctc gac acc att caa Leu Arg Gly Pro Met Asn Met Phe Met Arg Val Leu Asp Thr Ile Gln 280 285 290			979
tcc ggc tat gcg tcg ctg gcg cgc atc gtg gga gtt gtt gcg gat ccg Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly Val Val Ala Asp Pro 295 300 305			1027
ccg att cct gtg ccc gac agc ggt gtg aaa gca cct cag ggc aaa gtg Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala Pro Gln Gly Lys Val 310 315 320 325			1075
gaa ttg cgc aac gtc agc ttt agc tat ggc gat tcc tgg gcg gtg aaa Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp Ser Trp Ala Val Lys 330 335 340			1123
gac atc gac atc acg atc aat tcc ggc gaa act gtc gcg ctc gtg ggc Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr Val Ala Leu Val Gly 345 350 355			1171
gca tct ggc gca ggt aag acg acg gtc gcc gcc ttg ctg gcg ggc ttg Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala Leu Leu Ala Gly Leu 360 365 370			1219
cggt gtg cca gat caa ggg caa gtg ctt gtc gac gac ttc ccc gtc tct Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp Asp Phe Pro Val Ser 375 380 385			1267
cac ctc tct gac cgc gag cgt atc gcc cgc ttg gcc atg gtc agc cag His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu Ala Met Val Ser Gln 390 395 400 405			1315
gag gtt cat gtt ttc tcc ggc acg ctg cgc cag gat ctc acc ttg gct Glu Val His Val Phe Ser Gly Thr Leu Arg Gln Asp Leu Thr Leu Ala 410 415 420			1363
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 Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val Val Ala Gln Gln Leu
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 gcg ttg gcc cgg gtg ttg ttg ctc aat ccg gcg atc gtc atc atg gat 1555
 Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala Ile Val Ile Met Asp
 470 475 480 485
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 Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala Ser Ala Leu Glu Glu
 490 495 500
 gct gca gat gca gtg agc aag aac cgt tcc gca ttg gtg gtg gcg cac 1651
 Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala Leu Val Val Ala His
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 cgg ttg gat cag gca tgc cgg gct gat cag att ctg gtg atg gat aag 1699
 Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys
 520 525 530
 ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg 1747
 Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly
 535 540 545
 ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga 1789
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 tagttgactg ttcaatgcgt tga 1812

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<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

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 35 40 45
 Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val
 50 55 60
 Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile
 65 70 75 80
 Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro
 85 90 95
 Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser

100					105					110						
Thr	Asp	Asp	Val	Ser	Glu	Leu	Ser	Ala	Ala	Val	Thr	Glu	Thr	Val	Pro	
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Ile	Leu	Ser	Ser	Ser	Leu	Phe	Thr	Ile	Ala	Ala	Thr	Ile	Ile	Ala	Leu	
130					135					140						
Phe	Ser	Leu	Asp	Trp	Gln	Phe	Val	Leu	Ile	Pro	Val	Val	Val	Ala	Pro	
145					150					155					160	
Val	Tyr	Tyr	Phe	Ala	Ser	Lys	His	Tyr	Leu	Ser	Lys	Ala	Pro	Asp	Arg	
165					170					175						
Tyr	Ala	Ala	Glu	Arg	Ala	Ala	Met	Ala	Glu	Arg	Ala	Arg	Lys	Val	Leu	
180					185					190						
Glu	Ala	Ile	Arg	Gly	Arg	Ala	Thr	Val	Arg	Ala	Tyr	Ser	Met	Glu	Asp	
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Ala	Met	His	Asn	Gln	Ile	Asp	Gln	Ala	Ser	Trp	Ser	Val	Val	Val	Lys	
210					215					220						
Gly	Ile	Arg	Ala	Arg	Thr	Thr	Met	Leu	Ile	Leu	Asn	Met	Trp	Met	Leu	
225					230					235					240	
Phe	Ala	Glu	Phe	Leu	Met	Leu	Ala	Val	Ala	Leu	Val	Ile	Gly	Tyr	Lys	
245					250					255						
Leu	Val	Ile	Asp	Asn	Ala	Leu	Thr	Ile	Gly	Ala	Val	Thr	Gly	Ala	Val	
260					265					270						
Leu	Met	Ile	Ile	Arg	Leu	Arg	Gly	Pro	Met	Asn	Met	Phe	Met	Arg	Val	
275					280					285						
Leu	Asp	Thr	Ile	Gln	Ser	Gly	Tyr	Ala	Ser	Leu	Ala	Arg	Ile	Val	Gly	
290					295					300						
Val	Val	Ala	Asp	Pro	Pro	Ile	Pro	Val	Pro	Asp	Ser	Gly	Val	Lys	Ala	
305					310					315					320	
Pro	Gln	Gly	Lys	Val	Glu	Leu	Arg	Asn	Val	Ser	Phe	Ser	Tyr	Gly	Asp	
325					330					335						
Ser	Trp	Ala	Val	Lys	Asp	Ile	Asp	Ile	Thr	Ile	Asn	Ser	Gly	Glu	Thr	
340					345					350						
Val	Ala	Leu	Val	Gly	Ala	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Val	Ala	Ala	
355					360					365						
Leu	Leu	Ala	Gly	Leu	Arg	Val	Pro	Asp	Gln	Gly	Gln	Val	Leu	Val	Asp	
370					375					380						
Asp	Phe	Pro	Val	Ser	His	Leu	Ser	Asp	Arg	Glu	Arg	Ile	Ala	Arg	Leu	
385					390					395					400	
Ala	Met	Val	Ser	Gln	Glu	Val	His	Val	Phe	Ser	Gly	Thr	Leu	Arg	Gln	
405					410					415						
Asp	Leu	Thr	Leu	Ala	Lys	Pro	Asp	Ala	Ser	Asp	Glu	Glu	Leu	Ala	His	
420					425					430						

Ala Leu Gly Gln Val Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu
435 440 445

Gly Leu Asp Thr Val Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val
450 455 460

Val Ala Gln Gln Leu Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala
465 470 475 480

Ile Val Ile Met Asp Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala
485 490 495

Ser Ala Leu Glu Glu Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala
500 505 510

Leu Val Val Ala His Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile
515 520 525

Leu Val Met Asp Lys Gly Glu Val Val Glu Ser Gly Thr His Gln Glu
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Val Gly Arg

<210> 289

<211> 1812

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1789)

<223> FRXA00164

<400> 289

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Val Gly Arg Ile Pro
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cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163
Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly
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gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211
Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu Gly Arg Ile Val Asp
25 30 35

ctg gtg tcc gat ggc gcg cag atg cgt gat ttt gtt gag ctc agt gtg 259
Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe Val Glu Leu Ser Val
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att ctc att gcg gtg gca att gcc ggc gcg gtg ctc agt gcg tgc ggg 307
Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val Leu Ser Ala Cys Gly
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Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile Ile Ala Asn Leu Arg	
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gaa gat atg gtg ggc acc gcg ctt ggg ttg ccc acg cac cag gtg gaa	403
Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro Thr His Gln Val Glu	
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Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser Thr Asp Asp Val Ser	
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Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro Ile Leu Ser Ser Ser	
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Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu Phe Ser Leu Asp Trp	
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Gln Phe Val Leu Ile Pro Val Val Val Ala Pro Val Tyr Tyr Phe Ala	
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Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg Tyr Ala Ala Glu Arg	
170 175 180	
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Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu Glu Ala Ile Arg Gly	
185 190 195	
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Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp Ala Met His Asn Gln	
200 205 210	
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Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys Gly Ile Arg Ala Arg	
215 220 225	
acc acc atg ttg att ttg aac atg tgg atg ctg ttt gcg gaa ttc ctc	835
Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu Phe Ala Glu Phe Leu	
230 235 240 245	
atg ctc gcg gtc gcg ttg gtg atc ggc tac aag ctg gtc att gat aat	883
Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys Leu Val Ile Asp Asn	
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gcg ctg acg atc ggc gcg gtt acc ggt gcc gtg ctg atg att att cgt	931
Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val Leu Met Ile Ile Arg	
265 270 275	
ctg cgt ggc ccg atg aat atg ttc atg cgc gtg ctc gac acc att caa	979
Leu Arg Gly Pro Met Asn Met Phe Met Arg Val Leu Asp Thr Ile Gln	
280 285 290	
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Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly Val Val Ala Asp Pro	
295 300 305	

ccg att cct gtg ccc gac agc ggt gtg aaa gca cct cag ggc aaa gtg	1075
Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala Pro Gln Gly Lys Val	
310 315 320 325	
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Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp Ser Trp Ala Val Lys	
330 335 340	
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Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr Val Ala Leu Val Gly	
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gca tct ggc gca ggt aag acg acg gtc gcc gcc ttg ctg gcg ggc ttg	1219
Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala Leu Leu Ala Gly Leu	
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Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp Asp Phe Pro Val Ser	
375 380 385	
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His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu Ala Met Val Ser Gln	
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Glu Val His Val Phe Ser Gly Thr Leu Arg Gln Asp Leu Thr Leu Ala	
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Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His Ala Leu Gly Gln Val	
425 430 435	
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Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu Gly Leu Asp Thr Val	
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Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val Val Ala Gln Gln Leu	
455 460 465	
gcg ttg gcc cgg gtg ttg ttg ctc aat ccg gcg atc gtc atc atg gat	1555
Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala Ile Val Ile Met Asp	
470 475 480 485	
gaa gcc acg gca gaa gca gga tcg gcg ggt gcc agc gca ctg gaa gag	1603
Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala Ser Ala Leu Glu Glu	
490 495 500	
gct gca gat gca gtg agc aag aac cgt tcc gca ttg gtg gtg gcg cac	1651
Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala Leu Val Val Ala His	
505 510 515	
cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag	1699
Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys	
520 525 530	
ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg	1747
Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly	
535 540 545	
ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga	1789

Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser Val Gly Arg
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1812

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<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Leu Leu Ser Ala Gly Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu
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Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe
 35 40 45

Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val
 50 55 60

Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile
 65 70 75 80

Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro
 85 90 95

Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser
 100 105 110

Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro
 115 120 125

Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu
 130 135 140

Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro
 145 150 155 160

Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg
 165 170 175

Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu
 180 185 190

Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp
 195 200 205

Ala Met His Asn Gln Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys
 210 215 220

Gly Ile Arg Ala Arg Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu
 225 230 235 240

Phe Ala Glu Phe Leu Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys
 245 250 255

Leu Val Ile Asp Asn Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val

260					265					270					
Leu	Met	Ile	Ile	Arg	Leu	Arg	Gly	Pro	Met	Asn	Met	Phe	Met	Arg	Val
		275					280					285			
Leu	Asp	Thr	Ile	Gln	Ser	Gly	Tyr	Ala	Ser	Leu	Ala	Arg	Ile	Val	Gly
	290					295					300				
Val	Val	Ala	Asp	Pro	Pro	Ile	Pro	Val	Pro	Asp	Ser	Gly	Val	Lys	Ala
305					310					315					320
Pro	Gln	Gly	Lys	Val	Glu	Leu	Arg	Asn	Val	Ser	Phe	Ser	Tyr	Gly	Asp
				325					330					335	
Ser	Trp	Ala	Val	Lys	Asp	Ile	Asp	Ile	Thr	Ile	Asn	Ser	Gly	Glu	Thr
			340					345					350		
Val	Ala	Leu	Val	Gly	Ala	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Val	Ala	Ala
		355					360					365			
Leu	Leu	Ala	Gly	Leu	Arg	Val	Pro	Asp	Gln	Gly	Gln	Val	Leu	Val	Asp
	370					375					380				
Asp	Phe	Pro	Val	Ser	His	Leu	Ser	Asp	Arg	Glu	Arg	Ile	Ala	Arg	Leu
385					390					395					400
Ala	Met	Val	Ser	Gln	Glu	Val	His	Val	Phe	Ser	Gly	Thr	Leu	Arg	Gln
				405					410					415	
Asp	Leu	Thr	Leu	Ala	Lys	Pro	Asp	Ala	Ser	Asp	Glu	Glu	Leu	Ala	His
			420					425					430		
Ala	Leu	Gly	Gln	Val	Asn	Ala	Leu	Asp	Trp	Leu	Glu	Ser	Leu	Pro	Glu
		435					440					445			
Gly	Leu	Asp	Thr	Val	Val	Gly	Ala	Arg	Gly	Ile	Gln	Leu	Glu	Pro	Val
	450					455					460				
Val	Ala	Gln	Gln	Leu	Ala	Leu	Ala	Arg	Val	Leu	Leu	Leu	Asn	Pro	Ala
465					470					475					480
Ile	Val	Ile	Met	Asp	Glu	Ala	Thr	Ala	Glu	Ala	Gly	Ser	Ala	Gly	Ala
				485					490					495	
Ser	Ala	Leu	Glu	Glu	Ala	Ala	Asp	Ala	Val	Ser	Lys	Asn	Arg	Ser	Ala
			500					505					510		
Leu	Val	Val	Ala	His	Arg	Leu	Asp	Gln	Ala	Ser	Arg	Ala	Asp	Gln	Ile
			515				520					525			
Leu	Val	Met	Asp	Lys	Gly	Glu	Val	Val	Glu	Ser	Gly	Thr	His	Gln	Glu
	530					535					540				
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Val	Gly	Arg													

<210> 291

<211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1117)
 <223> RXN00243

<400> 291

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ttaacaaagc agcccatgat ggaaatgaag aggaacagaa gtg acc agc gaa caa 115
                               Val Thr Ser Glu Gln
                               1      5

gct tta gat cct atc cac cca ggt cag ttc cgt ctt tct cgg att cag 163
Ala Leu Asp Pro Ile His Pro Gly Gln Phe Arg Leu Ser Arg Ile Gln
                               10      15      20

ttg atc aac tgg gga acc ttc cac gga acg gtg gac att cct gtg acc 211
Leu Ile Asn Trp Gly Thr Phe His Gly Thr Val Asp Ile Pro Val Thr
                               25      30      35

agg gaa gga atc tta gtt acc ggt ggt tcg gga tca gga aaa tcc acg 259
Arg Glu Gly Ile Leu Val Thr Gly Gly Ser Gly Ser Gly Lys Ser Thr
                               40      45      50

ctg att gat gcg atc acg gcg gta ttg ctt ccg caa gga aag ctg agg 307
Leu Ile Asp Ala Ile Thr Ala Val Leu Leu Pro Gln Gly Lys Leu Arg
                               55      60      65

ttt aac tct gcc gca cag gct aat act ccg cgg aat aag gga cgc agt 355
Phe Asn Ser Ala Ala Gln Ala Asn Thr Pro Arg Asn Lys Gly Arg Ser
                               70      75      80      85

ttg gtt acc tat atc cgt ggc gct tgg cgt gcg cag gag gat ccg ctg 403
Leu Val Thr Tyr Ile Arg Gly Ala Trp Arg Ala Gln Glu Asp Pro Leu
                               90      95      100

cag gat cag att gtc tcc acg tac cta cgt ccc cgc gca acc tat tcg 451
Gln Asp Gln Ile Val Ser Thr Tyr Leu Arg Pro Arg Ala Thr Tyr Ser
                               105      110      115

ctg gtt gga ttg act tat tcc aac ggt gaa ggc gtc gag cac acc ttg 499
Leu Val Gly Leu Thr Tyr Ser Asn Gly Glu Gly Val Glu His Thr Leu
                               120      125      130

gtg gct att ttc tat ctg aaa tcg gga cac aat tta acc tcc gat att 547
Val Ala Ile Phe Tyr Leu Lys Ser Gly His Asn Leu Thr Ser Asp Ile
                               135      140      145

tct tca tat tat ggt gtg ttt ccc gtt gat caa gac atc aat gcg ctg 595
Ser Ser Tyr Tyr Gly Val Phe Pro Val Asp Gln Asp Ile Asn Ala Leu
                               150      155      160      165

ctg gat ttc ctg aaa gag ggc atc gat aaa cgc cag atc aga gct gct 643
Leu Asp Phe Leu Lys Glu Gly Ile Asp Lys Arg Gln Ile Arg Ala Ala
                               170      175      180

ttc aag gaa gcc atc ttt agc gag cag cat tct gta ttc tcc ggc agg 691

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Phe Lys Glu Ala Ile Phe Ser Glu Gln His Ser Val Phe Ser Gly Arg
 185 190 195
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 Phe Arg Ser Arg Leu Gly Ile Ser Ser Glu Glu Ala Leu Leu Leu Leu
 200 205 210
 cac cgc gcg cag tcg gcg aaa gat ctt caa agc ttg gat gat cta ttt 787
 His Arg Ala Gln Ser Ala Lys Asp Leu Gln Ser Leu Asp Asp Leu Phe
 215 220 225
 cgg gat tac atg ctg gtg gaa ccg gat acg ttc agc att gcc aaa act 835
 Arg Asp Tyr Met Leu Val Glu Pro Asp Thr Phe Ser Ile Ala Lys Thr
 230 235 240 245
 gcc gtg gaa caa ttc caa gac ctt gaa ggt gct tat gag cag gtc gaa 883
 Ala Val Glu Gln Phe Gln Asp Leu Glu Gly Ala Tyr Glu Gln Val Glu
 250 255 260
 gat att aaa cgg cag atc cac acc ctg gat cct ttg gtg cag ctg aag 931
 Asp Ile Lys Arg Gln Ile His Thr Leu Asp Pro Leu Val Gln Leu Lys
 265 270 275
 aat cgg cga gag aaa gcg caa cag tcc aaa gat cat gcc aat gca ctg 979
 Asn Arg Arg Glu Lys Ala Gln Gln Ser Lys Asp His Ala Asn Ala Leu
 280 285 290
 aag aag gcg ctg ccg act gtc ggg aat cgc att aag aag gaa gag caa 1027
 Lys Lys Ala Leu Pro Thr Val Gly Asn Arg Ile Lys Lys Glu Glu Gln
 295 300 305
 gaa ccg ctg gtt cga caa ttt act gtc gag caa acg cag cga agt cga 1075
 Glu Pro Leu Val Arg Gln Phe Thr Val Glu Gln Thr Gln Arg Ser Arg
 310 315 320 325
 agg tgg agt ccg cca aaa ttg aga cag atc gtg ccc gcg aaa 1117
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 tgaaaaccct cgcgcacgac aac 1140
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 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 292
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 Asp Ile Pro Val Thr Arg Glu Gly Ile Leu Val Thr Gly Gly Ser Gly
 35 40 45
 Ser Gly Lys Ser Thr Leu Ile Asp Ala Ile Thr Ala Val Leu Leu Pro
 50 55 60
 Gln Gly Lys Leu Arg Phe Asn Ser Ala Ala Gln Ala Asn Thr Pro Arg

65	70	75	80
Asn Lys Gly Arg Ser Leu Val Thr Tyr Ile Arg Gly Ala Trp Arg Ala	85	90	95
Gln Glu Asp Pro Leu Gln Asp Gln Ile Val Ser Thr Tyr Leu Arg Pro	100	105	110
Arg Ala Thr Tyr Ser Leu Val Gly Leu Thr Tyr Ser Asn Gly Glu Gly	115	120	125
Val Glu His Thr Leu Val Ala Ile Phe Tyr Leu Lys Ser Gly His Asn	130	135	140
Leu Thr Ser Asp Ile Ser Ser Tyr Tyr Gly Val Phe Pro Val Asp Gln	145	150	155
Asp Ile Asn Ala Leu Leu Asp Phe Leu Lys Glu Gly Ile Asp Lys Arg	165	170	175
Gln Ile Arg Ala Ala Phe Lys Glu Ala Ile Phe Ser Glu Gln His Ser	180	185	190
Val Phe Ser Gly Arg Phe Arg Ser Arg Leu Gly Ile Ser Ser Glu Glu	195	200	205
Ala Leu Leu Leu Leu His Arg Ala Gln Ser Ala Lys Asp Leu Gln Ser	210	215	220
Leu Asp Asp Leu Phe Arg Asp Tyr Met Leu Val Glu Pro Asp Thr Phe	225	230	235
Ser Ile Ala Lys Thr Ala Val Glu Gln Phe Gln Asp Leu Glu Gly Ala	245	250	255
Tyr Glu Gln Val Glu Asp Ile Lys Arg Gln Ile His Thr Leu Asp Pro	260	265	270
Leu Val Gln Leu Lys Asn Arg Arg Glu Lys Ala Gln Gln Ser Lys Asp	275	280	285
His Ala Asn Ala Leu Lys Lys Ala Leu Pro Thr Val Gly Asn Arg Ile	290	295	300
Lys Lys Glu Glu Gln Glu Pro Leu Val Arg Gln Phe Thr Val Glu Gln	305	310	315
Thr Gln Arg Ser Arg Arg Trp Ser Pro Pro Lys Leu Arg Gln Ile Val	325	330	335
Pro Ala Lys			

<210> 293
 <211> 1027
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(1027)

<223> FRXA00243

<400> 293

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ttaacaaagc agcccatgat ggaaatgaag aggaacagaa	gtg acc agc gaa caa	115
	Val Thr Ser Glu Gln	
	1 5	

gct tta gat cct atc cac cca ggt cag ttc cgt ctt tct cgg att cag	163
Ala Leu Asp Pro Ile His Pro Gly Gln Phe Arg Leu Ser Arg Ile Gln	
10 15 20	

ttg atc aac tgg gga acc ttc cac gga acg gtg gac att cct gtg acc	211
Leu Ile Asn Trp Gly Thr Phe His Gly Thr Val Asp Ile Pro Val Thr	
25 30 35	

agg gaa gga atc tta gtt acc ggt ggt tcg gga tca gga aaa tcc acg	259
Arg Glu Gly Ile Leu Val Thr Gly Gly Ser Gly Ser Gly Lys Ser Thr	
40 45 50	

ctg att gat gcg atc acg gcg gta ttg ctt ccg caa gga aag ctg agg	307
Leu Ile Asp Ala Ile Thr Ala Val Leu Leu Pro Gln Gly Lys Leu Arg	
55 60 65	

ttt aac tct gcc gca cag gct aat act ccg ccg aat aag gga cgc agt	355
Phe Asn Ser Ala Ala Gln Ala Asn Thr Pro Arg Asn Lys Gly Arg Ser	
70 75 80 85	

ttg gtt acc tat atc cgt ggc gct tgg cgt gcg cag gag gat ccg ctg	403
Leu Val Thr Tyr Ile Arg Gly Ala Trp Arg Ala Gln Glu Asp Pro Leu	
90 95 100	

cag gat cag att gtc tcc acg tac cta cgt ccc cgc gca acc tat tcg	451
Gln Asp Gln Ile Val Ser Thr Tyr Leu Arg Pro Arg Ala Thr Tyr Ser	
105 110 115	

ctg gtt gga ttg act tat tcc aac ggt gaa ggc gtc gag cac acc ttg	499
Leu Val Gly Leu Thr Tyr Ser Asn Gly Glu Gly Val Glu His Thr Leu	
120 125 130	

gtg gct att ttc tat ctg aaa tcg gga cac aat tta acc tcc gat att	547
Val Ala Ile Phe Tyr Leu Lys Ser Gly His Asn Leu Thr Ser Asp Ile	
135 140 145	

tct tca tat tat ggt gtg ttt ccc gtt gat caa gac atc aat gcg ctg	595
Ser Ser Tyr Tyr Gly Val Phe Pro Val Asp Gln Asp Ile Asn Ala Leu	
150 155 160 165	

ctg gat ttc ctg aaa gag ggc atc gat aaa cgc cag atc aga gct gct	643
Leu Asp Phe Leu Lys Glu Gly Ile Asp Lys Arg Gln Ile Arg Ala Ala	
170 175 180	

ttc aag gaa gcc atc ttt agc gag cag cat tct gta ttc tcc ggc agg	691
Phe Lys Glu Ala Ile Phe Ser Glu Gln His Ser Val Phe Ser Gly Arg	
185 190 195	

ttt aga agc cgt ttg ggg atc tcc agt gag gaa gct ttg ctg ttg ttg	739
Phe Arg Ser Arg Leu Gly Ile Ser Ser Glu Glu Ala Leu Leu Leu Leu	
200 205 210	

cac cgc gcg cag tcg gcg aaa gat ctt caa agc ttg gat gat cta ttt 787
 His Arg Ala Gln Ser Ala Lys Asp Leu Gln Ser Leu Asp Asp Leu Phe
 215 220 225

cgg gat tac atg ctg gtg gaa ccg gat acg ttc agc att gcc aaa act 835
 Arg Asp Tyr Met Leu Val Glu Pro Asp Thr Phe Ser Ile Ala Lys Thr
 230 235 240 245

gcc gtg gaa caa ttc caa gac ctt gaa ggt gct tat gag cag gtc gaa 883
 Ala Val Glu Gln Phe Gln Asp Leu Glu Gly Ala Tyr Glu Gln Val Glu
 250 255 260

gat att aaa cgg cag atc cac acc ctg gat cct ttg gtg cag ctg aag 931
 Asp Ile Lys Arg Gln Ile His Thr Leu Asp Pro Leu Val Gln Leu Lys
 265 270 275

aat cgg cga gag aaa gcg caa cag tcc aaa gat cat gcc aat gca ctg 979
 Asn Arg Arg Glu Lys Ala Gln Gln Ser Lys Asp His Ala Asn Ala Leu
 280 285 290

aag aag gcg ctg ccg act gtc ggg aat cgc att aag aag gaa gag caa 1027
 Lys Lys Ala Leu Pro Thr Val Gly Asn Arg Ile Lys Lys Glu Glu Gln
 295 300 305

<210> 294

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

Val Thr Ser Glu Gln Ala Leu Asp Pro Ile His Pro Gly Gln Phe Arg
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Leu Ser Arg Ile Gln Leu Ile Asn Trp Gly Thr Phe His Gly Thr Val
 20 25 30

Asp Ile Pro Val Thr Arg Glu Gly Ile Leu Val Thr Gly Gly Ser Gly
 35 40 45

Ser Gly Lys Ser Thr Leu Ile Asp Ala Ile Thr Ala Val Leu Leu Pro
 50 55 60

Gln Gly Lys Leu Arg Phe Asn Ser Ala Ala Gln Ala Asn Thr Pro Arg
 65 70 75 80

Asn Lys Gly Arg Ser Leu Val Thr Tyr Ile Arg Gly Ala Trp Arg Ala
 85 90 95

Gln Glu Asp Pro Leu Gln Asp Gln Ile Val Ser Thr Tyr Leu Arg Pro
 100 105 110

Arg Ala Thr Tyr Ser Leu Val Gly Leu Thr Tyr Ser Asn Gly Glu Gly
 115 120 125

Val Glu His Thr Leu Val Ala Ile Phe Tyr Leu Lys Ser Gly His Asn
 130 135 140

Leu Thr Ser Asp Ile Ser Ser Tyr Tyr Gly Val Phe Pro Val Asp Gln
 145 150 155 160

<210> 295
<211> 2325
<212> DNA
<213> *Corynebacterium glutamicum*

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<221> CDS
<222> (101)..(2302)
<223> RXA00259.
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Met Ser Gly Leu Phe
1 5
acc cca ttt tca gat gcg gca aaa aac aac acg gta aaa act gat gga 163
Thr Pro Phe Ser Asp Ala Ala Lys Asn Asn Thr Val Lys Thr Asp Gly
10 15 20
gat tca gta tct ggt cga gac ttg cct att act aag atc tct gag gat 211
Asp Ser Val Ser Gly Arg Asp Leu Pro Ile Thr Lys Ile Ser Glu Asp
25 30 35
cgt ttc gag cgt tct gcg tat tca gcc cag ctg gca aat ata atc tgc 259
Arg Phe Glu Arg Ser Ala Tyr Ser Ala Gln Leu Ala Asn Ile Ile Cys
40 45 50

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gat gtg gca cct tgg gga gcg agc act gtt ttc agt ctt act ggt cag	307
Asp Val Ala Pro Trp Gly Ala Ser Thr Val Phe Ser Leu Thr Gly Gln	
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tgg ggc agt ggt aag aca tct ctt gtt aat ttg att cgc tcg gaa gaa	355
Trp Gly Ser Gly Lys Thr Ser Leu Val Asn Leu Ile Arg Ser Glu Glu	
70 75 80 85	
tct cta tcg aac gaa aaa tgg aca atc gtt gat ttc aac ccg tgg gtg	403
Ser Leu Ser Asn Glu Lys Trp Thr Ile Val Asp Phe Asn Pro Trp Val	
90 95 100	
gcc tct gac ccg caa tct ttg att gag gag ttt tac cga gta atc gtt	451
Ala Ser Asp Pro Gln Ser Leu Ile Glu Glu Phe Tyr Arg Val Ile Val	
105 110 115	
ggg acg gta cct gat gat aag acc ggc caa aag atc aaa act gtt ctg	499
Gly Thr Val Pro Asp Asp Lys Thr Gly Gln Lys Ile Lys Thr Val Leu	
120 125 130	
cag aaa acc ttt agc acg att ggg tca att gca ggt ggg gtc gga ggg	547
Gln Lys Thr Phe Ser Thr Ile Gly Ser Ile Ala Gly Gly Val Gly Gly	
135 140 145	
ttt ggt gtc cta gaa gca ctt gcg ctc tca aaa gga gta gat gct gca	595
Phe Gly Val Leu Glu Ala Leu Ala Leu Ser Lys Gly Val Asp Ala Ala	
150 155 160 165	
aac gct gta tat aag aca tgg aaa cag gag caa gat tcg tgg cca acg	643
Asn Ala Val Tyr Lys Thr Trp Lys Gln Glu Gln Asp Ser Trp Pro Thr	
170 175 180	
ctg tat aca cgt gct gcg aac cat ttt aaa gat ctg aac aag cga att	691
Leu Tyr Thr Arg Ala Ala Asn His Phe Lys Asp Leu Asn Lys Arg Ile	
185 190 195	
ctc att gtc gtc gat gat att gat cgc ctc cat act gat gaa ttg gcg	739
Leu Ile Val Val Asp Asp Ile Asp Arg Leu His Thr Asp Glu Leu Ala	
200 205 210	
ctg tta atg aaa gta ata cgc ttg ctt gga cga ttc ccg cag gtg aat	787
Leu Leu Met Lys Val Ile Arg Leu Leu Gly Arg Phe Pro Gln Val Asn	
215 220 225	
tat ctt ttg gtt tat gaa gaa gaa tca ctg tta acg acg cta gcc aga	835
Tyr Leu Leu Val Tyr Glu Glu Glu Ser Leu Leu Thr Thr Leu Ala Arg	
230 235 240 245	
tcg aca gct gta ggt ggt agc gaa gat gat gct ttg cgt ttc atg gag	883
Ser Thr Ala Val Gly Gly Ser Glu Asp Asp Ala Leu Arg Phe Met Glu	
250 255 260	
aaa atc gtg cag tat cct ttc gat gtt ccg cct ctg aca tca ttt caa	931
Lys Ile Val Gln Tyr Pro Phe Asp Val Pro Pro Leu Thr Ser Phe Gln	
265 270 275	
ata gag aaa gag ctc agt gca tta ttt gac aag ctt ttc cag ggt gtt	979
Ile Glu Lys Glu Leu Ser Ala Leu Phe Asp Lys Leu Phe Gln Gly Val	
280 285 290	
tcg cta tcg ggt gat cct gaa gac ttt gca cta gtg aag tcg aga atg	1027

Ser	Leu	Ser	Gly	Asp	Pro	Glu	Asp	Phe	Ala	Leu	Val	Lys	Ser	Arg	Met		
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Phe	Asp	Val	Trp	Glu	Lys	Thr	Leu	Val	Thr	Pro	Arg	Leu	Leu	His	Arg		
310					315					320					325		
ttt	gct	gct	cta	cta	acc	aac	tgg	act	cgg	ata	tat	gga	tca	ggg	gaa	1123	
Phe	Ala	Ala	Leu	Leu	Thr	Asn	Trp	Thr	Arg	Ile	Tyr	Gly	Ser	Gly	Glu		
				330					335					340			
gtt	aac	ggc	gtt	gat	ctc	aca	ata	ctt	gcg	acc	att	cga	att	gtt	ttt	1171	
Val	Asn	Gly	Val	Asp	Leu	Thr	Ile	Leu	Ala	Thr	Ile	Arg	Ile	Val	Phe		
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ccg	tct	gtg	tat	aaa	cgt	ctt	tct	cga	gcg	aag	gaa	gta	ttg	ctt	caa	1219	
Pro	Ser	Val	Tyr	Lys	Arg	Leu	Ser	Arg	Ala	Lys	Glu	Val	Leu	Leu	Gln		
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gga	ggg	cga	acg	aca	ggc	tcg	cag	aaa	ccc	ggg	tgg	gaa	aag	caa	tta	1267	
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	375					380					385						
tgt	gag	ggg	atg	aac	aac	gag	cag	atg	gat	ctt	tta	aag	acc	atg	ctt	1315	
Cys	Glu	Gly	Met	Asn	Asn	Glu	Gln	Met	Asp	Leu	Leu	Lys	Thr	Met	Leu		
390					395				400						405		
ttg	ttc	ctt	ttc	cca	cgt	ctt	tcg	gat	cac	cct	agt	acg	aga	atg	cat	1363	
Leu	Phe	Leu	Phe	Pro	Arg	Leu	Ser	Asp	His	Pro	Ser	Thr	Arg	Met	His		
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cgt	gag	agg	ggg	atc	tcg	acg	gaa	gtt	tat	ttt	gac	acg	tac	ctc	atg	1411	
Arg	Glu	Arg	Gly	Ile	Ser	Thr	Glu	Val	Tyr	Phe	Asp	Thr	Tyr	Leu	Met		
			425					430					435				
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Phe	Gln	Arg	Pro	Gly	His	Val	Ile	Ser	Asp	Glu	Gln	Leu	Asp	Lys	Tyr		
	440						445					450					
cta	tct	aat	gcg	gac	gat	gct	atg	ggg	ttc	gtc	gat	tta	att	aac	tcc	1507	
Leu	Ser	Asn	Ala	Asp	Asp	Ala	Met	Gly	Phe	Val	Asp	Leu	Ile	Asn	Ser		
	455					460					465						
gat	gac	aat	gac	atg	gtg	gca	tca	gtg	atg	aaa	aag	ctt	cct	cta	gca	1555	
Asp	Asp	Asn	Asp	Met	Val	Ala	Ser	Val	Met	Lys	Lys	Leu	Pro	Leu	Ala		
470					475					480					485		
att	gat	cga	ctt	gat	gga	gag	ggg	gtt	agg	cac	atg	gca	gtt	gag	gtg	1603	
Ile	Asp	Arg	Leu	Asp	Gly	Glu	Gly	Val	Arg	His	Met	Ala	Val	Glu	Val		
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tta	ttc	acc	gct	gct	aat	ggg	atg	cat	gat	aaa	ggg	cgt	caa	gtg	cgt	1651	
Leu	Phe	Thr	Ala	Ala	Asn	Gly	Met	His	Asp	Lys	Gly	Arg	Gln	Val	Arg		
			505					510					515				
atg	agc	ggc	ata	ttc	agt	gac	ctg	tat	tcc	cat	gcg	tgc	tcg	att	ctt	1699	
Met	Ser	Gly	Ile	Phe	Ser	Asp	Leu	Tyr	Ser	His	Ala	Cys	Ser	Ile	Leu		
		520					525					530					
ggg	gca	ttg	cct	caa	tta	cca	gtg	gaa	caa	ctc	tat	gag	aaa	ttc	ttt	1747	
Gly	Ala	Leu	Pro	Gln	Leu	Pro	Val	Glu	Gln	Leu	Tyr	Glu	Lys	Phe	Phe		

535	540	545	
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gaa agg gct aga gcc tgt ggt aat gat gta agt ggc ctt gag ctt ttt Glu Arg Ala Arg Ala Cys Gly Asn Asp Val Ser Gly Leu Glu Leu Phe 570 575 580			1843
cgt aaa gtt aat ata aag acc gaa gct aga att tta agt gta ttg aag Arg Lys Val Asn Ile Lys Thr Glu Ala Arg Ile Leu Ser Val Leu Lys 585 590 595			1891
aat cag gac ccc tca gat tgg gat tta ggt cca tat tcg ctt ggt att Asn Gln Asp Pro Ser Asp Trp Asp Leu Gly Pro Tyr Ser Leu Gly Ile 600 605 610			1939
ttg gcg aaa agc tcg aat ttt tct tca gtg ctg aag tct ctg caa agt Leu Ala Lys Ser Ser Asn Phe Ser Ser Val Leu Lys Ser Leu Gln Ser 615 620 625			1987
ggt ata gag gaa cat cag ttt gat gtg ata gat att gga gtg ctt ttc Gly Ile Glu Glu His Gln Phe Asp Val Ile Asp Ile Gly Val Leu Phe 630 635 640 645			2035
tta acg act gtg tat tct tcg cga cag gga cca agc ggt ggt gca tgg Leu Thr Thr Val Tyr Ser Ser Arg Gln Gly Pro Ser Gly Gly Ala Trp 650 655 660			2083
ata gat tct ttt cag cat agt ctg ttt tca cgg tac gta cct gat tct Ile Asp Ser Phe Gln His Ser Leu Phe Ser Arg Tyr Val Pro Asp Ser 665 670 675			2131
cta cgg gct ata acc aag tct gaa gta gat gta gaa cta ggt aag ata Leu Arg Ala Ile Thr Lys Ser Glu Val Asp Val Glu Leu Gly Lys Ile 680 685 690			2179
cag ttc acg gat ttt agc tgg gaa ggg aag cga aaa gtt gtc gca tat Gln Phe Thr Asp Phe Ser Trp Glu Gly Lys Arg Lys Val Val Ala Tyr 695 700 705			2227
gca ctg gag act gga aga agt gat ttc act cga gaa cga tta ggg ggc Ala Leu Glu Thr Gly Arg Ser Asp Phe Thr Arg Glu Arg Leu Gly Gly 710 715 720 725			2275
tac agt atc gca gat tct ata gtc gat tgatgaggct gaggtcatga Tyr Ser Ile Ala Asp Ser Ile Val Asp 730			2322
ctt			2325

<210> 296

<211> 734

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Met	Ser	Gly	Leu	Phe	Thr	Pro	Phe	Ser	Asp	Ala	Ala	Lys	Asn	Asn	Thr
1					5				10						15

Val Lys Thr Asp Gly Asp Ser Val Ser Gly Arg Asp Leu Pro Ile Thr
 20 25 30
 Lys Ile Ser Glu Asp Arg Phe Glu Arg Ser Ala Tyr Ser Ala Gln Leu
 35 40 45
 Ala Asn Ile Ile Cys Asp Val Ala Pro Trp Gly Ala Ser Thr Val Phe
 50 55 60
 Ser Leu Thr Gly Gln Trp Gly Ser Gly Lys Thr Ser Leu Val Asn Leu
 65 70 75 80
 Ile Arg Ser Glu Glu Ser Leu Ser Asn Glu Lys Trp Thr Ile Val Asp
 85 90 95
 Phe Asn Pro Trp Val Ala Ser Asp Pro Gln Ser Leu Ile Glu Glu Phe
 100 105 110
 Tyr Arg Val Ile Val Gly Thr Val Pro Asp Asp Lys Thr Gly Gln Lys
 115 120 125
 Ile Lys Thr Val Leu Gln Lys Thr Phe Ser Thr Ile Gly Ser Ile Ala
 130 135 140
 Gly Gly Val Gly Gly Phe Gly Val Leu Glu Ala Leu Ala Leu Ser Lys
 145 150 155 160
 Gly Val Asp Ala Ala Asn Ala Val Tyr Lys Thr Trp Lys Gln Glu Gln
 165 170 175
 Asp Ser Trp Pro Thr Leu Tyr Thr Arg Ala Ala Asn His Phe Lys Asp
 180 185 190
 Leu Asn Lys Arg Ile Leu Ile Val Val Asp Asp Ile Asp Arg Leu His
 195 200 205
 Thr Asp Glu Leu Ala Leu Leu Met Lys Val Ile Arg Leu Leu Gly Arg
 210 215 220
 Phe Pro Gln Val Asn Tyr Leu Leu Val Tyr Glu Glu Glu Ser Leu Leu
 225 230 235 240
 Thr Thr Leu Ala Arg Ser Thr Ala Val Gly Gly Ser Glu Asp Asp Ala
 245 250 255
 Leu Arg Phe Met Glu Lys Ile Val Gln Tyr Pro Phe Asp Val Pro Pro
 260 265 270
 Leu Thr Ser Phe Gln Ile Glu Lys Glu Leu Ser Ala Leu Phe Asp Lys
 275 280 285
 Leu Phe Gln Gly Val Ser Leu Ser Gly Asp Pro Glu Asp Phe Ala Leu
 290 295 300
 Val Lys Ser Arg Met Phe Asp Val Trp Glu Lys Thr Leu Val Thr Pro
 305 310 315 320
 Arg Leu Leu His Arg Phe Ala Ala Leu Leu Thr Asn Trp Thr Arg Ile
 325 330 335

Tyr Gly Ser Gly Glu Val Asn Gly Val Asp Leu Thr Ile Leu Ala Thr
 340 345 350
 Ile Arg Ile Val Phe Pro Ser Val Tyr Lys Arg Leu Ser Arg Ala Lys
 355 360 365
 Glu Val Leu Leu Gln Gly Gly Arg Thr Thr Gly Ser Gln Lys Pro Gly
 370 375 380
 Trp Glu Lys Gln Leu Cys Glu Gly Met Asn Asn Glu Gln Met Asp Leu
 385 390 395 400
 Leu Lys Thr Met Leu Leu Phe Leu Phe Pro Arg Leu Ser Asp His Pro
 405 410 415
 Ser Thr Arg Met His Arg Glu Arg Gly Ile Ser Thr Glu Val Tyr Phe
 420 425 430
 Asp Thr Tyr Leu Met Phe Gln Arg Pro Gly His Val Ile Ser Asp Glu
 435 440 445
 Gln Leu Asp Lys Tyr Leu Ser Asn Ala Asp Asp Ala Met Gly Phe Val
 450 455 460
 Asp Leu Ile Asn Ser Asp Asp Asn Asp Met Val Ala Ser Val Met Lys
 465 470 475 480
 Lys Leu Pro Leu Ala Ile Asp Arg Leu Asp Gly Glu Gly Val Arg His
 485 490 495
 Met Ala Val Glu Val Leu Phe Thr Ala Ala Asn Gly Met His Asp Lys
 500 505 510
 Gly Arg Gln Val Arg Met Ser Gly Ile Phe Ser Asp Leu Tyr Ser His
 515 520 525
 Ala Cys Ser Ile Leu Gly Ala Leu Pro Gln Leu Pro Val Glu Gln Leu
 530 535 540
 Tyr Glu Lys Phe Phe Ser Glu Met Thr Leu Asn Glu Ala Ala Phe Trp
 545 550 555 560
 Leu Asn Gln Val Gly Glu Arg Ala Arg Ala Cys Gly Asn Asp Val Ser
 565 570 575
 Gly Leu Glu Leu Phe Arg Lys Val Asn Ile Lys Thr Glu Ala Arg Ile
 580 585 590
 Leu Ser Val Leu Lys Asn Gln Asp Pro Ser Asp Trp Asp Leu Gly Pro
 595 600 605
 Tyr Ser Leu Gly Ile Leu Ala Lys Ser Ser Asn Phe Ser Ser Val Leu
 610 615 620
 Lys Ser Leu Gln Ser Gly Ile Glu Glu His Gln Phe Asp Val Ile Asp
 625 630 635 640
 Ile Gly Val Leu Phe Leu Thr Thr Val Tyr Ser Ser Arg Gln Gly Pro
 645 650 655
 Ser Gly Gly Ala Trp Ile Asp Ser Phe Gln His Ser Leu Phe Ser Arg

660	665	670
Tyr Val Pro Asp Ser Leu Arg Ala Ile Thr Lys Ser Glu Val Asp Val 675	680	685
Glu Leu Gly Lys Ile Gln Phe Thr Asp Phe Ser Trp Glu Gly Lys Arg 690	695	700
Lys Val Val Ala Tyr Ala Leu Glu Thr Gly Arg Ser Asp Phe Thr Arg 705	710	715
Glu Arg Leu Gly Gly Tyr Ser Ile Ala Asp Ser Ile Val Asp 725	730	

<210> 297
 <211> 789
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(766)
 <223> RXN00410

<400> 297
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 cacagataac gctccgccgg tcctttcagc ccaagatctc atg atg atc tat gga 115
 Met Met Ile Tyr Gly
 1 5
 aaa gga tca aca gaa gtt cgg gct ctc gat ggc att tct gta cag att 163
 Lys Gly Ser Thr Glu Val Arg Ala Leu Asp Gly Ile Ser Val Gln Ile
 10 15 20
 cag tcc gac aaa tgg acc tcc atc atg ggg caa tca ggc tct ggc aaa 211
 Gln Ser Asp Lys Trp Thr Ser Ile Met Gly Gln Ser Gly Ser Gly Lys
 25 30 35
 aca act ctg ttg cag tgc ctt tcc gga ttg gcg cag cca acc tca ggc 259
 Thr Thr Leu Leu Gln Cys Leu Ser Gly Leu Ala Gln Pro Thr Ser Gly
 40 45 50
 aga gtg aca ctg aac aaa aac aac atc acg ttg agc tcc ctg tca gaa 307
 Arg Val Thr Leu Asn Lys Asn Asn Ile Thr Leu Ser Ser Leu Ser Glu
 55 60 65
 aat aag cgt gcc aag ctg cgt cgc acg cac atc agc atg gtg ttt cag 355
 Asn Lys Arg Ala Lys Leu Arg Arg Thr His Ile Ser Met Val Phe Gln
 70 75 80 85
 gat ttc aac ttg gtg cct att ttg tgc gtg aag gac aat att ttg ctg 403
 Asp Phe Asn Leu Val Pro Ile Leu Ser Val Lys Asp Asn Ile Leu Leu
 90 95 100
 ccg ttg cgt ctt gcg cat cgc agg gtg gat aag cag tgg ttt gaa cac 451
 Pro Leu Arg Leu Ala His Arg Arg Val Asp Lys Gln Trp Phe Glu His
 105 110 115
 atc acc agt gtg ttg aag att gat aat cgt atg cgc cat ttg cct ggc 499

Ile Thr Ser Val Leu Lys Ile Asp Asn Arg Met Arg His Leu Pro Gly
 120 125 130

gag ctg tct ggc ggt cag caa caa cgc gcc gcg att gcc cgg gcg ttg 547
 Glu Leu Ser Gly Gly Gln Gln Gln Arg Ala Ala Ile Ala Arg Ala Leu
 135 140 145

atg tct agg ccc gat att gtc att gcg gat gag cca aca gga agt ttg 595
 Met Ser Arg Pro Asp Ile Val Ile Ala Asp Glu Pro Thr Gly Ser Leu
 150 155 160 165

gat tcc gtc acc agc gat gca gtg ttg aat ttg ttc cgc agc att gtt 643
 Asp Ser Val Thr Ser Asp Ala Val Leu Asn Leu Phe Arg Ser Ile Val
 170 175 180

gat gat ttt ggg cag tca ctt gtg ttt gtc acc cac gat aaa gat gct 691
 Asp Asp Phe Gly Gln Ser Leu Val Phe Val Thr His Asp Lys Asp Ala
 185 190 195

gct cac cgt ggt gac gtg ttg atc aca atg cgt gat ggc aag atc atc 739
 Ala His Arg Gly Asp Val Leu Ile Thr Met Arg Asp Gly Lys Ile Ile
 200 205 210

gat acg gca gat ttg cgg gtg ggg cgt taatgttcag gcttgctttc 786
 Asp Thr Ala Asp Leu Arg Val Gly Arg
 215 220

gct 789

<210> 298
 <211> 222
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 298
 Met Met Ile Tyr Gly Lys Gly Ser Thr Glu Val Arg Ala Leu Asp Gly
 1 5 10 15

Ile Ser Val Gln Ile Gln Ser Asp Lys Trp Thr Ser Ile Met Gly Gln
 20 25 30

Ser Gly Ser Gly Lys Thr Thr Leu Leu Gln Cys Leu Ser Gly Leu Ala
 35 40 45

Gln Pro Thr Ser Gly Arg Val Thr Leu Asn Lys Asn Asn Ile Thr Leu
 50 55 60

Ser Ser Leu Ser Glu Asn Lys Arg Ala Lys Leu Arg Arg Thr His Ile
 65 70 75 80

Ser Met Val Phe Gln Asp Phe Asn Leu Val Pro Ile Leu Ser Val Lys
 85 90 95

Asp Asn Ile Leu Leu Pro Leu Arg Leu Ala His Arg Arg Val Asp Lys
 100 105 110

Gln Trp Phe Glu His Ile Thr Ser Val Leu Lys Ile Asp Asn Arg Met
 115 120 125

Arg His Leu Pro Gly Glu Leu Ser Gly Gly Gln Gln Gln Arg Ala Ala

130	135	140	
Ile Ala Arg Ala Leu Met Ser Arg Pro Asp Ile Val Ile Ala Asp Glu 145 150 155 160			
Pro Thr Gly Ser Leu Asp Ser Val Thr Ser Asp Ala Val Leu Asn Leu 165 170 175			
Phe Arg Ser Ile Val Asp Asp Phe Gly Gln Ser Leu Val Phe Val Thr 180 185 190			
His Asp Lys Asp Ala Ala His Arg Gly Asp Val Leu Ile Thr Met Arg 195 200 205			
Asp Gly Lys Ile Ile Asp Thr Ala Asp Leu Arg Val Gly Arg 210 215 220			
<210> 299			
<211> 789			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(766)			
<223> FRXA00410			
<400> 299			
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cacagataac gctccgccgg tcctttcagc ccaagatctc atg atg atc tat gga 115			
	Met Met Ile Tyr Gly		
	1 5		
aaa gga tca aca gaa gtt cgg gct ctc gat ggc att tct gta cag att 163			
Lys Gly Ser Thr Glu Val Arg Ala Leu Asp Gly Ile Ser Val Gln Ile			
10 15 20			
cag tcc gac aaa tgg acc tcc atc atg ggg caa tca ggc tct ggc aaa 211			
Gln Ser Asp Lys Trp Thr Ser Ile Met Gly Gln Ser Gly Ser Gly Lys			
25 30 35			
aca act ctg ttg cag tgc ctt tcc gga ttg gcg cag cca acc tca ggc 259			
Thr Thr Leu Leu Gln Cys Leu Ser Gly Leu Ala Gln Pro Thr Ser Gly			
40 45 50			
aga gtg aca ctg aac aaa aac aac atc acg ttg agc tcc ctg tca gaa 307			
Arg Val Thr Leu Asn Lys Asn Asn Ile Thr Leu Ser Ser Leu Ser Glu			
55 60 65			
aat aag cgt gcc aag ctg cgt cgc acg cac atc agc atg gtg ttt cag 355			
Asn Lys Arg Ala Lys Leu Arg Arg Thr His Ile Ser Met Val Phe Gln			
70 75 80 85			
gat ttc aac ttg*gtg cct att ttg tcg gtg aag gac aat att ttg ctg 403			
Asp Phe Asn Leu Val Pro Ile Leu Ser Val Lys Asp Asn Ile Leu Leu			
90 95 100			
ccg ttg cgt ctt gcg cat cgc agg gtg gat aag cag tgg ttt gaa cac 451			
Pro Leu Arg Leu Ala His Arg Arg Val Asp Lys Gln Trp Phe Glu His			

115	120	125
Arg His Leu Pro Gly Glu Leu Ser Gly Gly Gln Gln Gln Arg Ala Ala 130 135 140		
Ile Ala Arg Ala Leu Met Ser Arg Pro Asp Ile Val Ile Ala Asp Glu 145 150 155 160		
Pro Thr Gly Ser Leu Asp Ser Val Thr Ser Asp Ala Val Leu Asn Leu 165 170 175		
Phe Arg Ser Ile Val Asp Asp Phe Gly Gln Ser Leu Val Phe Val Thr 180 185 190		
His Asp Lys Asp Ala Ala His Arg Gly Asp Val Leu Ile Thr Met Arg 195 200 205		
Asp Gly Lys Ile Ile Asp Thr Ala Asp Leu Arg Val Gly Arg 210 215 220		

<210> 301
 <211> 1500
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1477)
 <223> RXN00456

<400> 301
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tcgtcgcaga cttttgctca ttgccctagg tgtacttggt gtg ctg cag gca ctg 115
 Val Leu Gln Ala Leu
 1 5

ctg gcg atc atg gtg tcg ttg agc gta gcc gcc ata ctt gag gga aac 163
 Leu Ala Ile Met Val Ser Leu Ser Val Ala Ala Ile Leu Glu Gly Asn
 10 15 20

cga gca ctt gtt gga ttg ctg ctt gct acc acg ttg ggt ttg ggg gtg 211
 Arg Ala Leu Val Gly Leu Leu Leu Ala Thr Thr Leu Gly Leu Gly Val
 25 30 35

gcg cag tgg att caa aaa gta gtg gca gaa gat cta ggc cag cat tat 259
 Ala Gln Trp Ile Gln Lys Val Val Ala Glu Asp Leu Gly Gln His Tyr
 40 45 50

gtg cat gag gtg cgt cgt gaa ttg gtg ggt gct gcg ctg gtg cct gga 307
 Val His Glu Val Arg Arg Glu Leu Val Gly Ala Ala Leu Val Pro Gly
 55 60 65

aat acg gcc tcg ttg ggc gtg act gtc acc cga gcc agc aat gat ctc 355
 Asn Thr Ala Ser Leu Gly Val Thr Val Thr Arg Ala Ser Asn Asp Leu
 70 75 80 85

acc gcg gtg cgc aat tgg gtg gct ttg ggc att gtt ccg atg gtc acc 403
 Thr Ala Val Arg Asn Trp Val Ala Leu Gly Ile Val Pro Met Val Thr
 90 95 100

ggg ctg ccg ttg att gcg att gtg ctg gtg gcg ttg ttt atc caa gat	451
Gly Leu Pro Leu Ile Ala Ile Val Leu Val Ala Leu Phe Ile Gln Asp	
105 110 115	
ctc cgc aca ggc gtg gct gtt act gtg cca ctg ctc atg tgt gta gcc	499
Leu Arg Thr Gly Val Ala Val Thr Val Pro Leu Leu Met Cys Val Ala	
120 125 130	
gtg ctg ccg gtg gtg gcg cgg tgg act ttg aaa aga gca cgt gaa cta	547
Val Leu Pro Val Val Ala Arg Trp Thr Leu Lys Arg Ala Arg Glu Leu	
135 140 145	
cgc aaa aaa cgt gga cgc atg gct gcg cgg atc gca gat tct gtc atg	595
Arg Lys Lys Arg Gly Arg Met Ala Ala Arg Ile Ala Asp Ser Val Met	
150 155 160 165	
gct gga gaa tta ctg cac gca aca gga gca ata gac cgt gag ctc aat	643
Ala Gly Glu Leu Leu His Ala Thr Gly Ala Ile Asp Arg Glu Leu Asn	
170 175 180	
gca gtc acc cga gat tcc gac cga gtg gtg ata gct gct gta aga cgt	691
Ala Val Thr Arg Asp Ser Asp Arg Val Val Ile Ala Ala Val Arg Arg	
185 190 195	
tcc tgg gcc acc ggt ttt agc cgc gca ttg atg gcc atg gca gcc tcg	739
Ser Trp Ala Thr Gly Phe Ser Arg Ala Leu Met Ala Met Ala Ala Ser	
200 205 210	
ctt ggc act gtc agc att gtg att tct ggc cac ctg gaa gta agt gag	787
Leu Gly Thr Val Ser Ile Val Ile Ser Gly His Leu Glu Val Ser Glu	
215 220 225	
gtt gcg gga ata atg atg ctt ctt ggc gtt ctt gcc act cca gtt gca	835
Val Ala Gly Ile Met Met Leu Leu Gly Val Leu Ala Thr Pro Val Ala	
230 235 240 245	
gaa ctt ggc cgc gtg gtg gaa tat cgc caa aat tat aaa gcc gcg aca	883
Glu Leu Gly Arg Val Val Glu Tyr Arg Gln Asn Tyr Lys Ala Ala Thr	
250 255 260	
cgc atc ctg att cca ctt ctg caa cga ggc tca gaa ttt aaa cac tcc	931
Arg Ile Leu Ile Pro Leu Leu Gln Arg Gly Ser Glu Phe Lys His Ser	
265 270 275	
caa caa aaa cta ccc ggg ttg caa gca aca gaa gga atc ccc ggt gtc	979
Gln Gln Lys Leu Pro Gly Leu Gln Ala Thr Glu Gly Ile Pro Gly Val	
280 285 290	
tat gtc aaa ggt att tcc gcc ctt cct gga gaa cgg atc tac ctc cac	1027
Tyr Val Lys Gly Ile Ser Ala Leu Pro Gly Glu Arg Ile Tyr Leu His	
295 300 305	
ggc tct gca gat gcg acg aga aaa tgg gtc acc tcg ttg tct gca atg	1075
Gly Ser Ala Asp Ala Thr Arg Lys Trp Val Thr Ser Leu Ser Ala Met	
310 315 320 325	
gag gaa ggc aca gat gta ata gtc aac ggt caa agg ctt tcg cag ctt	1123
Glu Glu Gly Thr Asp Val Ile Val Asn Gly Gln Arg Leu Ser Gln Leu	
330 335 340	

cct ttg aaa caa cga cgc gcc ctc atc gga atc gcc tca gca cac cac 1171
 Pro Leu Lys Gln Arg Arg Ala Leu Ile Gly Ile Ala Ser Ala His His
 345 350 355

cac tta agc cgt ggt tca gta tcg cgc ctg gtt ggt ttg cga gtg ccg 1219
 His Leu Ser Arg Gly Ser Val Ser Arg Leu Val Gly Leu Arg Val Pro
 360 365 370

gat gcc acc gtg gaa gaa att gag caa gca ctg gaa caa gtt ggt ctg 1267
 Asp Ala Thr Val Glu Glu Ile Glu Gln Ala Leu Glu Gln Val Gly Leu
 375 380 385

aac aac acc ggg aaa caa cgc ttg aaa aac ggc gga cac ccc tgg agt 1315
 Asn Asn Thr Gly Lys Gln Arg Leu Lys Asn Gly Gly His Pro Trp Ser
 390 395 400 405

act tcg cag atc aac aaa ctg aaa att gcc agc gcc acc ctt cga acc 1363
 Thr Ser Gln Ile Asn Lys Leu Lys Ile Ala Ser Ala Thr Leu Arg Thr
 410 415 420

cca ccg ctt ttg gta ctt gaa ggc atc acc cct gaa aac ctc ctc aac 1411
 Pro Pro Leu Leu Val Leu Glu Gly Ile Thr Pro Glu Asn Leu Leu Asn
 425 430 435

tat ccc gga gtg atc atc tcc acc gtt cag gag aac cca tcc gaa aca 1459
 Tyr Pro Gly Val Ile Ile Ser Thr Val Gln Glu Asn Pro Ser Glu Thr
 440 445 450

tgg cgg caa gtg aac atc taatctagaa acatggcagg acg 1500
 Trp Arg Gln Val Asn Ile
 455

<210> 302

<211> 459

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Val Leu Gln Ala Leu Leu Ala Ile Met Val Ser Leu Ser Val Ala Ala
 1 5 10 15

Ile Leu Glu Gly Asn Arg Ala Leu Val Gly Leu Leu Leu Ala Thr Thr
 20 25 30

Leu Gly Leu Gly Val Ala Gln Trp Ile Gln Lys Val Val Ala Glu Asp
 35 40 45

Leu Gly Gln His Tyr Val His Glu Val Arg Arg Glu Leu Val Gly Ala
 50 55 60

Ala Leu Val Pro Gly Asn Thr Ala Ser Leu Gly Val Thr Val Thr Arg
 65 70 75 80

Ala Ser Asn Asp Leu Thr Ala Val Arg Asn Trp Val Ala Leu Gly Ile
 85 90 95

Val Pro Met Val Thr Gly Leu Pro Leu Ile Ala Ile Val Leu Val Ala
 100 105 110

Leu Phe Ile Gln Asp Leu Arg Thr Gly Val Ala Val Thr Val Pro Leu

115	120	125
Leu Met Cys Val Ala Val 130	Leu Pro Val Val Ala Arg 135	Trp Thr Leu Lys 140
Arg Ala Arg Glu Leu Arg 145	Lys Lys Arg Gly Arg Met 150	Ala Ala Arg Ile 155
Ala Asp Ser Val Met Ala 165	Gly Glu Leu Leu His 170	Ala Thr Gly Ala Ile 175
Asp Arg Glu Leu Asn Ala 180	Val Thr Arg Asp Ser 185	Asp Arg Val Val Ile 190
Ala Ala Val Arg Arg Ser 195	Trp Ala Thr Gly Phe 200	Ser Arg Ala Leu Met 205
Ala Met Ala Ala Ser Leu 210	Gly Thr Val Ser Ile 215	Val Ile Ser Gly His 220
Leu Glu Val Ser Glu Val 225	Ala Gly Ile Met Met 230	Leu Leu Gly Val Leu 235
Ala Thr Pro Val Ala Glu 245	Leu Gly Arg Val Val 250	Glu Tyr Arg Gln Asn 255
Tyr Lys Ala Ala Thr Arg 260	Ile Leu Ile Pro Leu 265	Leu Gln Arg Gly Ser 270
Glu Phe Lys His Ser Gln 275	Gln Gln Lys Leu Pro 280	Gly Leu Gln Ala Thr 285
Gly Ile Pro Gly Val Tyr 290	Val Lys Gly Ile Ser 295	Ala Leu Pro Gly Glu 300
Arg Ile Tyr Leu His Gly 305	Ser Ala Asp Ala Thr 310	Arg Lys Trp Val Thr 315
Ser Leu Ser Ala Met Glu 325	Glu Glu Gly Thr Asp 330	Val Ile Val Asn Gly 335
Arg Leu Ser Gln Leu Pro 340	Leu Lys Gln Arg Arg 345	Ala Leu Ile Gly Ile 350
Ala Ser Ala His His His 355	Leu Ser Arg Gly Ser 360	Val Ser Arg Leu Val 365
Gly Leu Arg Val Pro Asp 370	Ala Thr Val Glu Glu 375	Ile Glu Gln Ala Leu 380
Glu Gln Val Gly Leu Asn 385	Asn Asn Thr Gly Lys 390	Gln Arg Leu Lys Asn 395
Gly His Pro Trp Ser Thr 405	Ser Gln Ile Asn Lys 410	Leu Lys Ile Ala Ser 415
Ala Thr Leu Arg Thr Pro 420	Pro Pro Leu Leu Val 425	Leu Glu Gly Ile Thr 430
Glu Asn Leu Leu Asn Tyr 435	Pro Gly Val Ile Ile 440	Ser Thr Val Gln Glu 445

Asn Pro Ser Glu Thr Trp Arg Gln Val Asn Ile
450 455

<210> 303
<211> 412
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(412)
<223> FRXA00456

<400> 303
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tcgtcgcaga cttttgctca ttgccctagg tgtacttggt gtg ctg cag gca ctg 115
Val Leu Gln Ala Leu
1 5
ctg gcg atc atg gtg tcg ttg agc gta gcc gcc ata ctt gag gga aac 163
Leu Ala Ile Met Val Ser Leu Ser Val Ala Ala Ile Leu Glu Gly Asn
10 15 20
cga gca ctt gtt gga ttg ctg ctt gct acc acg ttg ggt ttg ggg gtg 211
Arg Ala Leu Val Gly Leu Leu Leu Ala Thr Thr Leu Gly Leu Gly Val
25 30 35
gcg cag tgg att caa aaa gta gtg gca gaa gat cta ggc cag cat tat 259
Ala Gln Trp Ile Gln Lys Val Val Ala Glu Asp Leu Gly Gln His Tyr
40 45 50
gtg cat gag gtg cgt cgt gaa ttg gtg ggt gct gcg ctg gtg cct gga 307
Val His Glu Val Arg Arg Glu Leu Val Gly Ala Ala Leu Val Pro Gly
55 60 65
aat acg gcc tcg ttg ggc gtg act gtc acc cga gcc agc aat gat ctc 355
Asn Thr Ala Ser Leu Gly Val Thr Val Thr Arg Ala Ser Asn Asp Leu
70 75 80 85
acc gcg gtg cgc aat tgg gtg gct ttg ggc att gtt ccg atg gtc acc 403
Thr Ala Val Arg Asn Trp Val Ala Leu Gly Ile Val Pro Met Val Thr
90 95 100
ggg ctg ccg 412
Gly Leu Pro

<210> 304
<211> 104
<212> PRT
<213> Corynebacterium glutamicum

<400> 304
Val Leu Gln Ala Leu Leu Ala Ile Met Val Ser Leu Ser Val Ala Ala
1 5 10 15
Ile Leu Glu Gly Asn Arg Ala Leu Val Gly Leu Leu Leu Ala Thr Thr

20 25 30
 Leu Gly Leu Gly Val Ala Gln Trp Ile Gln Lys Val Val Ala Glu Asp
 35 40 45
 Leu Gly Gln His Tyr Val His Glu Val Arg Arg Glu Leu Val Gly Ala
 50 55 60
 Ala Leu Val Pro Gly Asn Thr Ala Ser Leu Gly Val Thr Val Thr Arg
 65 70 75 80
 Ala Ser Asn Asp Leu Thr Ala Val Arg Asn Trp Val Ala Leu Gly Ile
 85 90 95
 Val Pro Met Val Thr Gly Leu Pro
 100

<210> 305

<211> 1040

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (31)..(1017)

<223> FRXA00459

<400> 305

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 Val Cys Thr Arg Ala Ala Gly Gly
 1 5
 ggc gcg gtg act ttg aaa aga gca cgt gaa cta cgc aaa aaa cgt gga 102
 Gly Ala Val Thr Leu Lys Arg Ala Arg Glu Leu Arg Lys Lys Arg Gly
 10 15 20
 cgc atg gct gcg cgg atc gca gat tct gtc atg gct gga gaa tta ctg 150
 Arg Met Ala Ala Arg Ile Ala Asp Ser Val Met Ala Gly Glu Leu Leu
 25 30 35 40
 cac gca aca gga gca ata gac cgt gag ctc aat gca gtc acc cga gat 198
 His Ala Thr Gly Ala Ile Asp Arg Glu Leu Asn Ala Val Thr Arg Asp
 45 50 55
 tcc gac cga gtg gtg ata gct gct gta aga cgt tcc tgg gcc acc ggt 246
 Ser Asp Arg Val Val Ile Ala Ala Val Arg Arg Ser Trp Ala Thr Gly
 60 65 70
 ttt agc cgc gca ttg atg gcc atg gca gcc tcg ctt ggc act gtc agc 294
 Phe Ser Arg Ala Leu Met Ala Met Ala Ala Ser Leu Gly Thr Val Ser
 75 80 85
 att gtg att tct ggc cac ctg gaa gta agt gag gtt gcg gga ata atg 342
 Ile Val Ile Ser Gly His Leu Glu Val Ser Glu Val Ala Gly Ile Met
 90 95 100
 atg ctt ctt ggc gtt ctt gcc act cca gtt gca gaa ctt ggc cgc gtg 390
 Met Leu Leu Gly Val Leu Ala Thr Pro Val Ala Glu Leu Gly Arg Val
 105 110 115 120

gtg gaa tat cgc caa aat tat aaa gcc gcg aca cgc atc ctg att cca 438
 Val Glu Tyr Arg Gln Asn Tyr Lys Ala Ala Thr Arg Ile Leu Ile Pro
 125 130 135

ctt ctg caa cga ggc tca gaa ttt aaa cac tcc caa caa aaa cta ccc 486
 Leu Leu Gln Arg Gly Ser Glu Phe Lys His Ser Gln Gln Lys Leu Pro
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 Gly Leu Gln Ala Thr Glu Gly Ile Pro Gly Val Tyr Val Lys Gly Ile
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 Ser Ala Leu Pro Gly Glu Arg Ile Tyr Leu His Gly Ser Ala Asp Ala
 170 175 180

acg aga aaa tgg gtc acc tcg ttg tct gca atg gag gaa ggc aca gat 630
 Thr Arg Lys Trp Val Thr Ser Leu Ser Ala Met Glu Glu Gly Thr Asp
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gta ata gtc aac ggt caa agg ctt tcg cag ctt cct ttg aaa caa cga 678
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cgc gcc ctc atc gga atc gcc tca gca cac cac cac tta agc cgt ggt 726
 Arg Ala Leu Ile Gly Ile Ala Ser Ala His His His Leu Ser Arg Gly
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 Ser Val Ser Arg Leu Val Gly Leu Arg Val Pro Asp Ala Thr Val Glu
 235 240 245

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 Glu Ile Glu Gln Ala Leu Glu Gln Val Gly Leu Asn Asn Thr Gly Lys
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caa cgc ttg aaa aac ggc gga cac ccc tgg agt act tcg cag atc aac 870
 Gln Arg Leu Lys Asn Gly Gly His Pro Trp Ser Thr Ser Gln Ile Asn
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 Lys Leu Lys Ile Ala Ser Ala Thr Leu Arg Thr Pro Pro Leu Leu Val
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ctt gaa ggc atc acc cct gaa aac ctc ctc aac tat ccc gga gtg atc 966
 Leu Glu Gly Ile Thr Pro Glu Asn Leu Leu Asn Tyr Pro Gly Val Ile
 300 305 310

atc tcc acc gtt cag gag aac cca tcc gaa aca tgg cgg caa gtg aac 1014
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<212> PRT

<213> Corynebacterium glutamicum

<400> 306

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 Ser Val Met Ala Gly Glu Leu Leu His Ala Thr Gly Ala Ile Asp Arg
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 Glu Leu Asn Ala Val Thr Arg Asp Ser Asp Arg Val Val Ile Ala Ala
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 Val Arg Arg Ser Trp Ala Thr Gly Phe Ser Arg Ala Leu Met Ala Met
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 Ala Ala Ser Leu Gly Thr Val Ser Ile Val Ile Ser Gly His Leu Glu
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 Val Ser Glu Val Ala Gly Ile Met Met Leu Leu Gly Val Leu Ala Thr
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 Pro Val Ala Glu Leu Gly Arg Val Val Glu Tyr Arg Gln Asn Tyr Lys
 115 120 125
 Ala Ala Thr Arg Ile Leu Ile Pro Leu Leu Gln Arg Gly Ser Glu Phe
 130 135 140
 Lys His Ser Gln Gln Lys Leu Pro Gly Leu Gln Ala Thr Glu Gly Ile
 145 150 155 160
 Pro Gly Val Tyr Val Lys Gly Ile Ser Ala Leu Pro Gly Glu Arg Ile
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 Tyr Leu His Gly Ser Ala Asp Ala Thr Arg Lys Trp Val Thr Ser Leu
 180 185 190
 Ser Ala Met Glu Glu Gly Thr Asp Val Ile Val Asn Gly Gln Arg Leu
 195 200 205
 Ser Gln Leu Pro Leu Lys Gln Arg Arg Ala Leu Ile Gly Ile Ala Ser
 210 215 220
 Ala His His His Leu Ser Arg Gly Ser Val Ser Arg Leu Val Gly Leu
 225 230 235 240
 Arg Val Pro Asp Ala Thr Val Glu Glu Ile Glu Gln Ala Leu Glu Gln
 245 250 255
 Val Gly Leu Asn Asn Thr Gly Lys Gln Arg Leu Lys Asn Gly Gly His
 260 265 270
 Pro Trp Ser Thr Ser Gln Ile Asn Lys Leu Lys Ile Ala Ser Ala Thr
 275 280 285
 Leu Arg Thr Pro Pro Leu Leu Val Leu Glu Gly Ile Thr Pro Glu Asn
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<211> 771

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(748)

<223> RXN01604

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                                         1           5

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Glu Ile Ala Pro Asp Ser Gly Leu Thr Leu Leu Ser Thr Gly Arg Glu
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Leu Ala Lys His Val Ala Leu Ala Gly Ile Pro Glu Ile Asp Ser Leu
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Arg Trp Val Asp Val Glu Lys His Leu Gly Leu Asn Leu Asn Pro Lys
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acc tta atc ggc gac ctc agc gtg ctc gag cgt ttt aag ctg cgc atc 547
Thr Leu Ile Gly Asp Leu Ser Val Leu Glu Arg Phe Lys Leu Arg Ile
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Ala Leu Ala Leu Leu Ala Arg Pro Glu Ala Gln Leu Leu Val Val Asp
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 Asp Pro Asp Gln Val Arg Ser Met Glu Leu Arg Ala Glu Val Leu His
 170 175 180

gca ttg aaa ggc gtt gca gag gat ctc cct gtg gtc gtg gta tcc acc 691
 Ala Leu Lys Gly Val Ala Glu Asp Leu Pro Val Val Val Val Ser Thr
 185 190 195

aac cca gat ttt gat tcc ttg gcc gat acc gct ttg acc att acg ggg 739
 Asn Pro Asp Phe Asp Ser Leu Ala Asp Thr Ala Leu Thr Ile Thr Gly
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gct gga aac taatggcatt tttacacttt ggc 771
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<210> 308

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

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 20 25 30

Ser Thr Gly Arg Glu Ser Gln Ser Ser Ser Phe Ser Leu Val Leu Ser
 35 40 45

Gly Arg Met Arg Ala Ser Thr Gly Thr Ile Glu Leu Asn Gly Glu Pro
 50 55 60

Ile Lys Ala Thr Lys Leu Ala Lys His Val Ala Leu Ala Gly Ile Pro
 65 70 75 80

Glu Ile Asp Ser Leu Glu Arg Leu Val Thr Val Arg Thr Val Val Arg
 85 90 95

Glu Gln Leu Ala Trp Ser Ser Pro Trp Tyr Leu Met Val Pro Arg Asp
 100 105 110

Ile Ser Asp Ser Gly Arg Trp Val Asp Val Glu Lys His Leu Gly Leu
 115 120 125

Asn Leu Asn Pro Lys Thr Leu Ile Gly Asp Leu Ser Val Leu Glu Arg
 130 135 140

Phe Lys Leu Arg Ile Ala Leu Ala Leu Leu Ala Arg Pro Glu Ala Gln
 145 150 155 160

Leu Leu Val Val Asp Asp Pro Asp Gln Val Arg Ser Met Glu Leu Arg
 165 170 175

Ala Glu Val Leu His Ala Leu Lys Gly Val Ala Glu Asp Leu Pro Val
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Val Val Val Ser Thr Asn Pro Asp Phe Asp Ser Leu Ala Asp Thr Ala

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<222> (1)..(606)			
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Leu Leu Ser Thr Gly Arg Glu Ser Gln Ser Ser Ser Phe Ser Leu Val			
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Leu Ser Gly Arg Met Arg Ala Ser Thr Gly Thr Ile Glu Leu Asn Gly			
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Glu Pro Ile Lys Ala Thr Lys Leu Ala Lys His Val Ala Leu Ala Gly			
50 55 60			
 atc cct gaa atc gat tca ctc gag cga ctt gtc act gtg cgc acc gtt 240			
Ile Pro Glu Ile Asp Ser Leu Glu Arg Leu Val Thr Val Arg Thr Val			
65 70 75 80			
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Val Arg Glu Gln Leu Ala Trp Ser Ser Pro Trp Tyr Leu Met Val Pro			
85 90 95			
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Arg Asp Ile Ser Asp Ser Gly Arg Trp Val Asp Val Glu Lys His Leu			
100 105 110			
 ggc ctg aac ctg aac cct aaa acc tta atc ggc gac ctc agc gtg ctc 384			
Gly Leu Asn Leu Asn Pro Lys Thr Leu Ile Gly Asp Leu Ser Val Leu			
115 120 125			
 gag cgt ttt aag ctg cgc atc gcg ctg gcg ctg ctg gcg cgg cca gag 432			
Glu Arg Phe Lys Leu Arg Ile Ala Leu Ala Leu Ala Arg Pro Glu			
130 135 140			
 gcg caa ctg ttg gtc gtg gat gat ccc gat caa gtg cgc agc atg gaa 480			
Ala Gln Leu Leu Val Val Asp Asp Pro Asp Gln Val Arg Ser Met Glu			
145 150 155 160			
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Leu Arg Ala Glu Val Leu His Ala Leu Lys Gly Val Ala Glu Asp Leu			
165 170 175			

cct gtg gtc gtg gta tcc acc aac cca gat ttt gat tcc ttg gcc gat 576
 Pro Val Val Val Val Ser Thr Asn Pro Asp Phe Asp Ser Leu Ala Asp
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acc gct ttg acc att acg ggg gct gga aac taatggcatt ttacacttt 626
 Thr Ala Leu Thr Ile Thr Gly Ala Gly Asn
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ggc 629

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<212> PRT

<213> Corynebacterium glutamicum

<400> 310

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 20 25 30

Leu Ser Gly Arg Met Arg Ala Ser Thr Gly Thr Ile Glu Leu Asn Gly
 35 40 45

Glu Pro Ile Lys Ala Thr Lys Leu Ala Lys His Val Ala Leu Ala Gly
 50 55 60

Ile Pro Glu Ile Asp Ser Leu Glu Arg Leu Val Thr Val Arg Thr Val
 65 70 75 80

Val Arg Glu Gln Leu Ala Trp Ser Ser Pro Trp Tyr Leu Met Val Pro
 85 90 95

Arg Asp Ile Ser Asp Ser Gly Arg Trp Val Asp Val Glu Lys His Leu
 100 105 110

Gly Leu Asn Leu Asn Pro Lys Thr Leu Ile Gly Asp Leu Ser Val Leu
 115 120 125

Glu Arg Phe Lys Leu Arg Ile Ala Leu Ala Leu Leu Ala Arg Pro Glu
 130 135 140

Ala Gln Leu Leu Val Val Asp Asp Pro Asp Gln Val Arg Ser Met Glu
 145 150 155 160

Leu Arg Ala Glu Val Leu His Ala Leu Lys Gly Val Ala Glu Asp Leu
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Thr Ala Leu Thr Ile Thr Gly Ala Gly Asn
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<212> DNA

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<223> RXN02547

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 Leu Glu Leu Asn Asn
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gct gcg cgg ctg acc gtg gat gag tat ccg gcg gcg agg gaa gcg ctt 163
 Ala Ala Arg Leu Thr Val Asp Glu Tyr Pro Ala Ala Arg Glu Ala Leu
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gaa tct gca ggt cag agg aat gta gag gac cga acc cgt gcg gtt gat 211
 Glu Ser Ala Gly Gln Arg Asn Val Glu Asp Arg Thr Arg Ala Val Asp
 25 30 35

gag ttc aaa gcg gcg gat caa gag ctg tct tct ttg agt aaa ggc agc 259
 Glu Phe Lys Ala Ala Asp Gln Glu Leu Ser Ser Leu Ser Lys Gly Ser
 40 45 50

agt aat att gag tac cgt ttg ctg cag gtg cgg gaa aat ttg tgt cag 307
 Ser Asn Ile Glu Tyr Arg Leu Leu Gln Val Arg Glu Asn Leu Cys Gln
 55 60 65

gat ttg ggc gtg agc ccg cgg gat atg ccc ttt gcc ggt gag ctg att 355
 Asp Leu Gly Val Ser Pro Arg Asp Met Pro Phe Ala Gly Glu Leu Ile
 70 75 80 85

gat ccg aat aat gcg gaa tgg gaa ccc gtt gtg cag cgc att ttg ggt 403
 Asp Pro Asn Asn Ala Glu Trp Glu Pro Val Val Gln Arg Ile Leu Gly
 90 95 100

ggt ttt gct gcg gaa atg ttg gtt cct cat ggg ttg ttg cca cgg gtt 451
 Gly Phe Ala Ala Glu Met Leu Val Pro His Gly Leu Leu Pro Arg Val
 105 110 115

cgg gat tgg gta aat gcc aaa cat ttg gca gcg ctg ctg aaa ttc aac 499
 Arg Asp Trp Val Asn Ala Lys His Leu Ala Ala Leu Leu Lys Phe Asn
 120 125 130

ggc gtg gtg aca acg ggg gag tac aaa acc tcg cgt ttt ccg gcg gat 547
 Gly Val Val Thr Thr Gly Glu Tyr Lys Thr Ser Arg Phe Pro Ala Asp
 135 140 145

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 Ser Leu Ile Arg Lys Val Asp Val Val Glu Ser Pro Phe Arg Asp Trp
 150 155 160 165

gta aat caa gaa tta ggc aag cgt ttt aat att cgg tgc gtg cgc act 643
 Val Asn Gln Glu Leu Gly Lys Arg Phe Asn Ile Arg Cys Val Arg Thr
 170 175 180

cct gag gaa ttg tcg gcg ctg ggg cca cgc gat cag ggc gtg acc att 691
 Pro Glu Glu Leu Ser Ala Leu Gly Pro Arg Asp Gln Gly Val Thr Ile
 185 190 195

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Asn	Glu	Met	Ser	Thr	Arg	Asn	Leu	Gly	Gln	Ile	Ser	Arg	Arg	Leu	Arg		
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Leu	Ala	Gln	Ser	Glu	Phe	Asn	Glu	Gly	Arg	Phe	Leu	His	Ile	Asp	Ile		
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His	Val	Arg	Phe	Ile	Gly	Leu	Glu	Arg	Asp	Ser	Asp	Gly	Ala	Thr	Val		
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Phe	Asp	Arg	Ala	Asp	Pro	Ala	Phe	Thr	Arg	Gln	Thr	Met	Asn	Val	Phe		
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His	Ser	Phe	Gly	Phe	His	Met	Val	Leu	Ala	Thr	Pro	Leu	Lys	Leu	Ile		
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680

685

690

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<213> *Corynebacterium glutamicum*

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Gln Arg Ile Leu Gly Gly Phe Ala Ala Glu Met Leu Val Pro His Gly
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Leu Leu Pro Arg Val Arg Asp Trp Val Asn Ala Lys His Leu Ala Ala
 115 120 125

Leu Leu Lys Phe Asn Gly Val Val Thr Thr Gly Glu Tyr Lys Thr Ser
 130 135 140

Arg Phe Pro Ala Asp Ser Leu Ile Arg Lys Val Asp Val Val Glu Ser
 145 150 155 160

Pro Phe Arg Asp Trp Val Asn Gln Glu Leu Gly Lys Arg Phe Asn Ile
 165 170 175

Arg Cys Val Arg Thr Pro Glu Glu Leu Ser Ala Leu Gly Pro Arg Asp
 180 185 190

Gln Gly Val Thr Ile Leu Gly Val Arg Lys Phe Ala Gln Gln Thr Gly
 195 200 205

Asp Pro Thr Thr Arg Trp Glu Lys Asp Asp Arg Arg Lys Leu Gly Asp
 210 215 220

Arg Ser Thr Tyr Arg Leu Gly Ser Thr Asn Asp Ala Lys Val Glu Thr
 225 230 235 240

Leu Arg Glu Thr Val Lys Ala Gly Lys Ala Val Val Gln Ala Ala Asp
 245 250 255
 Asn Arg Ile Ala Ala Asn Arg Ala Glu Leu Arg Glu Leu Glu Arg Gln
 260 265 270
 Tyr Gln Ala Ser Gln Glu Ile Leu Lys Val Ser Trp Ala Gln Ile Asp
 275 280 285
 Val Glu Ser Ala Asp Ala Ala Ile Ala Glu Leu Asp Arg Leu Leu Glu
 290 295 300
 Glu Leu Asn Asn Thr Pro Glu Ala Thr Glu Leu Ser Ala Arg His Glu
 305 310 315 320
 Ala Ala Lys Gln Thr Leu Ala Arg Val Ser Asp Leu Leu Val Ala Ala
 325 330 335
 Gln Ser Glu Glu Thr Val Ala Ser Met Asn Leu Lys Arg Ala Glu Thr
 340 345 350
 Glu Leu Lys Arg Leu Glu Ser Leu Pro Val Ala Glu Val Ser Glu Glu
 355 360 365
 Ile Ala Arg Glu Val Glu Lys Leu Phe Leu Ala Asn Thr Arg Arg Val
 370 375 380
 His Ala Ala Asn Val Asp Glu Gln Thr Ile Ala Leu Arg Glu Asp Leu
 385 390 395 400
 Asp Lys Gln Ile Asp Ala Asn Glu Ala Glu Leu Arg Arg Cys Glu Asn
 405 410 415
 Gln Ile Val Gly Ile Leu Arg Ser Tyr Ile Glu Thr Trp Pro Ala Asn
 420 425 430
 Arg Ala Asp Leu Gln Ala Glu Pro Glu Phe Val Gly Glu Ala Ile Asn
 435 440 445
 Arg Leu Gly Glu Leu Arg Ser Asp Arg Leu Ala Glu Phe Thr Ala Lys
 450 455 460
 Phe Leu Gly Leu Met Asn Glu Met Ser Thr Arg Asn Leu Gly Gln Ile
 465 470 475 480
 Ser Arg Arg Leu Arg Asp Ala Arg Arg Glu Ile Glu Glu Arg Ile Glu
 485 490 495
 Pro Ile Asn Ala Ser Leu Ala Gln Ser Glu Phe Asn Glu Gly Arg Phe
 500 505 510
 Leu His Ile Asp Ile Arg Asp Gln Ser Gly Pro Ile Val Arg Glu Phe
 515 520 525
 Gln Gln Lys Leu Asp Ala Ala Thr Ser Gly Asp Leu Gly Thr Ser Thr
 530 535 540
 Glu Lys Gln Ala Phe Ala Arg Tyr Ala Leu Ile Ala Glu Ile Ile Ser
 545 550 555 560

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Ala	Ala	Arg	Leu	Thr	Val	Asp	Glu	Tyr	Pro	Ala	Ala	Arg	Glu	Ala	Leu	
1				5					10					15		
gaa	tct	gca	ggt	cag	agg	aat	gta	gag	gac	cga	acc	cgt	gcg	gtt	gat	96
Glu	Ser	Ala	Gly	Gln	Arg	Asn	Val	Glu	Asp	Arg	Thr	Arg	Ala	Val	Asp	
			20					25					30			
gag	ttc	aaa	gcg	gcg	gat	caa	gag	ctg	tct	tct	ttg	agt	aaa	ggc	agc	144
Glu	Phe	Lys	Ala	Ala	Asp	Gln	Glu	Leu	Ser	Ser	Leu	Ser	Lys	Gly	Ser	
		35					40					45				
agt	aat	att	gag	tac	cgt	ttg	ctg	cag	gtg	cgg	gaa	aat	ttg	tgt	cag	192
Ser	Asn	Ile	Glu	Tyr	Arg	Leu	Leu	Gln	Val	Arg	Glu	Asn	Leu	Cys	Gln	
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gat	ttg	ggc	gtg	agc	ccg	cgg	gat	atg	ccc	ttt	gcc	ggt	gag	ctg	att	240
Asp	Leu	Gly	Val	Ser	Pro	Arg	Asp	Met	Pro	Phe	Ala	Gly	Glu	Leu	Ile	
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gat ccg aat aat gcg gaa tgg gaa ccc gtt gtg cag cgc att ttg ggt	288
Asp Pro Asn Asn Ala Glu Trp Glu Pro Val Val Gln Arg Ile Leu Gly	
85 90 95	
ggt ttt gct gcg gaa atg ttg gtt cct cat ggg ttg ttg cca cgg gtt	336
Gly Phe Ala Ala Glu Met Leu Val Pro His Gly Leu Leu Pro Arg Val	
100 105 110	
cgg gat tgg gta aat gcc aaa cat ttg gca gcg ctg ctg aaa ttc aac	384
Arg Asp Trp Val Asn Ala Lys His Leu Ala Ala Leu Leu Lys Phe Asn	
115 120 125	
ggc gtg gtg aca acg ggg gag tac aaa acc tcg cgt ttt ccg gcg gat	432
Gly Val Val Thr Thr Gly Glu Tyr Lys Thr Ser Arg Phe Pro Ala Asp	
130 135 140	
tcc ctg atc cga aaa gtt gat gtt gtg gag tcg ccg ttt cgc gat tgg	480
Ser Leu Ile Arg Lys Val Asp Val Val Glu Ser Pro Phe Arg Asp Trp	
145 150 155 160	
gta aat caa gaa tta ggc aag cgt ttt aat att cgg tgc gtg cgc act	528
Val Asn Gln Glu Leu Gly Lys Arg Phe Asn Ile Arg Cys Val Arg Thr	
165 170 175	
cct gag gaa ttg tcg gcg ctg ggg cca cgc gat cag ggc gtg acc att	576
Pro Glu Glu Leu Ser Ala Leu Gly Pro Arg Asp Gln Gly Val Thr Ile	
180 185 190	
ttg ggt gtg cga aaa ttt gcg cag cag aca ggc gat ccg acg acg cgt	624
Leu Gly Val Arg Lys Phe Ala Gln Thr Gly Asp Pro Thr Thr Arg	
195 200 205	
tgg gaa aaa gat gat cgc cga aag ctg ggg gat cgt tcc aca tac cgt	672
Trp Glu Lys Asp Asp Arg Arg Lys Leu Gly Asp Arg Ser Thr Tyr Arg	
210 215 220	
ttg ggt tcc acc aat gat gcc aag gtg gaa acg ctt ccg gaa acc gtg	720
Leu Gly Ser Thr Asn Asp Ala Lys Val Glu Thr Leu Arg Glu Thr Val	
225 230 235 240	
aaa gct ggc aaa gca gtt gtg cag gca gct gat aat cgc att gct gca	768
Lys Ala Gly Lys Ala Val Val Gln Ala Ala Asp Asn Arg Ile Ala Ala	
245 250 255	
aac cgc gct gag ctg ccg gaa ctt gaa cgg cag tat caa gct tcg caa	816
Asn Arg Ala Glu Leu Arg Glu Leu Glu Arg Gln Tyr Gln Ala Ser Gln	
260 265 270	
gaa att ttg aaa gtg tcg tgg gct cag att gat gtg gaa tca gcc gac	864
Glu Ile Leu Lys Val Ser Trp Ala Gln Ile Asp Val Glu Ser Ala Asp	
275 280 285	
gcg gcg att gct gag ctg gac cga ttg ctg gaa gag ctg aac aac act	912
Ala Ala Ile Ala Glu Leu Asp Arg Leu Leu Glu Glu Leu Asn Asn Thr	
290 295 300	
cca gag gcc acc gag ctt tcc gcg ccg cat gag gcg gcg aag cag acg	960
Pro Glu Ala Thr Glu Leu Ser Ala Arg His Glu Ala Ala Lys Gln Thr	
305 310 315 320	

ctc gcg agg gtt tct gac ttg ctt gtc gca gct cag agt gag gaa acc	1008
Leu Ala Arg Val Ser Asp Leu Leu Val Ala Ala Gln Ser Glu Glu Thr	
325 330 335	
gtg gcg tcg atg aac ctg aaa cgc gcc gaa act gaa ttg aaa cgg ctc	1056
Val Ala Ser Met Asn Leu Lys Arg Ala Glu Thr Glu Leu Lys Arg Leu	
340 345 350	
gaa agc ctg ccg gtt gcg gag gtt tct gaa gaa atc gcg cgg gaa gtg	1104
Glu Ser Leu Pro Val Ala Glu Val Ser Glu Glu Ile Ala Arg Glu Val	
355 360 365	
gag aaa cta ttt ctt gcc aac acc cgc cgg gtt cac gcc gcc aac gtg	1152
Glu Lys Leu Phe Leu Ala Asn Thr Arg Arg Val His Ala Ala Asn Val	
370 375 380	
gat gag cag acc att gcg ctg cgc gag gat ctg gac aaa caa atc gat	1200
Asp Glu Gln Thr Ile Ala Leu Arg Glu Asp Leu Asp Lys Gln Ile Asp	
385 390 395 400	
gcc aat gag gca gaa ctt cga cgt tgt gaa aac caa att gtt ggc att	1248
Ala Asn Glu Ala Glu Leu Arg Arg Cys Glu Asn Gln Ile Val Gly Ile	
405 410 415	
ttg cgc agc tat att gaa acg tgg cct gcg aac cgc gct gac tta caa	1296
Leu Arg Ser Tyr Ile Glu Thr Trp Pro Ala Asn Arg Ala Asp Leu Gln	
420 425 430	
gcc gaa cct gag ttt gtt ggt gag gcc atc aac cgc ctc ggc gag ctt	1344
Ala Glu Pro Glu Phe Val Gly Glu Ala Ile Asn Arg Leu Gly Glu Leu	
435 440 445	
cgc agc gat cgt ttg gca gaa ttc acg gcc aaa ttc cta ggg ctc atg	1392
Arg Ser Asp Arg Leu Ala Glu Phe Thr Ala Lys Phe Leu Gly Leu Met	
450 455 460	
aac gag atg tcc acc cga aac ctc ggc caa atc tcg cgg cgt cta cgt	1440
Asn Glu Met Ser Thr Arg Asn Leu Gly Gln Ile Ser Arg Arg Leu Arg	
465 470 475 480	
gat gcg cgc cgg gaa atc gag gag cgc atc gag ccg atc aac gcc tcc	1488
Asp Ala Arg Arg Glu Ile Glu Glu Arg Ile Glu Pro Ile Asn Ala Ser	
485 490 495	
ttg gcg cag tcg gaa ttc aac gaa ggt cgc ttc ctg cac atc gac atc	1536
Leu Ala Gln Ser Glu Phe Asn Glu Gly Arg Phe Leu His Ile Asp Ile	
500 505 510	
cgt gat caa agt ggt ccg att gtg agg gaa ttc cag cag aaa ctt gat	1584
Arg Asp Gln Ser Gly Pro Ile Val Arg Glu Phe Gln Gln Lys Leu Asp	
515 520 525	
gcc gct acc agc ggt gac ctg gga acc agt acc gag aaa caa gcc ttc	1632
Ala Ala Thr Ser Gly Asp Leu Gly Thr Ser Thr Glu Lys Gln Ala Phe	
530 535 540	
gcc cgt tat gcg ctg atc gct gaa atc att tcc aaa ctc gcc tcc cac	1680
Ala Arg Tyr Ala Leu Ile Ala Glu Ile Ile Ser Lys Leu Ala Ser His	
545 550 555 560	
gac tcc gcc gac gcc cgc tgg cgc aac acc gtt cta gac acc cgc cgc	1728

Asp Ser Ala Asp Ala Arg Trp Arg Asn Thr Val Leu Asp Thr Arg Arg
 565 570 575
 cac gtt cgc ttc atc ggc ctc gag cgc gat tcc gac ggc gca acc gtc 1776
 His Val Arg Phe Ile Gly Leu Glu Arg Asp Ser Asp Gly Ala Thr Val
 580 585 590
 aac acc tac gtc gac tcc gca tca ctt tca ggc gga caa gcc cag aag 1824
 Asn Thr Tyr Val Asp Ser Ala Ser Leu Ser Gly Gly Gln Ala Gln Lys
 595 600 605
 ctg gtg ttt ttc tgc ctc gcc gct gcc ttg cgc tac cag cta gcc gaa 1872
 Leu Val Phe Phe Cys Leu Ala Ala Ala Leu Arg Tyr Gln Leu Ala Glu
 610 615 620
 ccc ggc gcc cat tat ccc acc tac gcc acc gtc att ctg gac gaa gcc 1920
 Pro Gly Ala His Tyr Pro Thr Tyr Ala Thr Val Ile Leu Asp Glu Ala
 625 630 635 640
 ttc gac cgc gcc gac ccc gcc ttc acc cgc caa acc atg aac gtc ttc 1968
 Phe Asp Arg Ala Asp Pro Ala Phe Thr Arg Gln Thr Met Asn Val Phe
 645 650 655
 cac agc ttc ggc ttc cac atg gtg ctc gcg acc ccg ctg aaa ctt atc 2016
 His Ser Phe Gly Phe His Met Val Leu Ala Thr Pro Leu Lys Leu Ile
 660 665 670
 caa acc ctc ggc gat tat gtc ggc tcc acc atc gtg gtc agc tac acc 2064
 Gln Thr Leu Gly Asp Tyr Val Gly Ser Thr Ile Val Val Ser Tyr Thr
 675 680 685
 gaa aaa cca aac gcc cag ggc gca att cag ggc aat tcc agt ttc tct 2112
 Glu Lys Pro Asn Ala Gln Gly Ala Ile Gln Gly Asn Ser Ser Phe Ser
 690 695 700
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 Arg Ile Glu Lys
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<400> 314
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 Glu Phe Lys Ala Ala Asp Gln Glu Leu Ser Ser Leu Ser Lys Gly Ser
 35 40 45
 Ser Asn Ile Glu Tyr Arg Leu Leu Gln Val Arg Glu Asn Leu Cys Gln
 50 55 60
 Asp Leu Gly Val Ser Pro Arg Asp Met Pro Phe Ala Gly Glu Leu Ile
 65 70 75 80

Asp Pro Asn Asn Ala Glu Trp Glu Pro Val Val Gln Arg Ile Leu Gly
 85 90 95
 Gly Phe Ala Ala Glu Met Leu Val Pro His Gly Leu Leu Pro Arg Val
 100 105 110
 Arg Asp Trp Val Asn Ala Lys His Leu Ala Ala Leu Leu Lys Phe Asn
 115 120 125
 Gly Val Val Thr Thr Gly Glu Tyr Lys Thr Ser Arg Phe Pro Ala Asp
 130 135 140
 Ser Leu Ile Arg Lys Val Asp Val Val Glu Ser Pro Phe Arg Asp Trp
 145 150 155 160
 Val Asn Gln Glu Leu Gly Lys Arg Phe Asn Ile Arg Cys Val Arg Thr
 165 170 175
 Pro Glu Glu Leu Ser Ala Leu Gly Pro Arg Asp Gln Gly Val Thr Ile
 180 185 190
 Leu Gly Val Arg Lys Phe Ala Gln Gln Thr Gly Asp Pro Thr Thr Arg
 195 200 205
 Trp Glu Lys Asp Asp Arg Arg Lys Leu Gly Asp Arg Ser Thr Tyr Arg
 210 215 220
 Leu Gly Ser Thr Asn Asp Ala Lys Val Glu Thr Leu Arg Glu Thr Val
 225 230 235 240
 Lys Ala Gly Lys Ala Val Val Gln Ala Ala Asp Asn Arg Ile Ala Ala
 245 250 255
 Asn Arg Ala Glu Leu Arg Glu Leu Glu Arg Gln Tyr Gln Ala Ser Gln
 260 265 270
 Glu Ile Leu Lys Val Ser Trp Ala Gln Ile Asp Val Glu Ser Ala Asp
 275 280 285
 Ala Ala Ile Ala Glu Leu Asp Arg Leu Leu Glu Glu Leu Asn Asn Thr
 290 295 300
 Pro Glu Ala Thr Glu Leu Ser Ala Arg His Glu Ala Ala Lys Gln Thr
 305 310 315 320
 Leu Ala Arg Val Ser Asp Leu Leu Val Ala Ala Gln Ser Glu Glu Thr
 325 330 335
 Val Ala Ser Met Asn Leu Lys Arg Ala Glu Thr Glu Leu Lys Arg Leu
 340 345 350
 Glu Ser Leu Pro Val Ala Glu Val Ser Glu Glu Ile Ala Arg Glu Val
 355 360 365
 Glu Lys Leu Phe Leu Ala Asn Thr Arg Arg Val His Ala Ala Asn Val
 370 375 380
 Asp Glu Gln Thr Ile Ala Leu Arg Glu Asp Leu Asp Lys Gln Ile Asp
 385 390 395 400
 Ala Asn Glu Ala Glu Leu Arg Arg Cys Glu Asn Gln Ile Val Gly Ile

405										410					415				
Leu	Arg	Ser	Tyr	Ile	Glu	Thr	Trp	Pro	Ala	Asn	Arg	Ala	Asp	Leu	Gln				
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Ala	Glu	Pro	Glu	Phe	Val	Gly	Glu	Ala	Ile	Asn	Arg	Leu	Gly	Glu	Leu				
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Arg	Ser	Asp	Arg	Leu	Ala	Glu	Phe	Thr	Ala	Lys	Phe	Leu	Gly	Leu	Met				
	450					455					460								
Asn	Glu	Met	Ser	Thr	Arg	Asn	Leu	Gly	Gln	Ile	Ser	Arg	Arg	Leu	Arg				
465				470						475					480				
Asp	Ala	Arg	Arg	Glu	Ile	Glu	Glu	Arg	Ile	Glu	Pro	Ile	Asn	Ala	Ser				
				485					490					495					
Leu	Ala	Gln	Ser	Glu	Phe	Asn	Glu	Gly	Arg	Phe	Leu	His	Ile	Asp	Ile				
		500						505					510						
Arg	Asp	Gln	Ser	Gly	Pro	Ile	Val	Arg	Glu	Phe	Gln	Gln	Lys	Leu	Asp				
		515					520					525							
Ala	Ala	Thr	Ser	Gly	Asp	Leu	Gly	Thr	Ser	Thr	Glu	Lys	Gln	Ala	Phe				
	530					535					540								
Ala	Arg	Tyr	Ala	Leu	Ile	Ala	Glu	Ile	Ile	Ser	Lys	Leu	Ala	Ser	His				
545				550						555					560				
Asp	Ser	Ala	Asp	Ala	Arg	Trp	Arg	Asn	Thr	Val	Leu	Asp	Thr	Arg	Arg				
			565					570						575					
His	Val	Arg	Phe	Ile	Gly	Leu	Glu	Arg	Asp	Ser	Asp	Gly	Ala	Thr	Val				
		580						585					590						
Asn	Thr	Tyr	Val	Asp	Ser	Ala	Ser	Leu	Ser	Gly	Gly	Gln	Ala	Gln	Lys				
		595					600					605							
Leu	Val	Phe	Phe	Cys	Leu	Ala	Ala	Ala	Leu	Arg	Tyr	Gln	Leu	Ala	Glu				
	610					615					620								
Pro	Gly	Ala	His	Tyr	Pro	Thr	Tyr	Ala	Thr	Val	Ile	Leu	Asp	Glu	Ala				
625					630					635					640				
Phe	Asp	Arg	Ala	Asp	Pro	Ala	Phe	Thr	Arg	Gln	Thr	Met	Asn	Val	Phe				
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His	Ser	Phe	Gly	Phe	His	Met	Val	Leu	Ala	Thr	Pro	Leu	Lys	Leu	Ile				
		660						665					670						
Gln	Thr	Leu	Gly	Asp	Tyr	Val	Gly	Ser	Thr	Ile	Val	Val	Ser	Tyr	Thr				
		675					680					685							
Glu	Lys	Pro	Asn	Ala	Gln	Gly	Ala	Ile	Gln	Gly	Asn	Ser	Ser	Phe	Ser				
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Arg	Ile	Glu	Lys																
705																			

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<211> 1152
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 <213> Corynebacterium glutamicum

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 <221> CDS
 <222> (101)..(1129)
 <223> RXN02571

<400> 315

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 Val Val Ala Leu Thr
 1 5

caa atc gtc gga ccg tcc ggc tcc ggg ctc acg cgg gaa ttg gaa aaa 163
 Gln Ile Val Gly Pro Ser Gly Ser Gly Leu Thr Arg Glu Leu Glu Lys
 10 15 20

cgc tac cgg gaa acg ccc gga gcg gtg atg ctg acc gcc gac ccg cgc 211
 Arg Tyr Arg Glu Thr Pro Gly Ala Val Met Leu Thr Ala Asp Pro Arg
 25 30 35

gcg cat atc acc tac ctg cgc gcg aca gtc gcc gag gag ctg gcc ttt 259
 Ala His Ile Thr Tyr Leu Arg Ala Thr Val Ala Glu Glu Leu Ala Phe
 40 45 50

ggg ctg gaa caa cgc ggc atc gta ccc gcg cag atg tgg gag cgc gtc 307
 Gly Leu Glu Gln Arg Gly Ile Val Pro Ala Gln Met Trp Glu Arg Val
 55 60 65

cga aac atc ggg ctc ggc ctc gag aat ctg cta gac cgc gca ccc gcg 355
 Arg Asn Ile Gly Leu Gly Leu Glu Asn Leu Leu Asp Arg Ala Pro Ala
 70 75 80 85

caa ctt tcc ggc ggg caa aca cgg cgg ctg gcg atc ggc acc gtc gcc 403
 Gln Leu Ser Gly Gly Gln Thr Arg Arg Leu Ala Ile Gly Thr Val Ala
 90 95 100

atc tta gag gcg cca acg atg ctt ctc gac gac ccc ctc tcc ggt ctt 451
 Ile Leu Glu Ala Pro Thr Met Leu Leu Asp Asp Pro Leu Ser Gly Leu
 105 110 115

gat acc tcc tcg cga gcc caa ctc atc aca atg ttg gaa tca tat gag 499
 Asp Thr Ser Ser Arg Ala Gln Leu Ile Thr Met Leu Glu Ser Tyr Glu
 120 125 130

ggc gat gtc atc gtc gct gcg cac aag cgg tgg ctc gac gcg ccg act 547
 Gly Asp Val Ile Val Ala Ala His Lys Arg Trp Leu Asp Ala Pro Thr
 135 140 145

gtg tac tta ggg gat ttg gag gag ctg tcc ctg cct gcg cgg gtg gaa 595
 Val Tyr Leu Gly Asp Leu Glu Glu Leu Ser Leu Pro Ala Arg Val Glu
 150 155 160 165

ttt tcc ggt cca tcg cga acg ttt tca gcg att aca gga acc cgc gga 643
 Phe Ser Gly Pro Ser Arg Thr Phe Ser Ala Ile Thr Gly Thr Arg Gly
 170 175 180

caa caa cgc cga cgc tgg tgg caa ttc aac gaa tcc caa cca cag ttt 691

Gln Gln Arg Arg Arg Trp Trp Gln Phe Asn Glu Ser Gln Pro Gln Phe
 185 190 195
 cag atc ggc ccc ctg gat att act gtt tct gca ggt caa gtg ctg tgg 739
 Gln Ile Gly Pro Leu Asp Ile Thr Val Ser Ala Gly Gln Val Leu Trp
 200 205 210
 ttg cag ggt ccc aat ggt tca ggg aag tcc aca ctc ctg cgt ggt ctt 787
 Leu Gln Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Leu Arg Gly Leu
 215 220 225
 gcc aat gaa ccc ggc act gaa ttg atg ctg caa aac cct agc gat caa 835
 Ala Asn Glu Pro Gly Thr Glu Leu Met Leu Gln Asn Pro Ser Asp Gln
 230 235 240 245
 gtc att gac tcc act gtt gct aat tgg gtg cca ggc agt aac agt gaa 883
 Val Ile Asp Ser Thr Val Ala Asn Trp Val Pro Gly Ser Asn Ser Glu
 250 255 260
 gaa cat ccg ctg gat tta tcc caa cgc gaa ctc cgc ctt gcc caa tgc 931
 Glu His Pro Leu Asp Leu Ser Gln Arg Glu Leu Arg Leu Ala Gln Cys
 265 270 275
 gac gca gcc ctg ggt aat aac ccg gaa gtt ttg ctt gct gat gaa ccc 979
 Asp Ala Ala Leu Gly Asn Asn Pro Glu Val Leu Leu Ala Asp Glu Pro
 280 285 290
 gac gtc ggc ctt gat gtc ggc ggt cga aac gcc atc cac cag cgc ttt 1027
 Asp Val Gly Leu Asp Val Gly Gly Arg Asn Ala Ile His Gln Arg Phe
 295 300 305
 gcg gat ttc tta ggg aat ggg gga gcg ctg atc ctg acc tgc cat gat 1075
 Ala Asp Phe Leu Gly Asn Gly Gly Ala Leu Ile Leu Thr Cys His Asp
 310 315 320 325
 gaa acc ttc gtg gca gag gta gct gaa tac gcg ata gtg aag gaa atg 1123
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 330 335 340
 ggg ctc taggtttctt tggaccaaac cac 1152
 Gly Leu

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<211> 343

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

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Thr Ala Asp Pro Arg Ala His Ile Thr Tyr Leu Arg Ala Thr Val Ala
 35 40 45

Glu Glu Leu Ala Phe Gly Leu Glu Gln Arg Gly Ile Val Pro Ala Gln
 50 55 60

Met Trp Glu Arg Val Arg Asn Ile Gly Leu Gly Leu Glu Asn Leu Leu
 65 70 75 80
 Asp Arg Ala Pro Ala Gln Leu Ser Gly Gly Gln Thr Arg Arg Leu Ala
 85 90 95
 Ile Gly Thr Val Ala Ile Leu Glu Ala Pro Thr Met Leu Leu Asp Asp
 100 105 110
 Pro Leu Ser Gly Leu Asp Thr Ser Ser Arg Ala Gln Leu Ile Thr Met
 115 120 125
 Leu Glu Ser Tyr Glu Gly Asp Val Ile Val Ala Ala His Lys Arg Trp
 130 135 140
 Leu Asp Ala Pro Thr Val Tyr Leu Gly Asp Leu Glu Glu Leu Ser Leu
 145 150 155 160
 Pro Ala Arg Val Glu Phe Ser Gly Pro Ser Arg Thr Phe Ser Ala Ile
 165 170 175
 Thr Gly Thr Arg Gly Gln Gln Arg Arg Arg Trp Trp Gln Phe Asn Glu
 180 185 190
 Ser Gln Pro Gln Phe Gln Ile Gly Pro Leu Asp Ile Thr Val Ser Ala
 195 200 205
 Gly Gln Val Leu Trp Leu Gln Gly Pro Asn Gly Ser Gly Lys Ser Thr
 210 215 220
 Leu Leu Arg Gly Leu Ala Asn Glu Pro Gly Thr Glu Leu Met Leu Gln
 225 230 235 240
 Asn Pro Ser Asp Gln Val Ile Asp Ser Thr Val Ala Asn Trp Val Pro
 245 250 255
 Gly Ser Asn Ser Glu Glu His Pro Leu Asp Leu Ser Gln Arg Glu Leu
 260 265 270
 Arg Leu Ala Gln Cys Asp Ala Ala Leu Gly Asn Asn Pro Glu Val Leu
 275 280 285
 Leu Ala Asp Glu Pro Asp Val Gly Leu Asp Val Gly Gly Arg Asn Ala
 290 295 300
 Ile His Gln Arg Phe Ala Asp Phe Leu Gly Asn Gly Gly Ala Leu Ile
 305 310 315 320
 Leu Thr Cys His Asp Glu Thr Phe Val Ala Glu Val Ala Glu Tyr Ala
 325 330 335
 Ile Val Lys Glu Met Gly Leu
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<210> 317

<211> 1152

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1129)

<223> FRXA02571

<400> 317

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Val Val Ala Leu Thr
1 5

caa atc gtc gga ccg tcc ggc tcc ggg ctc acg cgg gaa ttg gaa aaa 163
Gln Ile Val Gly Pro Ser Gly Ser Gly Leu Thr Arg Glu Leu Glu Lys
10 15 20

cgc tac cgg gaa acg ccc gga gcg gtg atg ctg acc gcc gac ccg cgc 211
Arg Tyr Arg Glu Thr Pro Gly Ala Val Met Leu Thr Ala Asp Pro Arg
25 30 35

gcg cat atc acc tac ctg cgc gcg aca gtc gcc gag gag ctg gcc ttt 259
Ala His Ile Thr Tyr Leu Arg Ala Thr Val Ala Glu Glu Leu Ala Phe
40 45 50

ggg ctg gaa caa cgc ggc atc gta ccc gcg cag atg tgg gag cgc gtc 307
Gly Leu Glu Gln Arg Gly Ile Val Pro Ala Gln Met Trp Glu Arg Val
55 60 65

cga aac atc ggg ctc ggc ctc gag aat ctg cta gac cgc gca ccc gcg 355
Arg Asn Ile Gly Leu Gly Leu Glu Asn Leu Leu Asp Arg Ala Pro Ala
70 75 80 85

caa ctt tcc ggc ggg caa aca cgg cgg ctg gcg atc ggc acc gtc gcc 403
Gln Leu Ser Gly Gly Gln Thr Arg Arg Leu Ala Ile Gly Thr Val Ala
90 95 100

atc tta gag gcg cca acg atg ctt ctc gac gac ccc ctc tcc ggt ctt 451
Ile Leu Glu Ala Pro Thr Met Leu Leu Asp Asp Pro Leu Ser Gly Leu
105 110 115

gat acc tcc tcg cga gcc caa ctc atc aca atg ttg gaa tca tat gag 499
Asp Thr Ser Ser Arg Ala Gln Leu Ile Thr Met Leu Glu Ser Tyr Glu
120 125 130

ggc gat gtc atc gtc gct gcg cac aag cgg tgg ctc gac gcg ccg act 547
Gly Asp Val Ile Val Ala Ala His Lys Arg Trp Leu Asp Ala Pro Thr
135 140 145

gtg tac tta ggg gat ttg gag gag ctg tcc ctg cct gcg cgg gtg gaa 595
Val Tyr Leu Gly Asp Leu Glu Glu Leu Ser Leu Pro Ala Arg Val Glu
150 155 160 165

ttt tcc ggt cca tcg cga acg ttt tca gcg att aca gga acc cgc gga 643
Phe Ser Gly Pro Ser Arg Thr Phe Ser Ala Ile Thr Gly Thr Arg Gly
170 175 180

caa caa cgc cga cgc tgg tgg caa ttc aac gaa tcc caa cca cag ttt 691
Gln Gln Arg Arg Arg Trp Trp Gln Phe Asn Glu Ser Gln Pro Gln Phe
185 190 195

cag atc ggc ccc ctg gat att act gtt tct gca ggt caa gtg ctg tgg 739

Gln Ile Gly Pro Leu Asp Ile Thr Val Ser Ala Gly Gln Val Leu Trp
 200 205 210

ttg cag ggt ccc aat ggt tca ggg aag tcc aca ctc ctg cgt ggt ctt 787
 Leu Gln Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Leu Arg Gly Leu
 215 220 225

gcc aat gaa ccc ggc act gaa ttg atg ctg caa aac cct agc gat caa 835
 Ala Asn Glu Pro Gly Thr Glu Leu Met Leu Gln Asn Pro Ser Asp Gln
 230 235 240 245

gtc att gac tcc act gtt gct aat tgg gtg cca ggc agt aac agt gaa 883
 Val Ile Asp Ser Thr Val Ala Asn Trp Val Pro Gly Ser Asn Ser Glu
 250 255 260

gaa cat ccg ctg gat tta tcg caa cgc gaa ctc cgc ctt gcc caa tgc 931
 Glu His Pro Leu Asp Leu Ser Gln Arg Glu Leu Arg Leu Ala Gln Cys
 265 270 275

gac gca gcc ctg ggt aat aac ccg gaa gtt ttg ctt gct gat gaa ccc 979
 Asp Ala Ala Leu Gly Asn Asn Pro Glu Val Leu Leu Ala Asp Glu Pro
 280 285 290

gac gtc ggc ctt gat gtc ggc ggt cga aac gcc atc cac cag cgc ttt 1027
 Asp Val Gly Leu Asp Val Gly Gly Arg Asn Ala Ile His Gln Arg Phe
 295 300 305

gcg gat ttc tta ggg aat ggg gga gcg ctg atc ctg acc tgc cat gat 1075
 Ala Asp Phe Leu Gly Asn Gly Gly Ala Leu Ile Leu Thr Cys His Asp
 310 315 320 325

gaa acc ttc gtg gca gag gta gct gaa tac gcg ata gtg aag gaa atg 1123
 Glu Thr Phe Val Ala Glu Val Ala Glu Tyr Ala Ile Val Lys Glu Met
 330 335 340

ggg ctc taggtttctt tggaccaaac cac 1152
 Gly Leu

<210> 318

<211> 343

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Val Val Ala Leu Thr Gln Ile Val Gly Pro Ser Gly Ser Gly Leu Thr
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Arg Glu Leu Glu Lys Arg Tyr Arg Glu Thr Pro Gly Ala Val Met Leu
 20 25 30

Thr Ala Asp Pro Arg Ala His Ile Thr Tyr Leu Arg Ala Thr Val Ala
 35 40 45

Glu Glu Leu Ala Phe Gly Leu Glu Gln Arg Gly Ile Val Pro Ala Gln
 50 55 60

Met Trp Glu Arg Val Arg Asn Ile Gly Leu Gly Leu Glu Asn Leu Leu
 65 70 75 80

Asp Arg Ala Pro Ala Gln Leu Ser Gly Gly Gln Thr Arg Arg Leu Ala
 85 90 95
 Ile Gly Thr Val Ala Ile Leu Glu Ala Pro Thr Met Leu Leu Asp Asp
 100 105 110
 Pro Leu Ser Gly Leu Asp Thr Ser Ser Arg Ala Gln Leu Ile Thr Met
 115 120 125
 Leu Glu Ser Tyr Glu Gly Asp Val Ile Val Ala Ala His Lys Arg Trp
 130 135 140
 Leu Asp Ala Pro Thr Val Tyr Leu Gly Asp Leu Glu Glu Leu Ser Leu
 145 150 155 160
 Pro Ala Arg Val Glu Phe Ser Gly Pro Ser Arg Thr Phe Ser Ala Ile
 165 170 175
 Thr Gly Thr Arg Gly Gln Gln Arg Arg Arg Trp Trp Gln Phe Asn Glu
 180 185 190
 Ser Gln Pro Gln Phe Gln Ile Gly Pro Leu Asp Ile Thr Val Ser Ala
 195 200 205
 Gly Gln Val Leu Trp Leu Gln Gly Pro Asn Gly Ser Gly Lys Ser Thr
 210 215 220
 Leu Leu Arg Gly Leu Ala Asn Glu Pro Gly Thr Glu Leu Met Leu Gln
 225 230 235 240
 Asn Pro Ser Asp Gln Val Ile Asp Ser Thr Val Ala Asn Trp Val Pro
 245 250 255
 Gly Ser Asn Ser Glu Glu His Pro Leu Asp Leu Ser Gln Arg Glu Leu
 260 265 270
 Arg Leu Ala Gln Cys Asp Ala Ala Leu Gly Asn Asn Pro Glu Val Leu
 275 280 285
 Leu Ala Asp Glu Pro Asp Val Gly Leu Asp Val Gly Gly Arg Asn Ala
 290 295 300
 Ile His Gln Arg Phe Ala Asp Phe Leu Gly Asn Gly Gly Ala Leu Ile
 305 310 315 320
 Leu Thr Cys His Asp Glu Thr Phe Val Ala Glu Val Ala Glu Tyr Ala
 325 330 335
 Ile Val Lys Glu Met Gly Leu
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<210> 319

<211> 1746

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1723)

<223> RXN02074

<400> 319

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              Met Arg Ser Leu Leu
              1           5

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cgt gat atc cct gcg gtg ggt tgg cta atc acc gcg acg att gtt gtg 163
Arg Asp Ile Pro Ala Val Gly Trp Leu Ile Thr Ala Thr Ile Val Val
 10 15 20

cgc acg ctc gtt gtt gcg ctg gtc atc gtt ggg atc ggc ttg ctt atc 211
 Arg Thr Leu Val Val Ala Leu Val Ile Val Gly Ile Gly Leu Leu Ile
 25 30 35

gac gtc ccc tgc ccc gct cat tca gcc atg ttg tgg tgg gtt ctg gca 259
Asp Val Pro Ser Pro Ala His Ser Ala Met Leu Trp Trp Val Leu Ala
40 45 50

ggt gcc acg gca gca gct gcg ctg ctg tgc gcg gaa gcg gtg ctc ccc 307
Gly Ala Thr Ala Ala Ala Ala Leu Leu Cys Ala Glu Ala Val Leu Pro
55 60 65

caa cgt att cgt gca cga gtt gaa cga tcc tgg cgg cgg cag ttg gct 355
Gln Arg Ile Arg Ala Arg Val Glu Arg Ser Trp Arg Arg Gln Leu Ala
70 75 80 85

gct aaa aat ctg gag ctg aat tcc agt tcg tca gat gat gcc cag ttg 403
Ala Lys Asn Leu Glu Leu Asn Ser Ser Ser Ser Asp Asp Ala Gln Leu
90 95 100

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atc aca ctg gca act gaa gcc acc tca aaa gca tcc act tac aca gtg    451
Ile Thr Leu Ala Thr Glu Ala Thr Ser Lys Ala Ser Thr Tyr Thr Val
      105                      110                      115

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atg ttt ctg ggg cct tac ttt gca gta ttt ttg gcc cca ctg aca gtt 499
Met Phe Leu Gly Pro Tyr Phe Ala Val Phe Leu Ala Pro Leu Thr Val
120 125 130

att gcc gtt gtc ggc gcg gct att tcc tgg ccg att gcg ggg ata ctg 547
Ile Ala Val Val Gly Ala Ala Ile Ser Trp Pro Ile Ala Gly Ile Leu
135 140 145

tgc	ctc	ggg	ttg	tgc	gtg	ata	cct	ttc	gtt	att	tct	tgg	gca	cag	cgc	595
Cys	Leu	Gly	Leu	Cys	Val	Ile	Pro	Phe	Val	Ile	Ser	Trp	Ala	Gln	Arg	
150					155					160					165	

atg ttg aaa ggc gct ggc gcg gga tac ggg cga gca tct ggg cag ttg 643
Met Leu Lys Gly Ala Gly Ala Gly Tyr Gly Arg Ala Ser Gly Gln Leu
170 175 180

gca ggc gtg ttt ttg gaa tcg gtg cgc aca cta ggc acc acg atg atg 691
Ala Gly Val Phe Leu Glu Ser Val Arg Thr Leu Gly Thr Thr Met Met
185 190 195

ctg aat gcc gct ggg cag cgc agg cag atc atc aca cag cgc gca gag 739
Leu Asn Ala Ala Gly Gln Arg Arg Gln Ile Ile Thr Gln Arg Ala Glu
200 205 210

aat atg cgc tcc caa gtg atg tca ttg ctg tac cga aat caa ttg atg 787

Asn	Met	Arg	Ser	Gln	Val	Met	Ser	Leu	Leu	Tyr	Arg	Asn	Gln	Leu	Met	
215						220					225					
att	ctg	gtg	acc	gac	ggc	gtg	ttt	gga	gtt	gcc	acc	aca	atg	gtt	gct	835
Ile	Leu	Val	Thr	Asp	Gly	Val	Phe	Gly	Val	Ala	Thr	Thr	Met	Val	Ala	
230					235					240					245	
gcg	gtg	ttt	gcc	att	gga	gga	ttc	ttt	tca	ggc	tct	ctt	act	ctc	ggc	883
Ala	Val	Phe	Ala	Ile	Gly	Gly	Phe	Phe	Ser	Gly	Ser	Leu	Thr	Leu	Gly	
				250					255					260		
caa	gct	gta	gca	ctc	gta	ttg	ctg	gcc	agg	ctg	ctt	att	gat	ccc	atc	931
Gln	Ala	Val	Ala	Leu	Val	Leu	Leu	Ala	Arg	Leu	Leu	Ile	Asp	Pro	Ile	
			265					270					275			
aac	cgc	atg	ggc	cgc	acg	ttt	tac	acc	ggc	atg	gca	ggc	aaa	ccc	tcg	979
Asn	Arg	Met	Gly	Arg	Thr	Phe	Tyr	Thr	Gly	Met	Ala	Gly	Lys	Pro	Ser	
		280					285					290				
ctg	atc	gcc	att	gaa	aaa	gcc	ctc	gcg	aca	acc	ttt	act	gat	cag	cca	1027
Leu	Ile	Ala	Ile	Glu	Lys	Ala	Leu	Ala	Thr	Thr	Phe	Thr	Asp	Gln	Pro	
	295					300					305					
act	caa	cag	gga	cag	cgc	cac	gat	ggg	gat	ctg	gtg	gtc	aac	aac	ttg	1075
Thr	Gln	Gln	Gly	Gln	Arg	His	Asp	Gly	Asp	Leu	Val	Val	Asn	Asn	Leu	
310					315					320					325	
aag	atc	gcc	cgc	gat	cac	agg	gac	att	gtg	cac	ggc	atc	tct	ttc	agc	1123
Lys	Ile	Ala	Arg	Asp	His	Arg	Asp	Ile	Val	His	Gly	Ile	Ser	Phe	Ser	
				330					335					340		
att	ccc	cgc	ggc	tcc	cac	atc	gcg	gtg	gta	ggc	ccc	agt	ggc	gct	ggc	1171
Ile	Pro	Arg	Gly	Ser	His	Ile	Ala	Val	Val	Gly	Pro	Ser	Gly	Ala	Gly	
			345					350					355			
aaa	tcc	tct	gtg	gct	cta	gcg	ttg	tcc	gga	ctt	tta	gag	ttt	gat	ggc	1219
Lys	Ser	Ser	Val	Ala	Leu	Ala	Leu	Ser	Gly	Leu	Leu	Glu	Phe	Asp	Gly	
	360						365					370				
gcg	att	tcc	ctc	ggc	ggc	cac	aac	tgt	gag	atg	tta	gat	ctt	cgc	gcc	1267
Ala	Ile	Ser	Leu	Gly	Gly	His	Asn	Cys	Glu	Met	Leu	Asp	Leu	Arg	Ala	
	375					380					385					
tca	gtc	agt	ttc	gtg	ccc	caa	tcc	ccc	acg	ctg	ttt	agc	gga	agc	atc	1315
Ser	Val	Ser	Phe	Val	Pro	Gln	Ser	Pro	Thr	Leu	Phe	Ser	Gly	Ser	Ile	
390					395					400					405	
aaa	agc	aat	atc	gat	ctg	gcg	cgc	acg	ggc	gtt	gat	tct	gat	cac	atc	1363
Lys	Ser	Asn	Ile	Asp	Leu	Ala	Arg	Thr	Gly	Val	Asp	Ser	Asp	His	Ile	
				410					415					420		
cac	gca	gca	ctt	tta	ggc	gaa	gaa	ctc	ccc	gcg	gac	ctc	aaa	gtc	ggc	1411
His	Ala	Ala	Leu	Leu	Gly	Glu	Glu	Leu	Pro	Ala	Asp	Leu	Lys	Val	Gly	
			425					430					435			
gaa	acc	ggc	aaa	ggc	gtc	tcc	ggc	ggc	caa	gca	gca	cgc	att	tcc	att	1459
Glu	Thr	Gly	Lys	Gly	Val	Ser	Gly	Gly	Gln	Ala	Ala	Arg	Ile	Ser	Ile	
	440						445					450				
gcc	cga	ggc	tta	gta	aag	aat	gct	gcc	gtg	att	gtt	ctc	gac	gag	gcg	1507
Ala	Arg	Gly	Leu	Val	Lys	Asn	Ala	Ala	Val	Ile	Val	Leu	Asp	Glu	Ala	

455 460 465
 acc gca caa ctc gac tac acc aac gcc cgc cag gtt cga cat ctt gcc 1555
 Thr Ala Gln Leu Asp Tyr Thr Asn Ala Arg Gln Val Arg His Leu Ala
 470 475 480 485
 aaa tcc ctt gag tgc acg ttg gtt gag atc acc cac cgc cca tca gaa 1603
 Lys Ser Leu Glu Cys Thr Leu Val Glu Ile Thr His Arg Pro Ser Glu
 490 495 500
 gcc ctc gat gca gac ttc atc att gtt tta gag gat ggc caa ttg acc 1651
 Ala Leu Asp Ala Asp Phe Ile Ile Val Leu Glu Asp Gly Gln Leu Thr
 505 510 515
 atg atg gat aca ccc agc aac gtt tcc cag cac aat gcg ttt ttc cgc 1699
 Met Met Asp Thr Pro Ser Asn Val Ser Gln His Asn Ala Phe Phe Arg
 520 525 530
 acc gct gtg atg gag gaa gaa caa tgatttcccg acttctccaa ttg 1746
 Thr Ala Val Met Glu Glu Gln
 535 540

<210> 320
 <211> 541
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 320
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 Ala Thr Ile Val Val Arg Thr Leu Val Val Ala Leu Val Ile Val Gly
 20 25 30
 Ile Gly Leu Leu Ile Asp Val Pro Ser Pro Ala His Ser Ala Met Leu
 35 40 45
 Trp Trp Val Leu Ala Gly Ala Thr Ala Ala Ala Ala Leu Leu Cys Ala
 50 55 60
 Glu Ala Val Leu Pro Gln Arg Ile Arg Ala Arg Val Glu Arg Ser Trp
 65 70 75 80
 Arg Arg Gln Leu Ala Ala Lys Asn Leu Glu Leu Asn Ser Ser Ser Ser
 85 90 95
 Asp Asp Ala Gln Leu Ile Thr Leu Ala Thr Glu Ala Thr Ser Lys Ala
 100 105 110
 Ser Thr Tyr Thr Val Met Phe Leu Gly Pro Tyr Phe Ala Val Phe Leu
 115 120 125
 Ala Pro Leu Thr Val Ile Ala Val Val Gly Ala Ala Ile Ser Trp Pro
 130 135 140
 Ile Ala Gly Ile Leu Cys Leu Gly Leu Cys Val Ile Pro Phe Val Ile
 145 150 155 160
 Ser Trp Ala Gln Arg Met Leu Lys Gly Ala Gly Ala Gly Tyr Gly Arg
 165 170 175

Ala Ser Gly Gln Leu Ala Gly Val Phe Leu Glu Ser Val Arg Thr Leu
 180 185 190
 Gly Thr Thr Met Met Leu Asn Ala Ala Gly Gln Arg Arg Gln Ile Ile
 195 200 205
 Thr Gln Arg Ala Glu Asn Met Arg Ser Gln Val Met Ser Leu Leu Tyr
 210 215 220
 Arg Asn Gln Leu Met Ile Leu Val Thr Asp Gly Val Phe Gly Val Ala
 225 230 235 240
 Thr Thr Met Val Ala Ala Val Phe Ala Ile Gly Gly Phe Phe Ser Gly
 245 250 255
 Ser Leu Thr Leu Gly Gln Ala Val Ala Leu Val Leu Leu Ala Arg Leu
 260 265 270
 Leu Ile Asp Pro Ile Asn Arg Met Gly Arg Thr Phe Tyr Thr Gly Met
 275 280 285
 Ala Gly Lys Pro Ser Leu Ile Ala Ile Glu Lys Ala Leu Ala Thr Thr
 290 295 300
 Phe Thr Asp Gln Pro Thr Gln Gln Gly Gln Arg His Asp Gly Asp Leu
 305 310 315 320
 Val Val Asn Asn Leu Lys Ile Ala Arg Asp His Arg Asp Ile Val His
 325 330 335
 Gly Ile Ser Phe Ser Ile Pro Arg Gly Ser His Ile Ala Val Val Gly
 340 345 350
 Pro Ser Gly Ala Gly Lys Ser Ser Val Ala Leu Ala Leu Ser Gly Leu
 355 360 365
 Leu Glu Phe Asp Gly Ala Ile Ser Leu Gly Gly His Asn Cys Glu Met
 370 375 380
 Leu Asp Leu Arg Ala Ser Val Ser Phe Val Pro Gln Ser Pro Thr Leu
 385 390 395 400
 Phe Ser Gly Ser Ile Lys Ser Asn Ile Asp Leu Ala Arg Thr Gly Val
 405 410 415
 Asp Ser Asp His Ile His Ala Ala Leu Leu Gly Glu Glu Leu Pro Ala
 420 425 430
 Asp Leu Lys Val Gly Glu Thr Gly Lys Gly Val Ser Gly Gly Gln Ala
 435 440 445
 Ala Arg Ile Ser Ile Ala Arg Gly Leu Val Lys Asn Ala Ala Val Ile
 450 455 460
 Val Leu Asp Glu Ala Thr Ala Gln Leu Asp Tyr Thr Asn Ala Arg Gln
 465 470 475 480
 Val Arg His Leu Ala Lys Ser Leu Glu Cys Thr Leu Val Glu Ile Thr
 485 490 495

His Arg Pro Ser Glu Ala Leu Asp Ala Asp Phe Ile Ile Val Leu Glu
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Asp Gly Gln Leu Thr Met Met Asp Thr Pro Ser Asn Val Ser Gln His
 515 520 525

Asn Ala Phe Phe Arg Thr Ala Val Met Glu Glu Glu Gln
 530 535 540

<210> 321
 <211> 1746
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1723)
 <223> FRXA02074

<400> 321

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 Met Arg Ser Leu Leu
 1 5

cgt gat atc cct gcg gtg ggt tgg cta atc acc gcg acg att gtt gtg 163
 Arg Asp Ile Pro Ala Val Gly Trp Leu Ile Thr Ala Thr Ile Val Val
 10 15 20

cgc acg ctc gtt gtt gcg ctg gtc atc gtt ggg atc ggc ttg ctt atc 211
 Arg Thr Leu Val Val Ala Leu Val Ile Val Gly Ile Gly Leu Leu Ile
 25 30 35

gac gtc ccc tcg ccc gct cat tca gcc atg ttg tgg tgg gtt ctg gca 259
 Asp Val Pro Ser Pro Ala His Ser Ala Met Leu Trp Trp Val Leu Ala
 40 45 50

ggt gcc acg gca gca gct gcg ctg ctg tgc gcg gaa gcg gtg ctc ccc 307
 Gly Ala Thr Ala Ala Ala Ala Leu Leu Cys Ala Glu Ala Val Leu Pro
 55 60 65

caa cgt att cgt gca cga gtt gaa cga tcc tgg cgg cgg cag ttg gct 355
 Gln Arg Ile Arg Ala Arg Val Glu Arg Ser Trp Arg Arg Gln Leu Ala
 70 75 80 85

gct aaa aat ctg gag ctg aat tcc agt tcg tca gat gat gcc cag ttg 403
 Ala Lys Asn Leu Glu Leu Asn Ser Ser Ser Ser Asp Asp Ala Gln Leu
 90 95 100

atc aca ctg gca act gaa gcc acc tca aaa gca tcc act tac aca gtg 451
 Ile Thr Leu Ala Thr Glu Ala Thr Ser Lys Ala Ser Thr Tyr Thr Val
 105 110 115

atg ttt ctg ggg cct tac ttt gca gta ttt ttg gcc cca ctg aca gtt 499
 Met Phe Leu Gly Pro Tyr Phe Ala Val Phe Leu Ala Pro Leu Thr Val
 120 125 130

att gcc gtt gtc ggc gcg gct att tcc tgg ccg att gcg ggg ata ctg 547
 Ile Ala Val Val Gly Ala Ala Ile Ser Trp Pro Ile Ala Gly Ile Leu

135	140	145	
tgc ctc ggg ttg tgc gtg ata cct ttc gtt att tct tgg gca cag cgc Cys Leu Gly Leu Cys Val Ile Pro Phe Val Ile Ser Trp Ala Gln Arg 150 155 160 165			595
atg ttg aaa ggc gct ggc gcg gga tac ggg cga gca tct ggg cag ttg Met Leu Lys Gly Ala Gly Ala Gly Tyr Gly Arg Ala Ser Gly Gln Leu 170 175 180			643
gca ggc gtg ttt ttg gaa tcg gtg cgc aca cta ggc acc acg atg atg Ala Gly Val Phe Leu Glu Ser Val Arg Thr Leu Gly Thr Thr Met Met 185 190 195			691
ctg aat gcc gct ggg cag cgc agg cag atc atc aca cag cgc gca gag Leu Asn Ala Ala Gly Gln Arg Arg Gln Ile Ile Thr Gln Arg Ala Glu 200 205 210			739
aat atg cgc tcc caa gtg atg tca ttg ctg tac cga aat cag ttg atg Asn Met Arg Ser Gln Val Met Ser Leu Leu Tyr Arg Asn Gln Leu Met 215 220 225			787
att ctg gtg acc gac ggc gtg ttt gga gtt gcc acc aca atg gtt gct Ile Leu Val Thr Asp Gly Val Phe Gly Val Ala Thr Thr Met Val Ala 230 235 240 245			835
gcg gtg ttt gcc att gga gga ttc ttt tca ggc tct ctt act ctc ggc Ala Val Phe Ala Ile Gly Gly Phe Phe Ser Gly Ser Leu Thr Leu Gly 250 255 260			883
caa gct gta gca ctc gta ttg ctg gcc agg ctg ctt att gat ccc atc Gln Ala Val Ala Leu Val Leu Leu Ala Arg Leu Leu Ile Asp Pro Ile 265 270 275			931
aac cgc atg ggt cgc acg ttt tac acc ggc atg gca ggc aaa ccc tcg Asn Arg Met Gly Arg Thr Phe Tyr Thr Gly Met Ala Gly Lys Pro Ser 280 285 290			979
ctg atc gcc att gaa aaa gcc ctc gcg aca acc ttt act gat cag cca Leu Ile Ala Ile Glu Lys Ala Leu Ala Thr Thr Phe Thr Asp Gln Pro 295 300 305			1027
act caa cag gga cag cgc cac gat ggg gat ctg gtg gtc aac aac ttg Thr Gln Gln Gly Gln Arg His Asp Gly Asp Leu Val Val Asn Asn Leu 310 315 320 325			1075
aag atc gcc cgc gat cac agg gac att gtg cac ggt atc tct ttc agc Lys Ile Ala Arg Asp His Arg Asp Ile Val His Gly Ile Ser Phe Ser 330 335 340			1123
att ccc cgc ggt tcc cac atc gcg gtg gta ggt ccc agt ggc gct ggt Ile Pro Arg Gly Ser His Ile Ala Val Val Gly Pro Ser Gly Ala Gly 345 350 355			1171
aaa tcc tct gtg gct cta gcg ttg tcc gga ctt tta gag ttt gat ggt Lys Ser Ser Val Ala Leu Ala Leu Ser Gly Leu Leu Glu Phe Asp Gly 360 365 370			1219
gcg att tcc ctc ggc ggc cac aac tgt gag atg tta gat ctt cgc gcc Ala Ile Ser Leu Gly Gly His Asn Cys Glu Met Leu Asp Leu Arg Ala 375 380 385			1267

tca gtc agt ttc gtg ccc caa tcc ccc acg ctg ttt agc gga agc atc 1315
 Ser Val Ser Phe Val Pro Gln Ser Pro Thr Leu Phe Ser Gly Ser Ile
 390 395 400 405

aaa agc aat atc gat ctg gcg cgc acg ggt gtt gat tct gat cac atc 1363
 Lys Ser Asn Ile Asp Leu Ala Arg Thr Gly Val Asp Ser Asp His Ile
 410 415 420

cac gca gca ctt tta ggc gaa gaa ctc ccc gcg gac ctc aaa gtc ggt 1411
 His Ala Ala Leu Leu Gly Glu Glu Leu Pro Ala Asp Leu Lys Val Gly
 425 430 435

gaa acc ggc aaa ggt gtc tcc ggc ggc caa gca gca cgc att tcc att 1459
 Glu Thr Gly Lys Gly Val Ser Gly Gly Gln Ala Ala Arg Ile Ser Ile
 440 445 450

gcc cga ggt tta gta aag aat gct gcc gtg att gtt ctc gac gag gcg 1507
 Ala Arg Gly Leu Val Lys Asn Ala Ala Val Ile Val Leu Asp Glu Ala
 455 460 465

acc gca caa ctc gac tac acc aac gcc cgc cag gtt cga cat ctt gcc 1555
 Thr Ala Gln Leu Asp Tyr Thr Asn Ala Arg Gln Val Arg His Leu Ala
 470 475 480 485

aaa tcc ctt gag tgc acg ttg gtt gag atc acc cac cgc cca tca gaa 1603
 Lys Ser Leu Glu Cys Thr Leu Val Glu Ile Thr His Arg Pro Ser Glu
 490 495 500

gcc ctc gat gca gac ttc atc att gtt tta gag gat ggc caa ttg acc 1651
 Ala Leu Asp Ala Asp Phe Ile Ile Val Leu Glu Asp Gly Gln Leu Thr
 505 510 515

atg atg gat aca ccc agc aac gtt tcc cag cac aat gcg ttt ttc cgc 1699
 Met Met Asp Thr Pro Ser Asn Val Ser Gln His Asn Ala Phe Phe Arg
 520 525 530

acc gct gtg atg gag gaa gaa caa tgatttcccg acttctccaa ttg 1746
 Thr Ala Val Met Glu Glu Glu Gln
 535 540

<210> 322

<211> 541

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Met Arg Ser Leu Leu Arg Asp Ile Pro Ala Val Gly Trp Leu Ile Thr
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Ala Thr Ile Val Val Arg Thr Leu Val Val Ala Leu Val Ile Val Gly
 20 25 30

Ile Gly Leu Leu Ile Asp Val Pro Ser Pro Ala His Ser Ala Met Leu
 35 40 45

Trp Trp Val Leu Ala Gly Ala Thr Ala Ala Ala Ala Leu Leu Cys Ala
 50 55 60

Glu Ala Val Leu Pro Gln Arg Ile Arg Ala Arg Val Glu Arg Ser Trp

65	70					75					80				
Arg Arg Gln Leu Ala Ala Lys Asn Leu Glu Leu Asn Ser Ser Ser Ser	85					90					95				
Asp Asp Ala Gln Leu Ile Thr Leu Ala Thr Glu Ala Thr Ser Lys Ala	100					105					110				
Ser Thr Tyr Thr Val Met Phe Leu Gly Pro Tyr Phe Ala Val Phe Leu	115					120					125				
Ala Pro Leu Thr Val Ile Ala Val Val Gly Ala Ala Ile Ser Trp Pro	130					135					140				
Ile Ala Gly Ile Leu Cys Leu Gly Leu Cys Val Ile Pro Phe Val Ile	145					150					155				
Ser Trp Ala Gln Arg Met Leu Lys Gly Ala Gly Ala Gly Tyr Gly Arg	165					170					175				
Ala Ser Gly Gln Leu Ala Gly Val Phe Leu Glu Ser Val Arg Thr Leu	180					185					190				
Gly Thr Thr Met Met Leu Asn Ala Ala Gly Gln Arg Arg Gln Ile Ile	195					200					205				
Thr Gln Arg Ala Glu Asn Met Arg Ser Gln Val Met Ser Leu Leu Tyr	210					215					220				
Arg Asn Gln Leu Met Ile Leu Val Thr Asp Gly Val Phe Gly Val Ala	225					230					235				
Thr Thr Met Val Ala Ala Val Phe Ala Ile Gly Gly Phe Phe Ser Gly	245					250					255				
Ser Leu Thr Leu Gly Gln Ala Val Ala Leu Val Leu Leu Ala Arg Leu	260					265					270				
Leu Ile Asp Pro Ile Asn Arg Met Gly Arg Thr Phe Tyr Thr Gly Met	275					280					285				
Ala Gly Lys Pro Ser Leu Ile Ala Ile Glu Lys Ala Leu Ala Thr Thr	290					295					300				
Phe Thr Asp Gln Pro Thr Gln Gln Gly Gln Arg His Asp Gly Asp Leu	305					310					315				
Val Val Asn Asn Leu Lys Ile Ala Arg Asp His Arg Asp Ile Val His	325					330					335				
Gly Ile Ser Phe Ser Ile Pro Arg Gly Ser His Ile Ala Val Val Gly	340					345					350				
Pro Ser Gly Ala Gly Lys Ser Ser Val Ala Leu Ala Leu Ser Gly Leu	355					360					365				
Leu Glu Phe Asp Gly Ala Ile Ser Leu Gly Gly His Asn Cys Glu Met	370					375					380				
Leu Asp Leu Arg Ala Ser Val Ser Phe Val Pro Gln Ser Pro Thr Leu	385					390					395				
											400				

Phe Ser Gly Ser Ile Lys Ser Asn Ile Asp Leu Ala Arg Thr Gly Val
 405 410 415
 Asp Ser Asp His Ile His Ala Ala Leu Leu Gly Glu Glu Leu Pro Ala
 420 425 430
 Asp Leu Lys Val Gly Glu Thr Gly Lys Gly Val Ser Gly Gly Gln Ala
 435 440 445
 Ala Arg Ile Ser Ile Ala Arg Gly Leu Val Lys Asn Ala Ala Val Ile
 450 455 460
 Val Leu Asp Glu Ala Thr Ala Gln Leu Asp Tyr Thr Asn Ala Arg Gln
 465 470 475 480
 Val Arg His Leu Ala Lys Ser Leu Glu Cys Thr Leu Val Glu Ile Thr
 485 490 495
 His Arg Pro Ser Glu Ala Leu Asp Ala Asp Phe Ile Ile Val Leu Glu
 500 505 510
 Asp Gly Gln Leu Thr Met Met Asp Thr Pro Ser Asn Val Ser Gln His
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 Asn Ala Phe Phe Arg Thr Ala Val Met Glu Glu Glu Gln
 530 535 540

<210> 323
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1504)
 <223> RXA02095

<400> 323
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 tactcccca acaggctcaa aaatactgaa aggctcacgc atg aaa act gag caa 115
 Met Lys Thr Glu Gln
 1 5
 tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag cca caa 163
 Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln
 10 15 20
 cgc atc cgc caa ctt att tcc gtg gcg tgg cag cga cct tgg ctc acc 211
 Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr
 25 30 35
 tca ttc acc gta atc agc gct tta gct gca acg ttg ttt gaa ctt aca 259
 Ser Phe Thr Val Ile Ser Ala Leu Ala Thr Leu Phe Glu Leu Thr
 40 45 50
 ctt cct ctt ttg acc ggt ggc gcc atc gat atc gcg ctc gga aat acc 307
 Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asn Thr
 55 60 65

gga gat act tta acc act gac ctg ctg gac cgg ttc act ccg agt gga	355
Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly	
70 75 80 85	
tta agc gtg ttg acc agc gtc att gcc ctt atc gtg ctt ctc gcg ttg	403
Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu	
90 95 100	
ctt cgc tat gcc agt caa ttt gga cgg cga tac acc gca ggc aag ctc	451
Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu	
105 110 115	
agc atg ggg gta cag cat gat gtc cgg ctt aaa acg atg cgc tca ttg	499
Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu	
120 125 130	
cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta	547
Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val	
135 140 145	
gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gcg	595
Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala	
150 155 160 165	
atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg	643
Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu	
170 175 180	
gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg	691
Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val	
185 190 195	
ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcg ctt	739
Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu	
200 205 210	
ttt gcg tcc acg tgg tcg gcc cag caa aag gct gcg gat ctg acc act	787
Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala Ala Asp Leu Thr Thr	
215 220 225	
cat gtg gaa gaa act gtc acg ggt atc cgc gtg gtc aag gca ttt gcg	835
His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala	
230 235 240 245	
cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta	883
Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu	
250 255 260	
ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc	931
Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro	
265 270 275	
atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc	979
Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly	
280 285 290	
ggc ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg	1027
Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val	
295 300 305	

gcg ttt tct tcc tat ctc act agc ttg tcg gcg gtg gct agg tcc ctg 1075
 Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala Val Ala Arg Ser Leu
 310 315 320 325

tcg ggc atg ctc atg cgc gtg cag ttg gcg ctg tct tct gtg gag cgc 1123
 Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg
 330 335 340

atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac 1171
 Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg Thr Asp Pro Ala His
 345 350 355

ccc ctg tca ctt ccc gac act ccc ctg ggt ctg tcg ttc aac aac gta 1219
 Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val
 360 365 370

gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt 1267
 Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly
 375 380 385

gaa acc gtt gtg ttg gtg ggc cct cca ggt tca ggc aag acc atg gct 1315
 Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala
 390 395 400 405

gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc 1363
 Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala
 410 415 420

ttt gat agc aac ggc cat cgc act cgc ttc gac gac ctc acc cac agc 1411
 Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser
 425 430 435

gat atc cgc agg aat ctc atc gcg gtt ttt gat gag ccg ttc ttg tac 1459
 Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr
 440 445 450

tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag 1504
 Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly Phe Gly Cys Gln
 455 460 465

tgatgagcag atcgaacacg cag 1527

<210> 324

<211> 468

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

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Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
 35 40 45

Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
 50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
 65 70 75 80
 Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile
 85 90 95
 Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr
 100 105 110
 Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
 115 120 125
 Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
 130 135 140
 Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val
 145 150 155 160
 Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys
 165 170 175
 Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr
 180 185 190
 Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr
 195 200 205
 Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala
 210 215 220
 Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val
 225 230 235 240
 Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu
 245 250 255
 Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr
 260 265 270
 Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val
 275 280 285
 Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr
 290 295 300
 Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala
 305 310 315 320
 Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu
 325 330 335
 Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg
 340 345 350
 Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu
 355 360 365
 Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu
 370 375 380
 Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser

[illegible]

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<211> 905
<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (1)..(882)  
<223> RXA02225
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Gln	Thr	Glu	Glu	Arg	Phe	Gly	Ala	Ala	Ala	Asp	Glu	Ala	Leu	Ala	Ile	
1				5					10					15		
atg	ttg	aag	gaa	gct	cgt	ctg	cag	tcg	ttg	ctg	act	ttt	gtg	cgc	caa	96
Met	Leu	Lys	Glu	Ala	Arg	Leu	Gln	Ser	Leu	Leu	Thr	Phe	Val	Arg	Gln	
			20					25					30			
ctt	gtc	cca	gcg	gtg	ttt	tct	gtg	ggg	ctt	ttg	gct	tat	gcg	tca	ctg	144
Leu	Val	Pro	Ala	Val	Phe	Ser	Val	Gly	Leu	Leu	Ala	Tyr	Ala	Ser	Leu	
		35					40					45				
ttg	gct	ttt	gac	ggg	gac	ata	act	ggg	ggg	gag	atg	atc	tcg	gtg	acg	192
Leu	Ala	Phe	Asp	Gly	Asp	Ile	Thr	Gly	Gly	Glu	Met	Ile	Ser	Val	Thr	
	50					55					60					
ttg	ctg	gtg	cca	cct	tcg	ttg	act	gtg	ttg	ggg	gtg	tcg	ctt	ggc	atg	240
Leu	Leu	Val	Pro	Pro	Ser	Leu	Thr	Val	Leu	Gly	Val	Ser	Leu	Gly	Met	
65					70					75				80		
atg	aca	gag	att	tgg	gct	agg	gga	cag	gct	tcg	aca	aaa	agg	gtc	caa	288
Met	Thr	Glu	Ile	Trp	Ala	Arg	Gly	Gln	Ala	Ser	Thr	Lys	Arg	Val	Gln	
				85					90					95		
aac	tta	gtc	act	gaa	ctg	gat	aag	gcg	gcc	gct	gag	cca	cga	cct	cag	336
Asn	Leu	Val	Thr	Glu	Leu	Asp	Lys	Ala	Ala	Ala	Glu	Pro	Arg	Pro	Gln	
			100					105					110			
cct	gcc	acc	ttt	gaa	ttt	gaa	gag	ggg	atc	acg	gtg	tgg	gat	cct	tcg	384
Pro	Ala	Thr	Phe	Glu	Phe	Glu	Glu	Gly	Ile	Thr	Val	Trp	Asp	Pro	Ser	
		115					120					125				

aca cct gag gca cgc gat gtg att gat cgg gag ttg gag gcg ctt cag 432
 Thr Pro Glu Ala Arg Asp Val Ile Asp Arg Glu Leu Glu Ala Leu Gln
 130 135 140

gtt cgc gaa gat gtc att gtg gct cct cac cgc gtc agc gtg ttt gaa 480
 Val Arg Glu Asp Val Ile Val Ala Pro His Arg Val Ser Val Phe Glu
 145 150 155 160

ggt gtg ctg aag gat aat ttg aat ccg atg ggc act atc gca ccg gag 528
 Gly Val Leu Lys Asp Asn Leu Asn Pro Met Gly Thr Ile Ala Pro Glu
 165 170 175

atg ctg cgc gct gct ctt cat gct gca agt tgt gag gac atc ttg agc 576
 Met Leu Arg Ala Ala Leu His Ala Ala Ser Cys Glu Asp Ile Leu Ser
 180 185 190

cga ttg ggt gct gat ctg aac atg ccg ggg gag ttt gag ctt cca gat 624
 Arg Leu Gly Ala Asp Leu Asn Met Pro Gly Glu Phe Glu Leu Pro Asp
 195 200 205

acc ttg atc ggc gag gcc gga ttg aat ctc tcc ggt ggc caa cgc cag 672
 Thr Leu Ile Gly Glu Ala Gly Leu Asn Leu Ser Gly Gly Gln Arg Gln
 210 215 220

agg att gct ttg gca cga ttc ttg gct gtt gat cct gag gtg ctc att 720
 Arg Ile Ala Leu Ala Arg Phe Leu Ala Val Asp Pro Glu Val Leu Ile
 225 230 235 240

ttg gat gaa ccg acc acg ggg ttg gat gcg gtg acc ctg gat gaa gtg 768
 Leu Asp Glu Pro Thr Thr Gly Leu Asp Ala Val Thr Leu Asp Glu Val
 245 250 255

gca cat cgc gtc gaa aag ctt cgt cga ggc cgg aaa acc gtc gtc att 816
 Ala His Arg Val Glu Lys Leu Arg Arg Gly Arg Lys Thr Val Val Ile
 260 265 270

acg tcg aac ccg acg tgg cac ggc gtc gca aag cag atg caa tct gat 864
 Thr Ser Asn Pro Thr Trp His Gly Val Ala Lys Gln Met Gln Ser Asp
 275 280 285

ttt tcg gaa ggg gtg aag tagatggcgc agcatgagcg cgt 905
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<210> 326

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

Gln Thr Glu Glu Arg Phe Gly Ala Ala Ala Asp Glu Ala Leu Ala Ile
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Met Leu Lys Glu Ala Arg Leu Gln Ser Leu Leu Thr Phe Val Arg Gln
 20 25 30

Leu Val Pro Ala Val Phe Ser Val Gly Leu Leu Ala Tyr Ala Ser Leu
 35 40 45

Leu Ala Phe Asp Gly Asp Ile Thr Gly Gly Glu Met Ile Ser Val Thr

50 55 60
 Leu Leu Val Pro Pro Ser Leu Thr Val Leu Gly Val Ser Leu Gly Met
 65 70 75 80
 Met Thr Glu Ile Trp Ala Arg Gly Gln Ala Ser Thr Lys Arg Val Gln
 85 90 95
 Asn Leu Val Thr Glu Leu Asp Lys Ala Ala Glu Pro Arg Pro Gln
 100 105 110
 Pro Ala Thr Phe Glu Phe Glu Glu Gly Ile Thr Val Trp Asp Pro Ser
 115 120 125
 Thr Pro Glu Ala Arg Asp Val Ile Asp Arg Glu Leu Glu Ala Leu Gln
 130 135 140
 Val Arg Glu Asp Val Ile Val Ala Pro His Arg Val Ser Val Phe Glu
 145 150 155 160
 Gly Val Leu Lys Asp Asn Leu Asn Pro Met Gly Thr Ile Ala Pro Glu
 165 170 175
 Met Leu Arg Ala Ala Leu His Ala Ala Ser Cys Glu Asp Ile Leu Ser
 180 185 190
 Arg Leu Gly Ala Asp Leu Asn Met Pro Gly Glu Phe Glu Leu Pro Asp
 195 200 205
 Thr Leu Ile Gly Glu Ala Gly Leu Asn Leu Ser Gly Gly Gln Arg Gln
 210 215 220
 Arg Ile Ala Leu Ala Arg Phe Leu Ala Val Asp Pro Glu Val Leu Ile
 225 230 235 240
 Leu Asp Glu Pro Thr Thr Gly Leu Asp Ala Val Thr Leu Asp Glu Val
 245 250 255
 Ala His Arg Val Glu Lys Leu Arg Arg Gly Arg Lys Thr Val Val Ile
 260 265 270
 Thr Ser Asn Pro Thr Trp His Gly Val Ala Lys Gln Met Gln Ser Asp
 275 280 285
 Phe Ser Glu Gly Val Lys
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<210> 327
 <211> 1050
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1027)
 <223> RXA02253

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tcttcacgcg tcaaaataag tagatcgcta ggatgtaacc	atg att caa tcc act	115
	Met Ile Gln Ser Thr	
	1 5	
ggg gtc acg cac act gat aag tct gca caa gaa aat cct gtg aag tac	163	
Gly Val Thr His Thr Asp Lys Ser Ala Gln Glu Asn Pro Val Lys Tyr		
	10 15 20	
agg gac aat ttc aca cct gtc atc atc acc ggt atg tca ggc gca ggt	211	
Arg Asp Asn Phe Thr Pro Val Ile Ile Thr Gly Met Ser Gly Ala Gly		
	25 30 35	
ctg agc aca gca gcc cga gtc ctc gaa gac ttg ggt tgg tat gtg gcg	259	
Leu Ser Thr Ala Ala Arg Val Leu Glu Asp Leu Gly Trp Tyr Val Ala		
	40 45 50	
cac aat att cca cca cag atc atc ctg gaa tta att gat atg tgc gct	307	
His Asn Ile Pro Pro Gln Ile Ile Leu Glu Leu Ile Asp Met Cys Ala		
	55 60 65	
cgg gaa gat tct ccc gtc gac aaa gtt gca gtc gtg tgc gat gtg cgc	355	
Arg Glu Asp Ser Pro Val Asp Lys Val Ala Val Val Cys Asp Val Arg		
	70 75 80 85	
tcc cgt gaa ttc cgc gga agc ctc acc cag gtt gtt tca gag ctg cgt	403	
Ser Arg Glu Phe Arg Gly Ser Leu Thr Gln Val Val Ser Glu Leu Arg		
	90 95 100	
gat aag cag ctc gat ccc acg gtg tta ttt ctg gaa gca cgc gat gag	451	
Asp Lys Gln Leu Asp Pro Thr Val Leu Phe Leu Glu Ala Arg Asp Glu		
	105 110 115	
gtg ctg atc aag cga ttc gat aat gtg cgc cgc acc cat cct ttg cag	499	
Val Leu Ile Lys Arg Phe Asp Asn Val Arg Arg Thr His Pro Leu Gln		
	120 125 130	
ggc agc caa acc ctt cag gtg ggt att gaa cgt gaa cga acc gtg ctg	547	
Gly Ser Gln Thr Leu Gln Val Gly Ile Glu Arg Glu Arg Thr Val Leu		
	135 140 145	
tct cct gtg aag gaa gac gct tca gtg gtc atc gat acc tcg gat ctg	595	
Ser Pro Val Lys Glu Asp Ala Ser Val Val Ile Asp Thr Ser Asp Leu		
	150 155 160 165	
tcc gtg cat gat ttg cgc cgc gcc atc gaa tcc tcg ttt agg aca atc	643	
Ser Val His Asp Leu Arg Arg Ala Ile Glu Ser Ser Phe Arg Thr Ile		
	170 175 180	
gcc acg cgc acc cag cac gtc acc att gaa tca ttc ggt ttc aaa cac	691	
Ala Thr Arg Thr Gln His Val Thr Ile Glu Ser Phe Gly Phe Lys His		
	185 190 195	
ggc tca cca cgc gac gcc gac ttt gtt gtg gac gtg cgt ttc ttg ccg	739	
Gly Ser Pro Arg Asp Ala Asp Phe Val Val Asp Val Arg Phe Leu Pro		
	200 205 210	
aac cca ttc tgg gtt cca gag ctg cgc cca ttt agg gga gtg gac aag	787	
Asn Pro Phe Trp Val Pro Glu Leu Arg Pro Phe Arg Gly Val Asp Lys		
	215 220 225	
cca gta tct gac tat gtg ctc tcc caa aaa ggc gca gaa gaa ttt ttg	835	

Pro Val Ser Asp Tyr Val Leu Ser Gln Lys Gly Ala Glu Glu Phe Leu
 230 235 240 245

aac aac ttt gtg gac atg ctc aaa gac atg ctt ccg gga tac cgc cac 883
 Asn Asn Phe Val Asp Met Leu Lys Asp Met Leu Pro Gly Tyr Arg His
 250 255 260

gaa gga aaa aac ttc atc aca atc ggt gtc ggc tgc acc ggt gga cac 931
 Glu Gly Lys Asn Phe Ile Thr Ile Gly Val Gly Cys Thr Gly Gly His
 265 270 275

cac aga tca gtt gcg gtg tct gaa gaa cta gcc aaa aga atc gca gat 979
 His Arg Ser Val Ala Val Ser Glu Glu Leu Ala Lys Arg Ile Ala Asp
 280 285 290

cag acc acg ctc gac gtg tct gta gta cac cgc gat att aac cgc cac 1027
 Gln Thr Thr Leu Asp Val Ser Val Val His Arg Asp Ile Asn Arg His
 295 300 305

taggaaaggg gccaaactaat tga 1050

<210> 328
 <211> 309
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 328

Met Ile Gln Ser Thr Gly Val Thr His Thr Asp Lys Ser Ala Gln Glu
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Asn Pro Val Lys Tyr Arg Asp Asn Phe Thr Pro Val Ile Ile Thr Gly
 20 25 30

Met Ser Gly Ala Gly Leu Ser Thr Ala Ala Arg Val Leu Glu Asp Leu
 35 40 45

Gly Trp Tyr Val Ala His Asn Ile Pro Pro Gln Ile Ile Leu Glu Leu
 50 55 60

Ile Asp Met Cys Ala Arg Glu Asp Ser Pro Val Asp Lys Val Ala Val
 65 70 75 80

Val Cys Asp Val Arg Ser Arg Glu Phe Arg Gly Ser Leu Thr Gln Val
 85 90 95

Val Ser Glu Leu Arg Asp Lys Gln Leu Asp Pro Thr Val Leu Phe Leu
 100 105 110

Glu Ala Arg Asp Glu Val Leu Ile Lys Arg Phe Asp Asn Val Arg Arg
 115 120 125

Thr His Pro Leu Gln Gly Ser Gln Thr Leu Gln Val Gly Ile Glu Arg
 130 135 140

Glu Arg Thr Val Leu Ser Pro Val Lys Glu Asp Ala Ser Val Val Ile
 145 150 155 160

Asp Thr Ser Asp Leu Ser Val His Asp Leu Arg Arg Ala Ile Glu Ser
 165 170 175

Ser Phe Arg Thr Ile Ala Thr Arg Thr Gln His Val Thr Ile Glu Ser
 180 185 190

Phe Gly Phe Lys His Gly Ser Pro Arg Asp Ala Asp Phe Val Val Asp
 195 200 205

Val Arg Phe Leu Pro Asn Pro Phe Trp Val Pro Glu Leu Arg Pro Phe
 210 215 220

Arg Gly Val Asp Lys Pro Val Ser Asp Tyr Val Leu Ser Gln Lys Gly
 225 230 235 240

Ala Glu Glu Phe Leu Asn Asn Phe Val Asp Met Leu Lys Asp Met Leu
 245 250 255

Pro Gly Tyr Arg His Glu Gly Lys Asn Phe Ile Thr Ile Gly Val Gly
 260 265 270

Cys Thr Gly Gly His His Arg Ser Val Ala Val Ser Glu Glu Leu Ala
 275 280 285

Lys Arg Ile Ala Asp Gln Thr Thr Leu Asp Val Ser Val Val His Arg
 290 295 300

Asp Ile Asn Arg His
 305

<210> 329
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> RXN01881

<400> 329
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 Met Ala Asn Leu Ile
 1 5

aat ctc gag aac gtc tcc aaa acc tgg gga tta aaa acg ctt ctc gac 163
 Asn Leu Glu Asn Val Ser Lys Thr Trp Gly Leu Lys Thr Leu Leu Asp
 10 15 20

ggg gtc tcc tta ggt gtt caa acc ggc gac cgc att ggc gtc gtc ggc 211
 Gly Val Ser Leu Gly Val Gln Thr Gly Asp Arg Ile Gly Val Val Gly
 25 30 35

ctc aat ggt ggc gga aaa acc acc ctg ctg gaa gta ctt act ggc atc 259
 Leu Asn Gly Gly Gly Lys Thr Thr Leu Leu Glu Val Leu Thr Gly Ile
 40 45 50

gaa aag ccg gat cag ggc cgt gtg tct cac aac tct gac ctg cgc atg 307
 Glu Lys Pro Asp Gln Gly Arg Val Ser His Asn Ser Asp Leu Arg Met
 55 60 65

gct gtg gtg acg cag cgt gct gaa ctc aat gat gac gac acc gtc gct 355
 Ala Val Val Thr Gln Arg Ala Glu Leu Asn Asp Asp Asp Thr Val Ala
 70 75 80 85

gac gtg gtg ctt gga cct ttg ggt ttg gaa gtt ttc gaa tgg gca tca 403
 Asp Val Val Leu Gly Pro Leu Gly Leu Glu Val Phe Glu Trp Ala Ser
 90 95 100

aac gcc acg gtg cgc gac gtc ctc ggt ggc ttg ggc att gtc gat ctt 451
 Asn Ala Thr Val Arg Asp Val Leu Gly Gly Leu Gly Ile Val Asp Leu
 105 110 115

ggc ctt gac acc aag gtg ggc aaa cct ttt ccg gtg ggc gaa gcg ccg 499
 Gly Leu Asp Thr Lys Val Gly Lys Pro Phe Pro Val Gly Glu Ala Pro
 120 125 130

acg cac caa cct ggc cgc cgc gct ggt tcg cga cct tgacctgac 545
 Thr His Gln Pro Gly Arg Arg Ala Gly Ser Arg Pro
 135 140 145

gtgctcgacg agc 558

<210> 330
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 330
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Lys Thr Leu Leu Asp Gly Val Ser Leu Gly Val Gln Thr Gly Asp Arg
 20 25 30

Ile Gly Val Val Gly Leu Asn Gly Gly Gly Lys Thr Thr Leu Leu Glu
 35 40 45

Val Leu Thr Gly Ile Glu Lys Pro Asp Gln Gly Arg Val Ser His Asn
 50 55 60

Ser Asp Leu Arg Met Ala Val Val Thr Gln Arg Ala Glu Leu Asn Asp
 65 70 75 80

Asp Asp Thr Val Ala Asp Val Val Leu Gly Pro Leu Gly Leu Glu Val
 85 90 95

Phe Glu Trp Ala Ser Asn Ala Thr Val Arg Asp Val Leu Gly Gly Leu
 100 105 110

Gly Ile Val Asp Leu Gly Leu Asp Thr Lys Val Gly Lys Pro Phe Pro
 115 120 125

Val Gly Glu Ala Pro Thr His Gln Pro Gly Arg Arg Ala Gly Ser Arg
 130 135 140

Pro
 145

<210> 331

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<211> 564
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(541)  
<223> FRXA01881
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<210> 332
<211> 147
<212> PRT
<213> Corynebacterium glutamicum
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<400> 332

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 Lys Thr Leu Leu Asp Gly Val Ser Leu Gly Val Gln Thr Gly Asp Arg
 20 25 30
 Ile Gly Val Val Gly Leu Asn Gly Gly Gly Lys Thr Thr Leu Leu Glu
 35 40 45
 Val Leu Thr Gly Ile Glu Lys Pro Asp Gln Gly Arg Val Ser His Asn
 50 55 60
 Ser Asp Leu Arg Met Ala Val Val Thr Gln Arg Ala Glu Leu Asn Asp
 65 70 75 80
 Asp Asp Thr Val Ala Asp Val Val Leu Gly Pro Leu Gly Leu Glu Val
 85 90 95
 Phe Glu Trp Ala Ser Asn Ala Thr Val Arg Asp Val Leu Gly Gly Leu
 100 105 110
 Gly Ile Val Asp Leu Gly Leu Asp Thr Lys Val Gly Gln Thr Phe Ser
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 Thr Leu Thr
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 <213> Corynebacterium glutamicum

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 <223> RXA00526

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 Met Ser Leu Ile Glu
 1 5
 atg cga aat att gtc aag acc tac aac att gga tct gaa ggt gaa ctc 163
 Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly Ser Glu Gly Glu Leu
 10 15 20
 acc gtg ttg cac ggt gtg gat ttc cat gtg gac cgt ggc gaa ttc gtg 211
 Thr Val Leu His Gly Val Asp Phe His Val Asp Arg Gly Glu Phe Val
 25 30 35
 tcg gtt gtg ggt acg tcc ggc tca ggt aaa tca acg atg atg aac atc 259
 Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser Thr Met Met Asn Ile
 40 45 50
 att ggg ttg ttg gat aag cca act gat ggc acg tac acc ttg gat ggc 307

Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr Tyr Thr Leu Asp Gly
 55 60 65

gtg gat gtg ttg gat atc agc gat gat gct ttg gcg agc cac cgc gct 355
 Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu Ala Ser His Arg Ala
 70 75 80 85

aaa tcg att ggt ttt gtg ttt cag aac ttc aat ctg att ggc cgg atc 403
 Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn Leu Ile Gly Arg Ile
 90 95 100

gat gcg ttg aag aat gtg gaa atg ccc atg atg tat gcg ggc att ccg 451
 Asp Ala Leu Lys Asn Val Glu Met Pro Met Met Tyr Ala Gly Ile Pro
 105 110 115

gct aag cag cgg aga agt cgt gcg gtt gaa tta ttg gaa atg gtc ggg 499
 Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu Leu Glu Met Val Gly
 120 125 130

atg ggt gag cgt ctc aac cat gag ccc aat gag ctt tcg ggt ggt cag 547
 Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu Leu Ser Gly Gly Gln
 135 140 145

aag cag cgc gtg gcc att gct cgc gcg ttg gcg aac gat cct gag atc 595
 Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala Asn Asp Pro Glu Ile
 150 155 160 165

att ctt gct gat gaa cca act ggt gcg ttg gat tct gca acg ggc cgg 643
 Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp Ser Ala Thr Gly Arg
 170 175 180

atg gtg atg gat att ttc cac cag ctc aac aag gag cag ggc aaa acc 691
 Met Val Met Asp Ile Phe His Gln Leu Asn Lys Glu Gln Gly Lys Thr
 185 190 195

atc gtg ttt att act cac aac cct gag ctt gct gat gaa tct gat cgg 739
 Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala Asp Glu Ser Asp Arg
 200 205 210

gtg gtc acc atg gtt gac ggg cgc atc att ggg tct gag gtg aaa cac 787
 Val Val Thr Met Val Asp Gly Arg Ile Ile Gly Ser Glu Val Lys His
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 Ser
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<210> 334

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

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Ser Glu Gly Glu Leu Thr Val Leu His Gly Val Asp Phe His Val Asp
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Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser

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                                         Met Ser Asn Thr Ala
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ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag 163
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys
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gca cag aat ttc gga cca tct gcc aaa agg ctt ttc gga att cta ggc 211

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His	Asp	Arg	Asn	Thr	Leu	Ile	Phe	Val	Ile	Phe	Leu	Ala	Val	Leu	Ser		
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Val	Val	Phe	Glu	Gly	Phe	Leu	Ser	Lys	Arg	Met	Pro	Ala	Gly	Ala	Ser		
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Lys	Glu	Asp	Ile	Ile	Ala	Gln	Leu	Gln	Ala	Ala	Gly	Lys	His	Asn	Gln		
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Ala	Ser	Met	Met	Glu	Asp	Met	Asn	Leu	Val	Pro	Gly	Ser	Gly	Ile	Asp		
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Phe	Glu	Lys	Leu	Ala	Met	Ile	Leu	Gly	Leu	Val	Ile	Gly	Ala	Tyr	Leu		
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Val	Gln	Ser	Ala	Met	His	Arg	Leu	Arg	Met	Glu	Val	Glu	Glu	Lys	Ile		
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Leu	Ser	Arg	Val	Thr	Asn	Asp	Val	Asp	Asn	Ile	Gly	Gln	Ser	Leu	Gln		
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Gln	Thr	Leu	Ser	Gln	Ala	Ile	Thr	Ser	Leu	Leu	Thr	Val	Ile	Gly	Val		
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Val	Ser	Ile	Pro	Val	Thr	Ile	Val	Val	Thr	Val	Val	Val	Ala	Ser	Arg		
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Ser	Gln	Lys	Leu	Phe	Ala	Glu	Gln	Trp	Lys	Gln	Thr	Gly	Ile	Leu	Asn		
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Ala	Arg	Leu	Glu	Glu	Thr	Tyr	Ser	Gly	His	Ala	Val	Val	Lys	Val	Phe		

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 Cys Val
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Leu Ala Val Leu Ser Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu
 50 55 60
 Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met
 65 70 75 80
 Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala
 85 90 95
 Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro
 100 105 110
 Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val
 115 120 125
 Ile Gly Ala Tyr Leu Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg
 130 135 140
 Met Leu Asn Arg Ile Val Gln Ser Ala Met His Arg Leu Arg Met Glu
 145 150 155 160
 Val Glu Glu Lys Ile His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile
 165 170 175
 Lys Arg Gly Asp Leu Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile
 180 185 190
 Gly Gln Ser Leu Gln Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu
 195 200 205
 Thr Val Ile Gly Val Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu
 210 215 220
 Ala Leu Val Ala Leu Val Ser Ile Pro Val Thr Ile Val Val Thr Val
 225 230 235 240

Val	Val	Ala	Ser	Arg 245	Ser	Gln	Lys	Leu	Phe 250	Ala	Glu	Gln	Trp	Lys 255	Gln
Thr	Gly	Ile	Leu 260	Asn	Ala	Arg	Leu	Glu 265	Glu	Thr	Tyr	Ser	Gly 270	His	Ala
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<210> 337
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<213> *Corynebacterium glutamicum*

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<223> FRXA00733
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Met Ser Asn Thr Ala																
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ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag																163
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys																
10 15 20																
gca cag aat ttc gga cca tct gcc aaa agg ctt ttc gga att cta ggc																211
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly																
25 30 35																
cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc																259
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser																
40 45 50																
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Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn																
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Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser																
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Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln																
90 95 100																
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Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp																
105 110 115																
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Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu																

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<210> 338
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 <213> Corynebacterium glutamicum

<400> 338
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 35 40 45
 Leu Ala Val Leu Ser Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu
 50 55 60
 Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met
 65 70 75 80
 Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala
 85 90 95
 Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro
 100 105 110
 Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1) .. (669)
 <223> RXA00735

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 Phe Tyr Asp Ile Asn Ser Gly Ser Ile Thr Leu Gly Glu Thr Ala Gln
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Asp Ala Val Asp Ile Arg Thr Met Ala Arg Glu Asp Leu Arg Ser Arg
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 acc ggc atg gtg ttg cag gat acg tgg ctg ttt gcc gga acc atc agg 192
 Thr Gly Met Val Leu Gln Asp Thr Trp Leu Phe Ala Gly Thr Ile Arg
 50 55 60
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 Asp Asn Ile Leu Tyr Gly Arg Pro Glu Ala Thr Glu Glu Glu Met Leu
 65 70 75 80
 gct gcg tcc aag gcc gcc tac gtg gat cgt ttt gtc cgt tcc ctg cca 288
 Ala Ala Ser Lys Ala Ala Tyr Val Asp Arg Phe Val Arg Ser Leu Pro
 85 90 95
 gaa ggc tac gac acc gta ctt gat gat gaa gcc atg aac cta tcg gtg 336
 Glu Gly Tyr Asp Thr Val Leu Asp Asp Glu Ala Met Asn Leu Ser Val
 100 105 110
 ggt gaa cgc cag ctg atc acc atc gcg cgt gca ttc ttg gct aat ccc 384
 Gly Glu Arg Gln Leu Ile Thr Ile Ala Arg Ala Phe Leu Ala Asn Pro
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 Arg Leu Leu Ile Leu Asp Glu Ala Thr Ser Ser Val Asp Thr Arg Thr
 130 135 140
 gaa ttg ttg att cag cgc gcc atg tcc aag ctg cgc caa gac cgc acc 480
 Glu Leu Leu Ile Gln Arg Ala Met Ser Lys Leu Arg Gln Asp Arg Thr
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 gcc ttc gtc atc gcg cac cgg ttg tcc acg att cgt gat gcc aac ctg 528
 Ala Phe Val Ile Ala His Arg Leu Ser Thr Ile Arg Asp Ala Asn Leu
 165 170 175
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 Ile Leu Met Met Lys Asp Gly Glu Ile Val Glu Gln Gly Asn His Arg
 180 185 190
 gag ttg atg gcc ctg gag ggc gca tat tgg gag ttg tat aac tcc caa 624
 Glu Leu Met Ala Leu Glu Gly Ala Tyr Trp Glu Leu Tyr Asn Ser Gln
 195 200 205
 ttc aac gcc ccc gcg aaa gaa gaa tta cag gct gac gga gat cac 669
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<210> 340

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

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Ala	Ala	Ser	Lys	Ala	Ala	Tyr	Val	Asp	Arg	Phe	Val	Arg	Ser	Leu	Pro
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Glu	Gly	Tyr	Asp	Thr	Val	Leu	Asp	Asp	Glu	Ala	Met	Asn	Leu	Ser	Val
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Arg	Leu	Leu	Ile	Leu	Asp	Glu	Ala	Thr	Ser	Ser	Val	Asp	Thr	Arg	Thr
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Glu	Leu	Leu	Ile	Gln	Arg	Ala	Met	Ser	Lys	Leu	Arg	Gln	Asp	Arg	Thr
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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA00878
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                                         Met Arg Leu Leu Gly
                                         1                               5

cga att tta aaa acc acg tct gcg ctt tgg ccc tac tat ctc gga att 163
Arg Ile Leu Lys Thr Thr Ser Ala Leu Trp Pro Tyr Tyr Leu Gly Ile
                        10                               15                               20

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Ile Val Val Ser Ile Val Ile Ala Ala Leu Ser Leu Leu Ser Pro Phe

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Asn	Thr	Val	Asp	Ala	Val	Thr	Arg	Thr	Ile	Ile	Phe	Leu	Ala	Leu	Ala					
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70						75						80			85					
tac	atc	ggg	gat	gtc	atg	gca	tct	cgt	atg	cgc	cag	att	ctg	gcc	acg	403				
Tyr	Ile	Gly	Asp	Val	Met	Ala	Ser	Arg	Met	Arg	Gln	Ile	Leu	Ala	Thr					
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cag	gtc	acc	ggc	acc	atc	atc	gcc	cgc	ctt	gat	cga	tca	atc	aac	ggc	499				
Gln	Val	Thr	Gly	Thr	Ile	Ile	Ala	Arg	Leu	Asp	Arg	Ser	Ile	Asn	Gly					
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Ile	Thr	Gln	Phe	Met	Gln	Ser	Phe	Ser	Asn	Asn	Phe	Phe	Pro	Met	Leu					
135						140						145								
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150						155						160			165					
ctg	gca	att	ctg	ctg	gcc	atg	ttg	ttc	ccg	att	tac	atg	tgg	ctg	acg	643				
Leu	Ala	Ile	Leu	Leu	Ala	Met	Leu	Phe	Pro	Ile	Tyr	Met	Trp	Leu	Thr					
			170						175						180					
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			185						190						195					
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215						220						225								
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Gly	Gly	Arg	Tyr	Gly	Lys	Thr	Val	Ala	Ile	Thr	Arg	Pro	Gln	Ser	Gly					
230			235						240						245					
tgg	tgg	cac	cgc	atg	gat	act	ctc	cgt	ggc	gcg	gca	cta	aat	atc	atc	883				
Trp	Trp	His	Arg	Met	Asp	Thr	Leu	Arg	Gly	Ala	Ala	Leu	Asn	Ile	Ile					
			250						255						260					
ttc	ctg	gcc	att	cac	ctg	ctg	att	ttc	tac	cgc	acc	ttg	cac	ggc	cat	931				
Phe	Leu	Ala	Ile	His	Leu	Leu	Ile	Phe	Tyr	Arg	Thr	Leu	His	Gly	His					
			265			270						275								

ttc acc atc ggc gac atg gtc atg ctc atc cag ctt gtc acc atg gcg	979
Phe Thr Ile Gly Asp Met Val Met Leu Ile Gln Leu Val Thr Met Ala	
280 285 290	
cag caa ccg gtg tac atg atg agc tac atc gtc gac tcc gcg cag cgc	1027
Gln Gln Pro Val Tyr Met Met Ser Tyr Ile Val Asp Ser Ala Gln Arg	
295 300 305	
gcc atc gcc ggc tcc cgc gac tac ttc gag gtc atg gcg cag cag gtc	1075
Ala Ile Ala Gly Ser Arg Asp Tyr Phe Glu Val Met Ala Gln Gln Val	
310 315 320 325	
gag ccc acc gcc aat aag gag ctt gtc gac gcc acc ctc gcc tca gac	1123
Glu Pro Thr Ala Asn Lys Glu Leu Val Asp Ala Thr Leu Ala Ser Asp	
330 335 340	
act cca cgc atc agt gtg ggc acg ccc gcc gcg ctg ccc gct gga gaa	1171
Thr Pro Arg Ile Ser Val Gly Thr Pro Ala Ala Leu Pro Ala Gly Glu	
345 350 355	
cca gcg atg gaa ttc aaa aac gtc acc ttc gcc tac gaa gaa ggc aag	1219
Pro Ala Met Glu Phe Lys Asn Val Thr Phe Ala Tyr Glu Glu Gly Lys	
360 365 370	
ccg gtt att tcc gac gtg tcc att acc gcc cgc cac gcc gag cgc atc	1267
Pro Val Ile Ser Asp Val Ser Ile Thr Ala Arg His Gly Glu Arg Ile	
375 380 385	
gcg ttg gtc ggt gaa tcc ggc ggc ggt aaa tcc acc ctg gtc aac ctt	1315
Ala Leu Val Gly Glu Ser Gly Gly Gly Lys Ser Thr Leu Val Asn Leu	
390 395 400 405	
ctg tta ggt ctg tac aaa cca aac agc gcc agc ctt gca gta tgt ggc	1363
Leu Leu Gly Leu Tyr Lys Pro Asn Ser Gly Ser Leu Ala Val Cys Gly	
410 415 420	
gtg gat gtt aaa gat ctg act tcc gag gaa ctt cgc gca tcc gtg ggt	1411
Val Asp Val Lys Asp Leu Thr Ser Glu Glu Leu Arg Ala Ser Val Gly	
425 430 435	
gtg gtc ttc cag gac gcc agc ttg ttc tct gga tct att gca gaa aac	1459
Val Val Phe Gln Asp Ala Ser Leu Phe Ser Gly Ser Ile Ala Glu Asn	
440 445 450	
atc gcc tac ggt cgc cca ggt gcc acc cgc gaa gag atc atc gaa gtg	1507
Ile Ala Tyr Gly Arg Pro Gly Ala Thr Arg Glu Glu Ile Ile Glu Val	
455 460 465	
gct aag aaa gcc aac gca cat gag ttc att tcc gcc ttc cct gaa gga	1555
Ala Lys Lys Ala Asn Ala His Glu Phe Ile Ser Ala Phe Pro Glu Gly	
470 475 480 485	
tat gaa acc gtc gtc ggt gaa cgc gga ctc aaa ctt tct ggt ggc cag	1603
Tyr Glu Thr Val Val Gly Glu Arg Gly Leu Lys Leu Ser Gly Gly Gln	
490 495 500	
aag cag cgc gtc tct gtg gca cgg gcc atg ctt aaa gat gcc cca ctt	1651
Lys Gln Arg Val Ser Val Ala Arg Ala Met Leu Lys Asp Ala Pro Leu	
505 510 515	

ctt gtt ctc gat gaa gcc acc tct gca ctg gat acc aag tct gag cag 1699
 Leu Val Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Lys Ser Glu Gln
 520 525 530

gca gtc caa gcc ggt ttg gaa cag ctg atg gaa aac cgc acc acc tta 1747
 Ala Val Gln Ala Gly Leu Glu Gln Leu Met Glu Asn Arg Thr Thr Leu
 535 540 545

atg atc gcc cac cgc ctg tcc acc atc gca ggc gtc gat acc atc gtg 1795
 Met Ile Ala His Arg Leu Ser Thr Ile Ala Gly Val Asp Thr Ile Val
 550 555 560 565

acc atc caa aac gga cgg gtt gaa gag gtc gga tct cct acc gag ctc 1843
 Thr Ile Gln Asn Gly Arg Val Glu Glu Val Gly Ser Pro Thr Glu Leu
 570 575 580

gca gtc tca ggc ggt atc tat tcc gaa ctg ctg cgc ctg acc aac tcc 1891
 Ala Val Ser Gly Gly Ile Tyr Ser Glu Leu Leu Arg Leu Thr Asn Ser
 585 590 595

aca gca gaa gcc gac cgg gag cgt ctg cgc gcc ttt ggt ttc act ggc 1939
 Thr Ala Glu Ala Asp Arg Glu Arg Leu Arg Ala Phe Gly Phe Thr Gly
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gat gca cca gct gaa gaa gag gac tagccccgcg aaagaacaat ccc 1986
 Asp Ala Pro Ala Glu Glu Glu Asp
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<210> 342

<211> 621

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

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Tyr Tyr Leu Gly Ile Ile Val Val Ser Ile Val Ile Ala Ala Leu Ser
 20 25 30

Leu Leu Ser Pro Phe Ile Leu Arg Glu Ala Thr Asp Ser Ile Val Ser
 35 40 45

Ala Val Thr Gly Ser Asn Thr Val Asp Ala Val Thr Arg Thr Ile Ile
 50 55 60

Phe Leu Ala Leu Ala Leu Phe Val Ala Ser Phe Leu Asn Thr Val Met
 65 70 75 80

Thr Asn Ile Gly Gly Tyr Ile Gly Asp Val Met Ala Ser Arg Met Arg
 85 90 95

Gln Ile Leu Ala Thr Arg Tyr Tyr Ala Lys Leu Leu Ala Leu Pro Gln
 100 105 110

Lys Tyr Phe Asp Asn Gln Val Thr Gly Thr Ile Ile Ala Arg Leu Asp
 115 120 125

Arg Ser Ile Asn Gly Ile Thr Gln Phe Met Gln Ser Phe Ser Asn Asn
 130 135 140

Phe Phe Pro Met Leu Ile Thr Met Val Ala Val Leu Ile Ile Ser Ala
 145 150 155 160
 Ile Phe Tyr Trp Pro Leu Ala Ile Leu Leu Ala Met Leu Phe Pro Ile
 165 170 175
 Tyr Met Trp Leu Thr Ala Leu Thr Ser Lys Arg Trp Gln Lys Tyr Glu
 180 185 190
 Gly Glu Lys Asn His Glu Ile Asp Val Ala Asn Gly Arg Phe Ala Glu
 195 200 205
 Val Val Gly Gln Val Lys Val Val Lys Ser Phe Val Ala Glu Thr Arg
 210 215 220
 Glu Leu Ala Asp Phe Gly Gly Arg Tyr Gly Lys Thr Val Ala Ile Thr
 225 230 235 240
 Arg Pro Gln Ser Gly Trp Trp His Arg Met Asp Thr Leu Arg Gly Ala
 245 250 255
 Ala Leu Asn Ile Ile Phe Leu Ala Ile His Leu Leu Ile Phe Tyr Arg
 260 265 270
 Thr Leu His Gly His Phe Thr Ile Gly Asp Met Val Met Leu Ile Gln
 275 280 285
 Leu Val Thr Met Ala Gln Gln Pro Val Tyr Met Met Ser Tyr Ile Val
 290 295 300
 Asp Ser Ala Gln Arg Ala Ile Ala Gly Ser Arg Asp Tyr Phe Glu Val
 305 310 315 320
 Met Ala Gln Gln Val Glu Pro Thr Ala Asn Lys Glu Leu Val Asp Ala
 325 330 335
 Thr Leu Ala Ser Asp Thr Pro Arg Ile Ser Val Gly Thr Pro Ala Ala
 340 345 350
 Leu Pro Ala Gly Glu Pro Ala Met Glu Phe Lys Asn Val Thr Phe Ala
 355 360 365
 Tyr Glu Glu Gly Lys Pro Val Ile Ser Asp Val Ser Ile Thr Ala Arg
 370 375 380
 His Gly Glu Arg Ile Ala Leu Val Gly Glu Ser Gly Gly Gly Lys Ser
 385 390 395 400
 Thr Leu Val Asn Leu Leu Leu Gly Leu Tyr Lys Pro Asn Ser Gly Ser
 405 410 415
 Leu Ala Val Cys Gly Val Asp Val Lys Asp Leu Thr Ser Glu Glu Leu
 420 425 430
 Arg Ala Ser Val Gly Val Val Phe Gln Asp Ala Ser Leu Phe Ser Gly
 435 440 445
 Ser Ile Ala Glu Asn Ile Ala Tyr Gly Arg Pro Gly Ala Thr Arg Glu
 450 455 460

Glu Ile Ile Glu Val Ala Lys Lys Ala Asn Ala His Glu Phe Ile Ser
 465 470 475 480
 Ala Phe Pro Glu Gly Tyr Glu Thr Val Val Gly Glu Arg Gly Leu Lys
 485 490 495
 Leu Ser Gly Gly Gln Lys Gln Arg Val Ser Val Ala Arg Ala Met Leu
 500 505 510
 Lys Asp Ala Pro Leu Leu Val Leu Asp Glu Ala Thr Ser Ala Leu Asp
 515 520 525
 Thr Lys Ser Glu Gln Ala Val Gln Ala Gly Leu Glu Gln Leu Met Glu
 530 535 540
 Asn Arg Thr Thr Leu Met Ile Ala His Arg Leu Ser Thr Ile Ala Gly
 545 550 555 560
 Val Asp Thr Ile Val Thr Ile Gln Asn Gly Arg Val Glu Glu Val Gly
 565 570 575
 Ser Pro Thr Glu Leu Ala Val Ser Gly Gly Ile Tyr Ser Glu Leu Leu
 580 585 590
 Arg Leu Thr Asn Ser Thr Ala Glu Ala Asp Arg Glu Arg Leu Arg Ala
 595 600 605
 Phe Gly Phe Thr Gly Asp Ala Pro Ala Glu Glu Glu Asp
 610 615 620

<210> 343
 <211> 1713
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1690)
 <223> RXN01191

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 Val Gly Gly Leu Val
 1 5
 gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg 163
 Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala
 10 15 20
 ctg ctt atc gtg gct ggc ggc gtt gtt tcg agc ctg ggc acg tgg tgg 211
 Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp
 25 30 35
 ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg 259
 Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu
 40 45 50
 cgc gag gat gtg ttg cgc gcg gcg gtg agt ttg gat gcg aac acg att 307

Arg	Glu	Asp	Val	Leu	Arg	Ala	Ala	Val	Ser	Leu	Asp	Ala	Asn	Thr	Ile		
55						60					65						
gaa	acg	gcg	ggg	cgc	ggc	gac	gtg	att	tcg	cgt	atc	gcg	gat	gat	tcg	355	
Glu	Thr	Ala	Gly	Arg	Gly	Asp	Val	Ile	Ser	Arg	Ile	Ala	Asp	Asp	Ser		
70					75					80					85		
cgg	gag	gtg	tcc	act	gcg	gcg	agc	acc	gtg	gtg	ccg	ctg	atg	gtg	cag	403	
Arg	Glu	Val	Ser	Thr	Ala	Ala	Ser	Thr	Val	Val	Pro	Leu	Met	Val	Gln		
				90					95					100			
gcg	ggc	ttt	acc	gtg	gtg	att	tcc	gcg	ttt	ggc	atg	gcg	gcg	gtt	gat	451	
Ala	Gly	Phe	Thr	Val	Val	Ile	Ser	Ala	Phe	Gly	Met	Ala	Ala	Val	Asp		
			105					110					115				
tgg	cgc	ctc	ggc	ctt	gtc	ggc	ttg	gtc	gcg	atc	ccg	ctg	tat	tgg	acc	499	
Trp	Arg	Leu	Gly	Leu	Val	Gly	Leu	Val	Ala	Ile	Pro	Leu	Tyr	Trp	Thr		
		120					125					130					
acg	ttg	cgc	gtc	tat	tta	ccc	cgc	tca	ggc	ccg	ctt	tat	acg	cgt	gag	547	
Thr	Leu	Arg	Val	Tyr	Leu	Pro	Arg	Ser	Gly	Pro	Leu	Tyr	Thr	Arg	Glu		
		135				140					145						
cgc	gag	gcc	ttt	ggg	gtg	cgc	acg	cag	cgg	ctt	gtc	ggc	gca	gtc	gaa	595	
Arg	Glu	Ala	Phe	Gly	Val	Arg	Thr	Gln	Arg	Leu	Val	Gly	Ala	Val	Glu		
150					155				160						165		
ggc	gcg	gaa	acc	ttg	cgc	gct	ttc	cgc	gca	gaa	gat	aca	gaa	tta	aag	643	
Gly	Ala	Glu	Thr	Leu	Arg	Ala	Phe	Arg	Ala	Glu	Asp	Thr	Glu	Leu	Lys		
			170					175						180			
cgt	atc	gac	gca	gcc	tcc	ggc	gaa	gcc	cgc	gac	att	tcc	att	tct	gtt	691	
Arg	Ile	Asp	Ala	Ala	Ser	Gly	Glu	Ala	Arg	Asp	Ile	Ser	Ile	Ser	Val		
			185					190					195				
ttc	agg	ttc	ctc	aca	tgg	gca	ttt	tcc	cgc	aac	aac	cgc	gcg	gaa	tgc	739	
Phe	Arg	Phe	Leu	Thr	Trp	Ala	Phe	Ser	Arg	Asn	Asn	Arg	Ala	Glu	Cys		
		200					205					210					
atc	acc	ctc	gtg	ctc	atc	ttg	ggc	acc	ggc	ttt	tac	ctg	gtc	aac	atc	787	
Ile	Thr	Leu	Val	Leu	Ile	Leu	Gly	Thr	Gly	Phe	Tyr	Leu	Val	Asn	Ile		
		215				220					225						
gat	ctg	gtc	acc	gtc	ggc	gca	gtc	tca	acc	gcc	gca	ctg	atc	ttc	cac	835	
Asp	Leu	Val	Thr	Val	Gly	Ala	Val	Ser	Thr	Ala	Ala	Leu	Ile	Phe	His		
230					235				240						245		
cga	ctc	ttc	ggc	cca	atc	ggc	acg	ctc	gtg	ggc	atg	ttc	tcc	gac	atc	883	
Arg	Leu	Phe	Gly	Pro	Ile	Gly	Thr	Leu	Val	Gly	Met	Phe	Ser	Asp	Ile		
				250				255						260			
caa	tcc	gcc	agc	gca	tcg	ctg	atc	cgc	atg	gtg	ggc	gtt	att	aac	gcg	931	
Gln	Ser	Ala	Ser	Ala	Ser	Leu	Ile	Arg	Met	Val	Gly	Val	Ile	Asn	Ala		
			265					270					275				
gca	tcg	aac	cag	gtc	agc	ggc	acc	tcg	ccg	gcg	tct	gcc	agc	acc	gct	979	
Ala	Ser	Asn	Gln	Val	Ser	Gly	Thr	Ser	Pro	Ala	Ser	Ala	Ser	Thr	Ala		
		280				285						290					
tta	acg	ctt	ttc	gac	gtc	tcc	cac	cac	tat	cac	act	gca	ccc	gtc	atc	1027	
Leu	Thr	Leu	Phe	Asp	Val	Ser	His	His	Tyr	His	Thr	Ala	Pro	Val	Ile		

295	300	305	
aag aat gca tcc gtg	cag ctg gaa cca ggg gaa cac atc gcc att gtg		1075
Lys Asn Ala Ser Val	Gln Leu Glu Pro Gly Glu His Ile Ala Ile Val		
310	315 320 325		
ggt gcg acc ggc gct	ggt aaa agc acg ctc gcc ctc att gcg gca ggc		1123
Gly Ala Thr Gly Ala	Gly Lys Ser Thr Leu Ala Leu Ile Ala Ala Gly		
	330 335 340		
ctg ctc agc cca act	tcc ggg cag gtg gct ctc ggc gga tcg agt ttt		1171
Leu Leu Ser Pro Thr	Ser Gly Gln Val Ala Leu Gly Gly Ser Ser Phe		
	345 350 355		
tct aac gtc gaa ccg	gaa gca ttg cgc cag aag atc gcg atg gtc agc		1219
Ser Asn Val Glu Pro	Glu Ala Leu Arg Gln Lys Ile Ala Met Val Ser		
	360 365 370		
caa gaa atc cac tgc	ttc cga gga tct gtt tta gat aat ctt cgt atc		1267
Gln Glu Ile His Cys	Phe Arg Gly Ser Val Leu Asp Asn Leu Arg Ile		
	375 380 385		
gca cgc ccc gaa gcc	acc gat gcg gac atc cac gcc gtt ctc gcc gat		1315
Ala Arg Pro Glu Ala	Thr Asp Ala Asp Ile His Ala Val Leu Ala Asp		
	390 395 400 405		
att ggt gat tcc tgg	ttg gag cgc tta ccg caa ggc ata gac acc atc		1363
Ile Gly Asp Ser Trp	Leu Glu Arg Leu Pro Gln Gly Ile Asp Thr Ile		
	410 415 420		
gtg ggt gat ggc gct	ttc cgt tta acc tct gtg gaa aac cag atc atg		1411
Val Gly Asp Gly Ala	Phe Arg Leu Thr Ser Val Glu Asn Gln Ile Met		
	425 430 435		
gcg ctt gct cgc gta	cat ttg gcc gac cta gca atc gtc atc ctt gat		1459
Ala Leu Ala Arg Val	His Leu Ala Asp Leu Ala Ile Val Ile Leu Asp		
	440 445 450		
gaa gca acg gct gaa	tca ggc tct gat cat gca aaa cag ctt gaa gat		1507
Glu Ala Thr Ala Glu	Ser Gly Ser Asp His Ala Lys Gln Leu Glu Asp		
	455 460 465		
gca gcc ctt aaa gtc	act gaa aac aga tca gcc atc atc gtg gct cac		1555
Ala Ala Leu Lys Val	Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His		
	470 475 480 485		
cgc ctc aac caa gcg	aaa acc gcc gat cgc atc atc gtc atg gac tcc		1603
Arg Leu Asn Gln Ala	Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser		
	490 495 500		
gga gaa atc ata gaa	tct gga acc cat gaa gag ctt cga gcg atc ggc		1651
Gly Glu Ile Ile Glu	Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly		
	505 510 515		
ggc cga tat gaa caa	ctg tgg act gcg tgg tct gcg cgc taattagcca		1700
Gly Arg Tyr Glu Gln	Leu Trp Thr Ala Trp Ser Ala Arg		
	520 525 530		
cccaagacca cgc			1713

<210> 344
 <211> 530
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 344

Val	Gly	Gly	Leu	Val	Asp	Lys	Leu	Leu	Ala	Thr	Pro	Ser	Met	Arg	Asp
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Val	Val	Val	Phe	Ala	Leu	Leu	Ile	Val	Ala	Gly	Gly	Val	Val	Ser	Ser
			20					25						30	
Leu	Gly	Thr	Trp	Trp	Gly	Ser	Ala	Leu	Met	Ala	Arg	Ala	Leu	Glu	Pro
			35				40					45			
Ala	Ile	Ala	Gly	Leu	Arg	Glu	Asp	Val	Leu	Arg	Ala	Ala	Val	Ser	Leu
			50			55					60				
Asp	Ala	Asn	Thr	Ile	Glu	Thr	Ala	Gly	Arg	Gly	Asp	Val	Ile	Ser	Arg
					70					75					80
Ile	Ala	Asp	Asp	Ser	Arg	Glu	Val	Ser	Thr	Ala	Ala	Ser	Thr	Val	Val
				85					90					95	
Pro	Leu	Met	Val	Gln	Ala	Gly	Phe	Thr	Val	Val	Ile	Ser	Ala	Phe	Gly
			100					105					110		
Met	Ala	Ala	Val	Asp	Trp	Arg	Leu	Gly	Leu	Val	Gly	Leu	Val	Ala	Ile
			115				120					125			
Pro	Leu	Tyr	Trp	Thr	Thr	Leu	Arg	Val	Tyr	Leu	Pro	Arg	Ser	Gly	Pro
						135				140					
Leu	Tyr	Thr	Arg	Glu	Arg	Glu	Ala	Phe	Gly	Val	Arg	Thr	Gln	Arg	Leu
				150						155				160	
Val	Gly	Ala	Val	Glu	Gly	Ala	Glu	Thr	Leu	Arg	Ala	Phe	Arg	Ala	Glu
				165					170					175	
Asp	Thr	Glu	Leu	Lys	Arg	Ile	Asp	Ala	Ala	Ser	Gly	Glu	Ala	Arg	Asp
			180				185						190		
Ile	Ser	Ile	Ser	Val	Phe	Arg	Phe	Leu	Thr	Trp	Ala	Phe	Ser	Arg	Asn
			195				200					205			
Asn	Arg	Ala	Glu	Cys	Ile	Thr	Leu	Val	Leu	Ile	Leu	Gly	Thr	Gly	Phe
			210			215					220				
Tyr	Leu	Val	Asn	Ile	Asp	Leu	Val	Thr	Val	Gly	Ala	Val	Ser	Thr	Ala
					230					235				240	
Ala	Leu	Ile	Phe	His	Arg	Leu	Phe	Gly	Pro	Ile	Gly	Thr	Leu	Val	Gly
				245					250					255	
Met	Phe	Ser	Asp	Ile	Gln	Ser	Ala	Ser	Ala	Ser	Leu	Ile	Arg	Met	Val
			260				265						270		
Gly	Val	Ile	Asn	Ala	Ala	Ser	Asn	Gln	Val	Ser	Gly	Thr	Ser	Pro	Ala
			275				280					285			
Ser	Ala	Ser	Thr	Ala	Leu	Thr	Leu	Phe	Asp	Val	Ser	His	His	Tyr	His

290 295 300
 Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu
 305 310 315 320
 His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala
 325 330 335
 Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu
 340 345 350
 Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys
 355 360 365
 Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu
 370 375 380
 Asp Asn Leu Arg Ile Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His
 385 390 395 400
 Ala Val Leu Ala Asp Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln
 405 410 415
 Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val
 420 425 430
 Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala
 435 440 445
 Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala
 450 455 460
 Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala
 465 470 475 480
 Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile
 485 490 495
 Ile Val Met Asp Ser Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu
 500 505 510
 Leu Arg Ala Ile Gly Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser
 515 520 525
 Ala Arg
 530

<210> 345
 <211> 1430
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1407)
 <223> FRXA01191

<400> 345
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 Val Ser Leu Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val

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att tcg cgt atc gcg gat gat tcg cgg gag gtg tcc act gcg gcg agc Ile Ser Arg Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser	20	25	30	96
acc gtg gtg ccg ctg atg gtg cag gcg ggc ttt acc gtg gtg att tcc Thr Val Val Pro Leu Met Val Gln Ala Gly Phe Thr Val Val Ile Ser	35	40	45	144
gcg ttt ggc atg gcg gcg gtt gat tgg cgc ctc ggc ctt gtc ggt ttg Ala Phe Gly Met Ala Ala Val Asp Trp Arg Leu Gly Leu Val Gly Leu	50	55	60	192
gtc gcg atc ccg ctg tat tgg acc acg ttg cgc gtc tat tta ccc cgc Val Ala Ile Pro Leu Tyr Trp Thr Thr Leu Arg Val Tyr Leu Pro Arg	65	70	75	240
tca ggt ccg ctt tat acg cgt gag cgc gag gcc ttt ggg gtg cgc acg Ser Gly Pro Leu Tyr Thr Arg Glu Arg Glu Ala Phe Gly Val Arg Thr	85	90	95	288
cag cgg ctt gtc ggc gca gtc gaa ggc gcg gaa acc ttg cgc gct ttc Gln Arg Leu Val Gly Ala Val Glu Gly Ala Glu Thr Leu Arg Ala Phe	100	105	110	336
cgc gca gaa gat aca gaa tta aag cgt atc gac gca gcc tcc ggc gaa Arg Ala Glu Asp Thr Glu Leu Lys Arg Ile Asp Ala Ala Ser Gly Glu	115	120	125	384
gcc cgc gac att tcc att tct gtt ttc agg ttc ctc aca tgg gca ttt Ala Arg Asp Ile Ser Ile Ser Val Phe Arg Phe Leu Thr Trp Ala Phe	130	135	140	432
tcc cgc aac aac cgc gcg gaa tgc atc acc ctc gtg ctc atc ttg ggc Ser Arg Asn Asn Arg Ala Glu Cys Ile Thr Leu Val Leu Ile Leu Gly	145	150	155	480
acc ggc ttt tac ctg gtc aac atc gat ctg gtc acc gtc ggc gca gtc Thr Gly Phe Tyr Leu Val Asn Ile Asp Leu Val Thr Val Gly Ala Val	165	170	175	528
tca acc gcc gca ctg atc ttc cac cga ctc ttc ggt cca atc ggc acg Ser Thr Ala Ala Leu Ile Phe His Arg Leu Phe Gly Pro Ile Gly Thr	180	185	190	576
ctc gtg ggc atg ttc tcc gac atc caa tcc gcc agc gca tcg ctg atc Leu Val Gly Met Phe Ser Asp Ile Gln Ser Ala Ser Ala Ser Leu Ile	195	200	205	624
cgc atg gtg ggc gtt att aac gcg gca tcg aac cag gtc agc ggc acc Arg Met Val Gly Val Ile Asn Ala Ala Ser Asn Gln Val Ser Gly Thr	210	215	220	672
tcg ccg gcg tct gcc agc acc gct tta acg ctt ttc gac gtc tcc cac Ser Pro Ala Ser Ala Ser Thr Ala Leu Thr Leu Phe Asp Val Ser His	225	230	235	720
cac tat cac act gca ccc gtc atc aag aat gca tcc gtg cag ctg gaa His Tyr His Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu	245	250	255	768

cca ggg gaa cac atc gcc att gtg ggt gcg acc ggc gct ggt aaa agc 816
 Pro Gly Glu His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser
 260 265 270

acg ctc gcc ctc att gcg gca ggc ctg ctc agc cca act tcc ggg cag 864
 Thr Leu Ala Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln
 275 280 285

gtg gct ctc ggc gga tcg agt ttt tct aac gtc gaa ccg gaa gca ttg 912
 Val Ala Leu Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu
 290 295 300

cgc cag aag atc gcg atg gtc agc caa gaa atc cac tgc ttc cga gga 960
 Arg Gln Lys Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly
 305 310 315 320

tct gtt tta gat aat ctt cgt atc gca cgc ccc gaa gcc acc gat gcg 1008
 Ser Val Leu Asp Asn Leu Arg Ile Ala Arg Pro Glu Ala Thr Asp Ala
 325 330 335

gac atc cac gcc gtt ctc gcc gat att ggt gat tcc tgg ttg gag cgc 1056
 Asp Ile His Ala Val Leu Ala Asp Ile Gly Asp Ser Trp Leu Glu Arg
 340 345 350

tta ccg caa ggc ata gac acc atc gtg ggt gat ggc gct ttc cgt tta 1104
 Leu Pro Gln Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu
 355 360 365

acc tct gtg gaa aac cag atc atg gcg ctt gct cgc gta cat ttg gcc 1152
 Thr Ser Val Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala
 370 375 380

gac cta gca atc gtc atc ctt gat gaa gca acg gct gaa tca ggc tct 1200
 Asp Leu Ala Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser
 385 390 395 400

gat cat gca aaa cag ctt gaa gat gca gcc ctt aaa gtc act gaa aac 1248
 Asp His Ala Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn
 405 410 415

aga tca gcc atc atc gtg gct cac cgc ctc aac caa gcg aaa acc gcc 1296
 Arg Ser Ala Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala
 420 425 430

gat cgc atc atc gtc atg gac tcc gga gaa atc ata gaa tct gga acc 1344
 Asp Arg Ile Ile Val Met Asp Ser Gly Glu Ile Ile Glu Ser Gly Thr
 435 440 445

cat gaa gag ctt cga gcg atc ggc ggt cga tat gaa caa ctg tgg act 1392
 His Glu Glu Leu Arg Ala Ile Gly Gly Arg Tyr Glu Gln Leu Trp Thr
 450 455 460

gcg tgg tct gcg cgc taattagcca cccaagacca cgc 1430
 Ala Trp Ser Ala Arg
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<210> 346

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Val Ser Leu Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val
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Ile Ser Arg Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser
 20 25 30

Thr Val Val Pro Leu Met Val Gln Ala Gly Phe Thr Val Val Ile Ser
 35 40 45

Ala Phe Gly Met Ala Ala Val Asp Trp Arg Leu Gly Leu Val Gly Leu
 50 55 60

Val Ala Ile Pro Leu Tyr Trp Thr Thr Leu Arg Val Tyr Leu Pro Arg
 65 70 75 80

Ser Gly Pro Leu Tyr Thr Arg Glu Arg Glu Ala Phe Gly Val Arg Thr
 85 90 95

Gln Arg Leu Val Gly Ala Val Glu Gly Ala Glu Thr Leu Arg Ala Phe
 100 105 110

Arg Ala Glu Asp Thr Glu Leu Lys Arg Ile Asp Ala Ala Ser Gly Glu
 115 120 125

Ala Arg Asp Ile Ser Ile Ser Val Phe Arg Phe Leu Thr Trp Ala Phe
 130 135 140

Ser Arg Asn Asn Arg Ala Glu Cys Ile Thr Leu Val Leu Ile Leu Gly
 145 150 155 160

Thr Gly Phe Tyr Leu Val Asn Ile Asp Leu Val Thr Val Gly Ala Val
 165 170 175

Ser Thr Ala Ala Leu Ile Phe His Arg Leu Phe Gly Pro Ile Gly Thr
 180 185 190

Leu Val Gly Met Phe Ser Asp Ile Gln Ser Ala Ser Ala Ser Leu Ile
 195 200 205

Arg Met Val Gly Val Ile Asn Ala Ala Ser Asn Gln Val Ser Gly Thr
 210 215 220

Ser Pro Ala Ser Ala Ser Thr Ala Leu Thr Leu Phe Asp Val Ser His
 225 230 235 240

His Tyr His Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu
 245 250 255

Pro Gly Glu His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser
 260 265 270

Thr Leu Ala Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln
 275 280 285

Val Ala Leu Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu
 290 295 300

Arg Gln Lys Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly

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<210> 347

<211> 1047

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXN01212

<400> 347

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catatggctc taccagcgcc aatgcgaagt aggaagaatt atg cct atg aca acg 115
Met Pro Met Thr Thr
1 5

aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac 163
Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr
10 15 20

acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt 211
Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe
25 30 35

ggt ctg ctc ggc acc aac ggg gcc ggc aaa acc tcc acc ttg gaa gtc 259
 Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val
 40 45 50

atc gaa gga ctt tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly 55 60 65	307
ctt gac ccc gtt gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile 70 75 80 85	355
atg ctg caa tca ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr 90 95 100	403
atg gac atg tgg cac ggc acc tgc acg tat ccg cgc gcc att aaa gat Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp 105 110 115	451
gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly 120 125 130	499
gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu 135 140 145	547
ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu 150 155 160 165	595
gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys 170 175 180	643
cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala 185 190 195	691
gaa ttc ctc tgc gac cgg att gcc atc atg aac gcc ggt gag atc gca Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala 200 205 210	739
gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile 215 220 225	787
agt ttc gtg ctg cgt ggc ggg cag gtg gag ttg ccg gtc ttg agt ggg Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly 230 235 240 245	835
gct gaa atc atc cgc gac aac aac cac gtc cgc atc gcc acc acc acc Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr 250 255 260	883
ctg cag cag cac acc tta gaa ata ctt acc tgg gct gca gag acc ggg Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly 265 270 275	931
atc gcg ctg gaa ggc ttc gct gca aaa ccc gcc acc ttg gaa tcc gta Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val 280 285 290	979

ttc atg gac atc gcc tca ctc gag aac acc tcg ctg caa acc gcc 1024
 Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser Leu Gln Thr Ala
 295 300 305

tagaatcttt aaggagacca caa 1047

<210> 348

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

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Thr Tyr Gly Asp Tyr Thr Ala Val Lys Gly Leu Asn Phe His Val Gln
 20 25 30

Arg Gly Glu Val Phe Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr
 35 40 45

Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr
 50 55 60

Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg
 65 70 75 80

Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu
 85 90 95

Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro
 100 105 110

Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu
 115 120 125

Asn Val Lys Val Gly Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp
 130 135 140

Leu Ala Cys Ala Leu Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu
 145 150 155 160

Pro Thr Thr Gly Leu Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu
 165 170 175

Leu Leu Asp Leu Lys Gln Arg Gly Val Thr Met Met Leu Thr Thr His
 180 185 190

Tyr Leu Glu Glu Ala Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn
 195 200 205

Ala Gly Glu Ile Ala Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg
 210 215 220

Glu Lys Ser Ile Ile Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu
 225 230 235 240

Pro Val Leu Ser Gly Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg
 245 250 255

Ile Ala Thr Thr Thr Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp
 260 265 270

Ala Ala Glu Thr Gly Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala
 275 280 285

Thr Leu Glu Ser Val Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser
 290 295 300

Leu Gln Thr Ala
 305

<210> 349
 <211> 813
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(813)
 <223> FRXA01212

<400> 349
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acc aac ggg gcc ggc aaa acc tcc acc ttg gaa gtc atc gaa gga ctt 96
 Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val Ile Glu Gly Leu
 20 25 30

tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg ctt gac ccc gtt 144
 Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly Leu Asp Pro Val
 35 40 45

gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc atg ctg caa tca 192
 Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile Met Leu Gln Ser
 50 55 60

ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc atg gac atg tgg 240
 Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr Met Asp Met Trp
 65 70 75 80

cac ggc acc tgc acg tat ccg cgc gcc att aaa gat gtg ctt gcc gac 288
 His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp Val Leu Ala Asp
 85 90 95

gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc gcg ctt tcc gga 336
 Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly Ala Leu Ser Gly
 100 105 110

ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg ctt ggc gac ccc 384
 Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu Leu Gly Asp Pro
 115 120 125

tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc gac cca gaa tct 432
 Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu Asp Pro Glu Ser
 130 135 140

agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa cag cgc ggc gtc 480

Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys Gln Arg Gly Val
 145 150 155 160
 acc atg atg ctg acc acc cac tac ctg gag gaa gcc gaa ttc ctc tgc 528
 Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala Glu Phe Leu Cys
 165 170 175
 gac cgg att gcc atc atg aac gcc ggt gag atc gca gtg gaa ggc acc 576
 Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala Val Glu Gly Thr
 180 185 190
 ttg gat gaa ctg gtg gcc cgc gag aag tgc atc atc agt ttc gtg ctg 624
 Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile Ser Phe Val Leu
 195 200 205
 cgt ggc ggg cag gtg gag ttg ccg gtc ttg agt ggg gct gaa atc atc 672
 Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly Ala Glu Ile Ile
 210 215 220
 cgc gac aac aac cac gtc cgc atc gcc acc acc acc ctg cag cag cac 720
 Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Leu Gln Gln His
 225 230 235 240
 acc tta gaa ata ctt acc tgg gct gca gag acc ggg atc gcg ctg gaa 768
 Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly Ile Ala Leu Glu
 245 250 255
 ggc ttc gct gca aaa ccc gcc acc ttg gaa tcc gta ttc atg gac 813
 Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val Phe Met Asp
 260 265 270

<210> 350

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

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 Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val Ile Glu Gly Leu
 20 25 30
 Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly Leu Asp Pro Val
 35 40 45
 Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile Met Leu Gln Ser
 50 55 60
 Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr Met Asp Met Trp
 65 70 75 80
 His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp Val Leu Ala Asp
 85 90 95
 Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly Ala Leu Ser Gly
 100 105 110
 Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu Leu Gly Asp Pro
 115 120 125

Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu Asp Pro Glu Ser
 130 135 140

Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys Gln Arg Gly Val
 145 150 155 160

Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala Glu Phe Leu Cys
 165 170 175

Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala Val Glu Gly Thr
 180 185 190

Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile Ser Phe Val Leu
 195 200 205

Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly Ala Glu Ile Ile
 210 215 220

Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr Leu Gln Gln His
 225 230 235 240

Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly Ile Ala Leu Glu
 245 250 255

Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val Phe Met Asp
 260 265 270

<210> 351
 <211> 999
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(976)
 <223> RXA02749

<400> 351
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agcgatgcgc cgattacttg tttttgctac aaattttaact atg tca ccc atc cta 115
 Met Ser Pro Ile Leu
 1 5

aaa gtg cgg gac ctc gtc aaa cgc tat ggc gac acc gtt gcg gtt gac 163
 Lys Val Arg Asp Leu Val Lys Arg Tyr Gly Asp Thr Val Ala Val Asp
 10 15 20

ggt tta aat ttt gat gtt tca caa ggg gaa att ttt gcc ttt cta ggg 211
 Gly Leu Asn Phe Asp Val Ser Gln Gly Glu Ile Phe Ala Phe Leu Gly
 25 30 35

gag aac ggc gca gga aaa aca acc acg att tca tgc ctg att ggc att 259
 Glu Asn Gly Ala Gly Lys Thr Thr Thr Ile Ser Cys Leu Ile Gly Ile
 40 45 50

gat caa gcc acc tct ggg gag atc gaa ctg cag ggt ggc caa gta gat 307
 Asp Gln Ala Thr Ser Gly Glu Ile Glu Leu Gln Gly Gly Gln Val Asp
 55 60 65

tct gaa aaa ctt gga gtg gtg ttt caa caa tcc gtc tta gac cct ttg	355
Ser Glu Lys Leu Gly Val Val Phe Gln Gln Ser Val Leu Asp Pro Leu	
70 75 80 85	
ctg agt gcc aaa gaa aac ttg gaa aca cgc gga cag ctg tac cca ggg	403
Leu Ser Ala Lys Glu Asn Leu Glu Thr Arg Gly Gln Leu Tyr Pro Gly	
90 95 100	
gtg ggg aag cag cgg gtt gca cag ctc att gag caa atc ggg atg gaa	451
Val Gly Lys Gln Arg Val Ala Gln Leu Ile Glu Gln Ile Gly Met Glu	
105 110 115	
ggg ttt gcg gac cgc cga tac gga gtg ttg tcg ggc ggt gaa aaa cgt	499
Gly Phe Ala Asp Arg Arg Tyr Gly Val Leu Ser Gly Gly Glu Lys Arg	
120 125 130	
cgc acc gac atc gca cga gct tta ctg cac agc cca gac att ctt ttt	547
Arg Thr Asp Ile Ala Arg Ala Leu Leu His Ser Pro Asp Ile Leu Phe	
135 140 145	
ctt gat gaa ccc aca gca ggc ctc gac ccc aga tca cga cgc caa gtt	595
Leu Asp Glu Pro Thr Ala Gly Leu Asp Pro Arg Ser Arg Arg Gln Val	
150 155 160 165	
tgg gac acc atc aat tcc ctg cgt aac gat gtg ggc ctc act gtc ttt	643
Trp Asp Thr Ile Asn Ser Leu Arg Asn Asp Val Gly Leu Thr Val Phe	
170 175 180	
ttg acc act cac tac atg gaa gaa aca gaa ctg gct gat tca gtt cta	691
Leu Thr Thr His Tyr Met Glu Glu Thr Glu Leu Ala Asp Ser Val Leu	
185 190 195	
atc att gac cgt ggc aaa gag gtc gca tca gga acc ccg atg gaa ctg	739
Ile Ile Asp Arg Gly Lys Glu Val Ala Ser Gly Thr Pro Met Glu Leu	
200 205 210	
cgc gcc cgt tac acc aca aca gaa ttg act ctt aga aca aac gac cct	787
Arg Ala Arg Tyr Thr Thr Thr Glu Leu Thr Leu Arg Thr Asn Asp Pro	
215 220 225	
act cat tcg ggt aaa gag ttg gcc cac ttg agc cca gaa atc gac ggt	835
Thr His Ser Gly Lys Glu Leu Ala His Leu Ser Pro Glu Ile Asp Gly	
230 235 240 245	
gac cga ctg cgg atc aag ttg gaa aat ggg ctc gaa gct gcg cgc ctg	883
Asp Arg Leu Arg Ile Lys Leu Glu Asn Gly Leu Glu Ala Ala Arg Leu	
250 255 260	
gca aca gaa cta gat ggg gtt ctc gac gta gag atc cgc cac ggt tcc	931
Ala Thr Glu Leu Asp Gly Val Leu Asp Val Glu Ile Arg His Gly Ser	
265 270 275	
atg gac gat gta ttt cta gca gtt aca gct gaa cgg aaa cga tca	976
Met Asp Asp Val Phe Leu Ala Val Thr Ala Glu Arg Lys Arg Ser	
280 285 290	
tgattacagt tctgacacgc aga	999

<210> 352

<211> 292

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Met Ser Pro Ile Leu Lys Val Arg Asp Leu Val Lys Arg Tyr Gly Asp
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 20 25 30

Phe Ala Phe Leu Gly Glu Asn Gly Ala Gly Lys Thr Thr Thr Ile Ser
 35 40 45

Cys Leu Ile Gly Ile Asp Gln Ala Thr Ser Gly Glu Ile Glu Leu Gln
 50 55 60

Gly Gly Gln Val Asp Ser Glu Lys Leu Gly Val Val Phe Gln Gln Ser
 65 70 75 80

Val Leu Asp Pro Leu Leu Ser Ala Lys Glu Asn Leu Glu Thr Arg Gly
 85 90 95

Gln Leu Tyr Pro Gly Val Gly Lys Gln Arg Val Ala Gln Leu Ile Glu
 100 105 110

Gln Ile Gly Met Glu Gly Phe Ala Asp Arg Arg Tyr Gly Val Leu Ser
 115 120 125

Gly Gly Glu Lys Arg Arg Thr Asp Ile Ala Arg Ala Leu Leu His Ser
 130 135 140

Pro Asp Ile Leu Phe Leu Asp Glu Pro Thr Ala Gly Leu Asp Pro Arg
 145 150 155 160

Ser Arg Arg Gln Val Trp Asp Thr Ile Asn Ser Leu Arg Asn Asp Val
 165 170 175

Gly Leu Thr Val Phe Leu Thr Thr His Tyr Met Glu Glu Thr Glu Leu
 180 185 190

Ala Asp Ser Val Leu Ile Ile Asp Arg Gly Lys Glu Val Ala Ser Gly
 195 200 205

Thr Pro Met Glu Leu Arg Ala Arg Tyr Thr Thr Thr Glu Leu Thr Leu
 210 215 220

Arg Thr Asn Asp Pro Thr His Ser Gly Lys Glu Leu Ala His Leu Ser
 225 230 235 240

Pro Glu Ile Asp Gly Asp Arg Leu Arg Ile Lys Leu Glu Asn Gly Leu
 245 250 255

Glu Ala Ala Arg Leu Ala Thr Glu Leu Asp Gly Val Leu Asp Val Glu
 260 265 270

Ile Arg His Gly Ser Met Asp Asp Val Phe Leu Ala Val Thr Ala Glu
 275 280 285

Arg Lys Arg Ser
 290

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<210> 353
<211> 1920
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1897)  
<223> RXA02224
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				Met	Ala	Gln	His	Glu								
				1				5								
cgc gtt gcg gat gcg ctg cag ccg gcg tcg ttg gcg gag tcg tgg cgt	163															
Arg Val Ala Asp Ala Leu Gln Pro Ala Ser Leu Ala Glu Ser Trp Arg																
	10							15						20		
gag ctg aaa acg atg cct tcg ggg ccc aag gcc tgg tgg tat gtg agt	211															
Glu Leu Lys Thr Met Pro Ser Gly Pro Lys Ala Trp Trp Tyr Val Ser																
	25						30					35				
ttc gtg gtt att agc gtg gtc acg gtc gtg gcg atg gtc ggc acg tcc	259															
Phe Val Val Ile Ser Val Val Thr Val Val Ala Met Val Gly Thr Ser																
	40					45				50						
aac ttg ttg ggc tat tcc gtt gat ctg atc aat ggg cag tcg ttg ccg	307															
Asn Leu Leu Gly Tyr Ser Val Asp Leu Ile Asn Gly Gln Ser Leu Pro																
	55				60			65								
ctg atc ggt tca gga tcg acc gca atg atc tgg ttg ctt ggt ttg gtg	355															
Leu Ile Gly Ser Gly Ser Thr Ala Met Ile Trp Leu Leu Gly Leu Val																
	70				75			80						85		
ggc gct gga att tta gca gaa act gcc ggt cgc gcg ctg ctg caa ttg	403															
Gly Ala Gly Ile Leu Ala Glu Thr Ala Gly Arg Ala Leu Leu Gln Leu																
	90						95						100			
gtg atc aac acc ttg gca cgt cgc ctg tcg gtg gat ctg cgg aaa gct	451															
Val Ile Asn Thr Leu Ala Arg Arg Leu Ser Val Asp Leu Arg Lys Ala																
	105						110					115				
gcg ctg tct tcg gcg ttg cgt gca ccg gtt cct gat gtc atg gaa ttg	499															
Ala Leu Ser Ser Ala Leu Arg Ala Pro Val Pro Asp Val Met Glu Leu																
	120					125				130						
ggc acg gga aac gtg att agc cgc ctg acg caa gac atc gat aac act	547															
Gly Thr Gly Asn Val Ile Ser Arg Leu Thr Gln Asp Ile Asp Asn Thr																
	135				140			145								
gtg cgc atc gtc ggc atg gta ggt gtg cgt ttg gtg atc acc att ttg	595															
Val Arg Ile Val Gly Met Val Gly Val Arg Leu Val Ile Thr Ile Leu																
	150				155			160						165		
att ctg ccc agc tcc ttg ttc gcg ttg atg acc att cac tgg acc ttt	643															
Ile Leu Pro Ser Ser Leu Phe Ala Leu Met Thr Ile His Trp Thr Phe																

170										175										180									
gtg	atc	ctg	ttc	atc	gca	gtg	att	gtg	gtg	ctg	att	ccc	agc	ggg	cgg					691									
Val	Ile	Leu	Phe	Ile	Ala	Val	Ile	Val	Val	Leu	Ile	Pro	Ser	Gly	Arg														
			185																										
aaa	gcc	gtg	cga	gct	att	cct	tcg	gca	aca	aat	att	gtg	tcc	agt	acg					739									
Lys	Ala	Val	Arg	Ala	Ile	Pro	Ser	Ala	Thr	Asn	Ile	Val	Ser	Ser	Thr														
		200					205						210																
gag	gcg	cgt	cga	aac	aat	ctg	ctc	ctc	gat	acg	atc	cgt	ggc	att	gaa					787									
Glu	Ala	Arg	Arg	Asn	Asn	Leu	Leu	Leu	Asp	Thr	Ile	Arg	Gly	Ile	Glu														
		215					220					225																	
aca	ctg	cgt	gtg	ctc	aag	ctc	ggg	gcg	tgg	ggg	gtg	cag	cgg	atg	cgc					835									
Thr	Leu	Arg	Val	Leu	Lys	Leu	Gly	Ala	Trp	Gly	Val	Gln	Arg	Met	Arg														
					235					240																			
caa	gcg	tcg	tgg	act	gcg	gtg	caa	gca	aca	gct	gat	cgc	gcg	ccg	att					883									
Gln	Ala	Ser	Trp	Thr	Ala	Val	Gln	Ala	Thr	Ala	Asp	Arg	Ala	Pro	Ile														
				250					255						260														
ttc	act	cgt	ctg	ctc	gcc	ctt	ggg	tcg	att	gct	tat	ggc	ctg	ctg	cta					931									
Phe	Thr	Arg	Leu	Leu	Ala	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Leu	Leu	Leu														
			265					270																					
att	ggc	gtg	ttt	ggg	ctc	agt	gcg	ttt	tgg	gtt	gcc	cag	gat	gcg	atg					979									
Ile	Gly	Val	Phe	Gly	Leu	Ser	Ala	Phe	Trp	Val	Ala	Gln	Asp	Ala	Met														
		280					285					290																	
agc	att	gga	gcg	gca	acg	gca	gca	gtt	ttc	gtg	gtt	gtg	cgc	atg	gaa					1027									
Ser	Ile	Gly	Ala	Ala	Thr	Ala	Ala	Val	Phe	Val	Val	Val	Arg	Met	Glu														
		295					300					305																	
att	cac	gtg	ttc	aac	gtg	ctg	ttc	ttc	gca	tcg	gaa	att	cag	agt	gcg					1075									
Ile	His	Val	Phe	Asn	Val	Leu	Phe	Phe	Ala	Ser	Glu	Ile	Gln	Ser	Ala														
		310				315				320					325														
tct	act	tct	ctt	ggg	cgc	gcg	gtg	tcc	ctt	gcc	cag	atg	gct	cgt	cgc					1123									
Ser	Thr	Ser	Leu	Gly	Arg	Ala	Val	Ser	Leu	Ala	Gln	Met	Ala	Arg	Arg														
				330					335					340															
acc	gaa	cag	ctg	tct	gag	tct	gcc	gat	tgc	aca	gaa	cca	ccc	tcc	gtg					1171									
Thr	Glu	Gln	Leu	Ser	Glu	Ser	Ala	Asp	Cys	Thr	Glu	Pro	Pro	Ser	Val														
			345					350					355																
act	gtg	cag	gac	gtg	acg	ttt	aaa	tat	ccc	ggc	ggc	gtg	gcc	att	ttg					1219									
Thr	Val	Gln	Asp	Val	Thr	Phe	Lys	Tyr	Pro	Gly	Gly	Val	Ala	Ile	Leu														
		360					365					370																	
gag	gat	ttc	aat	ctg	gtc	ttg	gaa	gca	gga	aca	acc	aca	gcg	ctg	gtc					1267									
Glu	Asp	Phe	Asn	Leu	Val	Leu	Glu	Ala	Gly	Thr	Thr	Thr	Ala	Leu	Val														
		375				380						385																	
ggg	act	tct	ggg	gcg	gga	aaa	tcc	acg	ctc	gcg	ggc	gtc	att	gcg	ggg					1315									
Gly	Thr	Ser	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Ala	Gly	Val	Ile	Ala	Gly														
		390				395				400					405														
ctg	cag	cgc	cct	gat	tcc	ggc	gcc	gtt	ttg	gtc	ggg	ggc	atc	aac	acc					1363									
Leu	Gln	Arg	Pro	Asp	Ser	Gly	Ala	Val	Leu	Val	Gly	Gly	Ile	Asn	Thr														
			410						415					420															

gcc acc gtc acc gac acg tgg act acc cgc cag gtt gcg ctg atc agc 1411
 Ala Thr Val Thr Asp Thr Trp Thr Thr Arg Gln Val Ala Leu Ile Ser
 425 430 435

cag gaa gtc cac ctt ttc gca ggc act ctg gca gag gat ctt cgc atg 1459
 Gln Glu Val His Leu Phe Ala Gly Thr Leu Ala Glu Asp Leu Arg Met
 440 445 450

gcc aat gcg cac gcc acc gac gcg cag ctc cac gca gcg ctc gag tcg 1507
 Ala Asn Ala His Ala Thr Asp Ala Gln Leu His Ala Ala Leu Glu Ser
 455 460 465

gtc ggg ctc ggg caa atg aca act gct ttt cga cgt ttc ttt cca tcc 1555
 Val Gly Leu Gly Gln Met Thr Thr Ala Phe Arg Arg Phe Phe Pro Ser
 470 475 480 485

gga tta gac acc aaa att ggc gcc ggc gca gaa gaa ctc acc cct gaa 1603
 Gly Leu Asp Thr Lys Ile Gly Ala Gly Ala Glu Glu Leu Thr Pro Glu
 490 495 500

atc caa cag caa atc tct ctt gcc cgc atc gtg ctc cgc aat cca cct 1651
 Ile Gln Gln Gln Ile Ser Leu Ala Arg Ile Val Leu Arg Asn Pro Pro
 505 510 515

gtg ttg atc atg gat gaa gcc acc agt gaa gcc ggc agc gat gat gcc 1699
 Val Leu Ile Met Asp Glu Ala Thr Ser Glu Ala Gly Ser Asp Asp Ala
 520 525 530

cgc atg ttg gaa aaa gcc gcc aca gaa atc gca cga aac cgc acc acc 1747
 Arg Met Leu Glu Lys Ala Ala Thr Glu Ile Ala Arg Asn Arg Thr Thr
 535 540 545

ttg gtt gtt gcg cac cgc ctt gac caa gca gtt gtc gca gat cgc atc 1795
 Leu Val Val Ala His Arg Leu Asp Gln Ala Val Val Ala Asp Arg Ile
 550 555 560 565

atc gtg atg gaa caa ggc aca atc acc gaa gac ggc act cac cag gaa 1843
 Ile Val Met Glu Gln Gly Thr Ile Thr Glu Asp Gly Thr His Gln Glu
 570 575 580

tta ctt gct ttt gag ggc cgc tac gcg cag ctg tat caa cga tgg agt 1891
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 585 590 595

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 Ala Gln

<210> 354

<211> 599

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

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 20 25 30

Trp Trp Tyr Val Ser Phe Val Val Ile Ser Val Val Thr Val Val Ala
 35 40 45
 Met Val Gly Thr Ser Asn Leu Leu Gly Tyr Ser Val Asp Leu Ile Asn
 50 55 60
 Gly Gln Ser Leu Pro Leu Ile Gly Ser Gly Ser Thr Ala Met Ile Trp
 65 70 75 80
 Leu Leu Gly Leu Val Gly Ala Gly Ile Leu Ala Glu Thr Ala Gly Arg
 85 90 95
 Ala Leu Leu Gln Leu Val Ile Asn Thr Leu Ala Arg Arg Leu Ser Val
 100 105 110
 Asp Leu Arg Lys Ala Ala Leu Ser Ser Ala Leu Arg Ala Pro Val Pro
 115 120 125
 Asp Val Met Glu Leu Gly Thr Gly Asn Val Ile Ser Arg Leu Thr Gln
 130 135 140
 Asp Ile Asp Asn Thr Val Arg Ile Val Gly Met Val Gly Val Arg Leu
 145 150 155 160
 Val Ile Thr Ile Leu Ile Leu Pro Ser Ser Leu Phe Ala Leu Met Thr
 165 170 175
 Ile His Trp Thr Phe Val Ile Leu Phe Ile Ala Val Ile Val Val Leu
 180 185 190
 Ile Pro Ser Gly Arg Lys Ala Val Arg Ala Ile Pro Ser Ala Thr Asn
 195 200 205
 Ile Val Ser Ser Thr Glu Ala Arg Arg Asn Asn Leu Leu Leu Asp Thr
 210 215 220
 Ile Arg Gly Ile Glu Thr Leu Arg Val Leu Lys Leu Gly Ala Trp Gly
 225 230 235 240
 Val Gln Arg Met Arg Gln Ala Ser Trp Thr Ala Val Gln Ala Thr Ala
 245 250 255
 Asp Arg Ala Pro Ile Phe Thr Arg Leu Leu Ala Leu Gly Ser Ile Ala
 260 265 270
 Tyr Gly Leu Leu Leu Ile Gly Val Phe Gly Leu Ser Ala Phe Trp Val
 275 280 285
 Ala Gln Asp Ala Met Ser Ile Gly Ala Ala Thr Ala Ala Val Phe Val
 290 295 300
 Val Val Arg Met Glu Ile His Val Phe Asn Val Leu Phe Phe Ala Ser
 305 310 315 320
 Glu Ile Gln Ser Ala Ser Thr Ser Leu Gly Arg Ala Val Ser Leu Ala
 325 330 335
 Gln Met Ala Arg Arg Thr Glu Gln Leu Ser Glu Ser Ala Asp Cys Thr
 340 345 350

Glu Pro Pro Ser Val Thr Val Gln Asp Val Thr Phe Lys Tyr Pro Gly
 355 360 365
 Gly Val Ala Ile Leu Glu Asp Phe Asn Leu Val Leu Glu Ala Gly Thr
 370 375 380
 Thr Thr Ala Leu Val Gly Thr Ser Gly Ala Gly Lys Ser Thr Leu Ala
 385 390 395 400
 Gly Val Ile Ala Gly Leu Gln Arg Pro Asp Ser Gly Ala Val Leu Val
 405 410 415
 Gly Gly Ile Asn Thr Ala Thr Val Thr Asp Thr Trp Thr Thr Arg Gln
 420 425 430
 Val Ala Leu Ile Ser Gln Glu Val His Leu Phe Ala Gly Thr Leu Ala
 435 440 445
 Glu Asp Leu Arg Met Ala Asn Ala His Ala Thr Asp Ala Gln Leu His
 450 455 460
 Ala Ala Leu Glu Ser Val Gly Leu Gly Gln Met Thr Thr Ala Phe Arg
 465 470 475 480
 Arg Phe Phe Pro Ser Gly Leu Asp Thr Lys Ile Gly Ala Gly Ala Glu
 485 490 495
 Glu Leu Thr Pro Glu Ile Gln Gln Gln Ile Ser Leu Ala Arg Ile Val
 500 505 510
 Leu Arg Asn Pro Pro Val Leu Ile Met Asp Glu Ala Thr Ser Glu Ala
 515 520 525
 Gly Ser Asp Asp Ala Arg Met Leu Glu Lys Ala Ala Thr Glu Ile Ala
 530 535 540
 Arg Asn Arg Thr Thr Leu Val Val Ala His Arg Leu Asp Gln Ala Val
 545 550 555 560
 Val Ala Asp Arg Ile Ile Val Met Glu Gln Gly Thr Ile Thr Glu Asp
 565 570 575
 Gly Thr His Gln Glu Leu Leu Ala Phe Glu Gly Arg Tyr Ala Gln Leu
 580 585 590
 Tyr Gln Arg Trp Ser Ala Gln
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1630)
 <223> RXN01602

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	Met Ala Lys Thr His	
	1 5	
att cgg tta cag gac ctt tcc ctg tca tac acc tca acc ccg tta att	163	
Ile Arg Leu Gln Asp Leu Ser Leu Ser Tyr Thr Ser Thr Pro Leu Ile		
10 15 20		
acg aag ctc aat atc act gtt tct tct gga cag tgc gca gtg att gtt	211	
Thr Lys Leu Asn Ile Thr Val Ser Ser Gly Gln Cys Ala Val Ile Val		
25 30 35		
ggg gag aat ggt cga ggt aaa acc aca ctt ctg cga gca ctg gct cga	259	
Gly Glu Asn Gly Arg Gly Lys Thr Thr Leu Leu Arg Ala Leu Ala Arg		
40 45 50		
gaa ttc ccg cca tct gca ggt gag att ctc act cat ggc acg gta gca	307	
Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr His Gly Thr Val Ala		
55 60 65		
att gct cat caa cac atg cct gca ggt gat ctg tcc gtc gga gag atc	355	
Ile Ala His Gln His Met Pro Ala Gly Asp Leu Ser Val Gly Glu Ile		
70 75 80 85		
tgt gat gag gca att cgt gat tca aag aat gct ctc gaa gag ctt gag	403	
Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala Leu Glu Glu Leu Glu		
90 95 100		
aga gct gga gct cta ctt gag aca aac act gcg cac gca ctt gat gga	451	
Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala His Ala Leu Asp Gly		
105 110 115		
tat caa caa gcc ctt gat gcc gct gaa gtg ctt gac gca tgg aac gct	499	
Tyr Gln Gln Ala Leu Asp Ala Ala Glu Val Leu Asp Ala Trp Asn Ala		
120 125 130		
gaa cat cga tta gaa aaa gct ctg cgc agc ttt ggc gcg atc acc gat	547	
Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe Gly Ala Ile Thr Asp		
135 140 145		
aga tcc cgt gca ctc agt gag cta tcg atc ggg caa agg tat cgg gta	595	
Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly Gln Arg Tyr Arg Val		
150 155 160 165		
cgg ctg gcc tgc ctc atc ggt ggc gat gct gat att ttg ctt ctc gat	643	
Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp Ile Leu Leu Leu Asp		
170 175 180		
gaa ccc acc aat cat ctt gac cgg ggc gcg ctt aac tat ctc acc gaa	691	
Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu Asn Tyr Leu Thr Glu		
185 190 195		
gcc ata acc tcc cac aaa ggt gtg gta ctt gtt gtt tct cat gat caa	739	
Ala Ile Thr Ser His Lys Gly Val Val Leu Val Val Ser His Asp Gln		
200 205 210		
gca ctg atc aaa gat gtc gcg gat ttc atc atc gat att gat tca acc	787	
Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile Asp Ile Asp Ser Thr		
215 220 225		

cca gac ggc cta cca cgg atc tat cat gag ggt ttt gat tct tat cga	835
Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly Phe Asp Ser Tyr Arg	
230 235 240 245	
cgc caa agg agt gcg ctt ctt gaa act tgg agg cag gat tat gcc gct	883
Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg Gln Asp Tyr Ala Ala	
250 255 260	
gca caa act gtg caa cag caa ttg cag gag gat cta gag cac gca cgc	931
Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp Leu Glu His Ala Arg	
265 270 275	
cag cgg gtg aat tct tcg tgg aaa cct cca aaa gga acg gga aaa cac	979
Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys Gly Thr Gly Lys His	
280 285 290	
act cgc gca tct cgg gct ccc gga gtg gtg cag gcc tta aag cga gca	1027
Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln Ala Leu Lys Arg Ala	
295 300 305	
cag gat gcg ttg gat agc aaa gcg ttg gac gtt ccc ccg gct ccg gcc	1075
Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val Pro Pro Ala Pro Ala	
310 315 320 325	
cca ttg ctt ctg cct acc ttg aaa gtg cga cca gat aaa ccc atg gtg	1123
Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro Asp Lys Pro Met Val	
330 335 340	
gac ttt tcg gac ctt ttt gta ccc cac cgc ttg cgt ctg cca ggc tca	1171
Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu Arg Leu Pro Gly Ser	
345 350 355	
cat tca gtg gta tca ggt gac aaa ata gtg atc act ggt gac aac ggc	1219
His Ser Val Val Ser Gly Asp Lys Ile Val Ile Thr Gly Asp Asn Gly	
360 365 370	
gct ggc aaa tca acg ctc atc gaa gtc ttg tct ggg gtt ttg act ccg	1267
Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser Gly Val Leu Thr Pro	
375 380 385	
gca agt ggt tcg gtt gca aac cat gcc cga act ggg gtt ctc ggc caa	1315
Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr Gly Val Leu Gly Gln	
390 395 400 405	
gaa tca ctt gtc ggc gag gtg cca tca ata gca cga gat cac gca gtt	1363
Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala Arg Asp His Ala Val	
410 415 420	
aag tgg gga ctt tta agt gtt gag gag agc cga ttt gcc cta cag gaa	1411
Lys Trp Gly Leu Leu Ser Val Glu Glu Ser Arg Phe Ala Leu Gln Glu	
425 430 435	
ttc tca att ggt caa cgc aga aga cta gat ttg gcc atg tcg tta gct	1459
Phe Ser Ile Gly Gln Arg Arg Arg Leu Asp Leu Ala Met Ser Leu Ala	
440 445 450	
ggc aat cct gaa ctg ttg ctt ctc gat gaa cct tcg aac cat ctg tct	1507
Gly Asn Pro Glu Leu Leu Leu Leu Asp Glu Pro Ser Asn His Leu Ser	
455 460 465	
atg cac ttg gtt tcc gca ctt aca gag tgg ctg gac acg acc gcg gct	1555

Met His Leu Val Ser Ala Leu Thr Glu Trp Leu Asp Thr Thr Ala Ala
 470 475 480 485

gca gtg atc atg gta acg cat gat cga cag cta ctc cgc gat acg gct 1603
 Ala Val Ile Met Val Thr His Asp Arg Gln Leu Leu Arg Asp Thr Ala
 490 495 500

cat tgg agg cac atc gag ttg aaa tct taagaattcg caagggcttt 1650
 His Trp Arg His Ile Glu Leu Lys Ser
 505 510

cac 1653

<210> 356

<211> 510

<212> PRT

<213> Corynebacterium glutamicum

<400> 356

Met Ala Lys Thr His Ile Arg Leu Gln Asp Leu Ser Leu Ser Tyr Thr
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Ser Thr Pro Leu Ile Thr Lys Leu Asn Ile Thr Val Ser Ser Gly Gln
 20 25 30

Cys Ala Val Ile Val Gly Glu Asn Gly Arg Gly Lys Thr Thr Leu Leu
 35 40 45

Arg Ala Leu Ala Arg Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr
 50 55 60

His Gly Thr Val Ala Ile Ala His Gln His Met Pro Ala Gly Asp Leu
 65 70 75 80

Ser Val Gly Glu Ile Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala
 85 90 95

Leu Glu Glu Leu Glu Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala
 100 105 110

His Ala Leu Asp Gly Tyr Gln Gln Ala Leu Asp Ala Ala Glu Val Leu
 115 120 125

Asp Ala Trp Asn Ala Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe
 130 135 140

Gly Ala Ile Thr Asp Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly
 145 150 155 160

Gln Arg Tyr Arg Val Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp
 165 170 175

Ile Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu
 180 185 190

Asn Tyr Leu Thr Glu Ala Ile Thr Ser His Lys Gly Val Val Leu Val
 195 200 205

Val Ser His Asp Gln Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile
 210 215 220

Asp Ile Asp Ser Thr Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly
 225 230 235 240
 Phe Asp Ser Tyr Arg Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg
 245 250 255
 Gln Asp Tyr Ala Ala Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp
 260 265 270
 Leu Glu His Ala Arg Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys
 275 280 285
 Gly Thr Gly Lys His Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln
 290 295 300
 Ala Leu Lys Arg Ala Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val
 305 310 315 320
 Pro Pro Ala Pro Ala Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro
 325 330 335
 Asp Lys Pro Met Val Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu
 340 345 350
 Arg Leu Pro Gly Ser His Ser Val Val Ser Gly Asp Lys Ile Val Ile
 355 360 365
 Thr Gly Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser
 370 375 380
 Gly Val Leu Thr Pro Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr
 385 390 395 400
 Gly Val Leu Gly Gln Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala
 405 410 415
 Arg Asp His Ala Val Lys Trp Gly Leu Leu Ser Val Glu Glu Ser Arg
 420 425 430
 Phe Ala Leu Gln Glu Phe Ser Ile Gly Gln Arg Arg Arg Leu Asp Leu
 435 440 445
 Ala Met Ser Leu Ala Gly Asn Pro Glu Leu Leu Leu Leu Asp Glu Pro
 450 455 460
 Ser Asn His Leu Ser Met His Leu Val Ser Ala Leu Thr Glu Trp Leu
 465 470 475 480
 Asp Thr Thr Ala Ala Ala Val Ile Met Val Thr His Asp Arg Gln Leu
 485 490 495
 Leu Arg Asp Thr Ala His Trp Arg His Ile Glu Leu Lys Ser
 500 505 510

<210> 357

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXN02515

<400> 357

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tcagtttaaa attcgcttca accctgaaag attgtgacag atg agc act ctt gaa 115
                                         Met Ser Thr Leu Glu
                                         1           5

atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163
Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu
              10              15              20

cct aag gaa atc ctc aag ggc gtc aac ctc acc atc aac tct ggt gag 211
Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr Ile Asn Ser Gly Glu
              25              30              35

atc cac gcc atc atg ggc cct aac ggt tcc ggc aag tcc act ctt gct 259
Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala
              40              45              50

tac acc ctt ggt gga cac cca cgc tac gag gta acc gca ggc gag gtc 307
Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val
              55              60              65

ctc ctc gac ggc gag aac atc ctg gag atg gaa gtt gat gag cgt gca 355
Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala
              70              75              80              85

cgc gct ggt ctc ttc ctg gcc atg cag tat cca act gaa atc cct ggc 403
Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro Thr Glu Ile Pro Gly
              90              95              100

gtt tcc gtt gct aac ttc ctg cgt tcc gca gcg acc gca atc cgc ggc 451
Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly
              105              110              115

gag gct cct aag ctt cgc gag tgg gtt aag gaa gtc cgc acc gct cag 499
Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu Val Arg Thr Ala Gln
              120              125              130

gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa 547
Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu
              135              140              145

ggg ttc tcc ggt ggc gag aag aag cgc cac gag gtt ctg cag ctt gat 595
Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu Val Leu Gln Leu Asp
              150              155              160              165

ctg ctg aag cca aag ttc gcg atc atg gat gag acc gac tcc ggc ctt 643
Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu Thr Asp Ser Gly Leu
              170              175              180

gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag 691
Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys
              185              190              195

cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc 739

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Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile
 200 205 210

ctc aac tac gtt aag cct gac ttc att cac gtt ttc gcg aat ggc cag 787
 Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val Phe Ala Asn Gly Gln
 215 220 225

att gtg acc acc ggt ggc gct gag ctt gct gac aag ctc gag gct gac 835
 Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp Lys Leu Glu Ala Asp
 230 235 240 245

ggc tac gac cag ttc atc aag taacatgtcc gatttcctca atg 879
 Gly Tyr Asp Gln Phe Ile Lys
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<210> 358
 <211> 252
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 358
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Asp Glu Ser Ala Glu Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr
 20 25 30

Ile Asn Ser Gly Glu Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly
 35 40 45

Lys Ser Thr Leu Ala Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val
 50 55 60

Thr Ala Gly Glu Val Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu
 65 70 75 80

Val Asp Glu Arg Ala Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro
 85 90 95

Thr Glu Ile Pro Gly Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala
 100 105 110

Thr Ala Ile Arg Gly Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu
 115 120 125

Val Arg Thr Ala Gln Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn
 130 135 140

Arg Ser Val Asn Glu Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu
 145 150 155 160

Val Leu Gln Leu Asp Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu
 165 170 175

Thr Asp Ser Gly Leu Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly
 180 185 190

Ile Asn Ser Tyr Lys Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr
 195 200 205

His Tyr Lys Arg Ile Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val
 210 215 220
 Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp
 225 230 235 240
 Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys
 245 250

<210> 359
 <211> 1386
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1363)
 <223> RXN00525

<400> 359

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 Met Ser Leu Ala Glu
 1 5

tca att ctt ttg gcg ctc acc agc ctg aga agc aac aag atg cgt gca 163
 Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser Asn Lys Met Arg Ala
 10 15 20

ttg ttg acg ctg tta gga gtc atc att ggt atc gca tca gtc atc gga 211
 Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile Ala Ser Val Ile Gly
 25 30 35

att ttg acc att ggt aaa gcc ctg cag gat caa act ttg aat agt ttg 259
 Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln Thr Leu Asn Ser Leu
 40 45 50

gaa agc ttg ggc gcg aat gat ctg tcg gcg cag gtg gag gaa cgc ccc 307
 Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln Val Glu Glu Arg Pro
 55 60 65

gac gaa gat tcc ccc gaa ccc gat atg ttc gct ttt tct ggg gct gca 355
 Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala Phe Ser Gly Ala Ala
 70 75 80 85

aac tct agt ggc aat ctg att ccg gaa gaa aca gtt gat acg ctg cgc 403
 Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr Val Asp Thr Leu Arg
 90 95 100

gat cgt ttc gca ggc agc atc acg gga atc agc gtt ggc gga atg ggt 451
 Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser Val Gly Gly Met Gly
 105 110 115

acg caa ggc act ctc atc ggc gac acc gca gat ctt aaa tcc gat ctc 499
 Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp Leu Lys Ser Asp Leu
 120 125 130

ctc ggc gtc aac gag gat tat atg tgg atg aat ggc gtc gaa atg aac 547
 Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn Gly Val Glu Met Asn

135	140	145	
tac ggc cgc gcc atc acg caa gac gat gtt gcc gct cag cgc ccc gtt			595
Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala Ala Gln Arg Pro Val			
150	155	160	165
gcg gtc atc gcc cca gac acc ttt aat acg ctt ttc gac gca aac ccc			643
Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu Phe Asp Ala Asn Pro			
	170	175	180
aac ctc gct ctg ggg tcc gaa gta gct ttt gaa ctc aac ggt caa gag			691
Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu Leu Asn Gly Gln Glu			
	185	190	195
aca ttt ttg cgg gtt atc ggt gtg tat aaa gaa gcc gca gca ggt gga			739
Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu Ala Ala Ala Gly Gly			
	200	205	210
ctt gtg gga agc aat cca acc gtc cac acc tac acc cca tat acg gtg			787
Leu Val Gly Ser Asn Pro Thr Val His Thr Tyr Thr Pro Tyr Thr Val			
	215	220	225
gcc aat gac atc acc cac acg gaa gat gga ttg aac acg tta agt atc			835
Ala Asn Asp Ile Thr His Thr Glu Asp Gly Leu Asn Thr Leu Ser Ile			
	230	235	240
cgt gca gct cag ggc gta gac cag gat tca ctt aag ggt tca ctg caa			883
Arg Ala Ala Gln Gly Val Asp Gln Asp Ser Leu Lys Gly Ser Leu Gln			
	250	255	260
acc tac ttc gac gtc ctg tac gcc aac aat gac tcg cac cac gtt gcc			931
Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn Asp Ser His His Val Ala			
	265	270	275
atg ttg gac ttc cgt aaa cag atc gaa gag ttc aac acc att ctc ggc			979
Met Leu Asp Phe Arg Lys Gln Ile Glu Glu Phe Asn Thr Ile Leu Gly			
	280	285	290
gca atg agt ttg ggt atc tca gcc atc ggc gga att tcc ttg ctt gtc			1027
Ala Met Ser Leu Gly Ile Ser Ala Ile Gly Gly Ile Ser Leu Leu Val			
	295	300	305
ggt ggc atc gga gtg atg aac att atg ttg gtg tct gtc acc gag cga			1075
Gly Gly Ile Gly Val Met Asn Ile Met Leu Val Ser Val Thr Glu Arg			
	310	315	320
acc cgc gaa atc ggt gtc cga aaa gcc ctc ggc gct cgt cga cgt gac			1123
Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly Ala Arg Arg Arg Asp			
	330	335	340
att cgc ctg caa ttc gtc gtt gaa gcc atg atc att tgt ttc atc ggt			1171
Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile Ile Cys Phe Ile Gly			
	345	350	355
ggc atc ctc ggc gtg ctt ttg ggc ggc att ttg gga ttg atc atg tcc			1219
Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu Gly Leu Ile Met Ser			
	360	365	370
agc gct att ggc tac att tcc ttg cca cca ctg agt gga atc gtg atc			1267
Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu Ser Gly Ile Val Ile			
	375	380	385

gcc ttg gta ttt tcc atg gct atc ggc ctg ttt ttc ggc tac tac ccc 1315
 Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe Phe Gly Tyr Tyr Pro
 390 395 400 405

gcc aac aag gca gca aag ctc gat cca att gac gcc ttg cgt tat gag 1363
 Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp Ala Leu Arg Tyr Glu
 410 415 420

taaaagcctc gtttttaagg tag 1386

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<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

Met Ser Leu Ala Glu Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser
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Asn Lys Met Arg Ala Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile
 20 25 30

Ala Ser Val Ile Gly Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln
 35 40 45

Thr Leu Asn Ser Leu Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln
 50 55 60

Val Glu Glu Arg Pro Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala
 65 70 75 80

Phe Ser Gly Ala Ala Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr
 85 90 95

Val Asp Thr Leu Arg Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser
 100 105 110

Val Gly Gly Met Gly Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp
 115 120 125

Leu Lys Ser Asp Leu Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn
 130 135 140

Gly Val Glu Met Asn Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala
 145 150 155 160

Ala Gln Arg Pro Val Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu
 165 170 175

Phe Asp Ala Asn Pro Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu
 180 185 190

Leu Asn Gly Gln Glu Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu
 195 200 205

Ala Ala Ala Gly Gly Leu Val Gly Ser Asn Pro Thr Val His Thr Tyr
 210 215 220

Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Glu Asp Gly Leu

225	230	235	240
Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser Leu	245	250	255
Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn Asp	260	265	270
Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu Phe	275	280	285
Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly Gly	290	295	300
Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu Val	305	310	315
Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly	325	330	335
Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile	340	345	350
Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu	355	360	365
Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu	370	375	380
Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe	385	390	395
Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp	405	410	415
Ala Leu Arg Tyr Glu	420		
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<223> RXN02096			
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ccgttcttgt actcctcttc cataccgcga gaacatctcg atg ggt ttg gat gtc 115			
Met Gly Leu Asp Val 1 5			
agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat 163			
Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp 10 15 20			
ttt atc gat cgc ctt cca aac aaa tac gag gaa gtc att ggc gaa cgc 211			

Phe	Ile	Asp	Arg	Leu	Pro	Asn	Lys	Tyr	Glu	Glu	Val	Ile	Gly	Glu	Arg		
			25					30					35				
ggc	ctg	acg	ctt	tct	ggt	ggt	caa	cgc	caa	cgc	atc	gcc	ctc	gca	cgg	259	
Gly	Leu	Thr	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala	Leu	Ala	Arg		
		40					45					50					
gct	ttc	ctg	gcg	cat	ccc	aaa	gtg	ttg	gtg	ctt	gat	gat	gcc	acc	tct	307	
Ala	Phe	Leu	Ala	His	Pro	Lys	Val	Leu	Val	Leu	Asp	Asp	Ala	Thr	Ser		
	55					60					65						
gcc	att	gat	gcc	tcc	act	gag	gac	cgc	att	ttc	cag	gcc	ttg	cgc	gaa	355	
Ala	Ile	Asp	Ala	Ser	Thr	Glu	Asp	Arg	Ile	Phe	Gln	Ala	Leu	Arg	Glu		
70					75					80				85			
gaa	ctg	cac	gat	gtc	acc	att	ttg	atc	atc	gcg	cac	cgc	cac	tcc	act	403	
Glu	Leu	His	Asp	Val	Thr	Ile	Leu	Ile	Ile	Ala	His	Arg	His	Ser	Thr		
				90					95					100			
ttg	gag	ctc	ggc	gat	cgg	gtt	ggt	ctg	gtc	gaa	gat	gga	cgg	gta	aca	451	
Leu	Glu	Leu	Gly	Asp	Arg	Val	Gly	Leu	Val	Glu	Asp	Gly	Arg	Val	Thr		
			105					110					115				
gca	ctg	gga	ccg	ttg	agt	gag	atg	cgt	gat	cac	gct	cgt	ttc	tcg	cat	499	
Ala	Leu	Gly	Pro	Leu	Ser	Glu	Met	Arg	Asp	His	Ala	Arg	Phe	Ser	His		
		120					125					130					
ctg	atg	gct	ctt	gat	ttc	cag	gat	tct	cac	gat	ccg	gaa	ttc	acc	ctc	547	
Leu	Met	Ala	Leu	Asp	Phe	Gln	Asp	Ser	His	Asp	Pro	Glu	Phe	Thr	Leu		
	135					140					145						
gac	aac	ggt	tca	cta	ccc	agc	caa	gag	caa	ttg	tgg	ccg	gag	gtc	tcc	595	
Asp	Asn	Gly	Ser	Leu	Pro	Ser	Gln	Glu	Gln	Leu	Trp	Pro	Glu	Val	Ser		
150					155					160					165		
aca	gaa	aag	cag	tac	aag	att	ctt	gcg	cct	gcc	cct	ggt	cga	ggc	cgt	643	
Thr	Glu	Lys	Gln	Tyr	Lys	Ile	Leu	Ala	Pro	Ala	Pro	Gly	Arg	Gly	Arg		
				170					175					180			
ggc	atg	tcc	atg	cca	gca	acc	cct	gag	ctg	ctc	gcc	cag	att	gag	gcg	691	
Gly	Met	Ser	Met	Pro	Ala	Thr	Pro	Glu	Leu	Leu	Ala	Gln	Ile	Glu	Ala		
			185					190					195				
ctg	cca	gca	gca	acg	gaa	gaa	aca	cga	gtt	gat	gcc	ggg	agg	cta	cgc	739	
Leu	Pro	Ala	Ala	Thr	Glu	Glu	Thr	Arg	Val	Asp	Ala	Gly	Arg	Leu	Arg		
		200					205					210					
acc	agt	acc	tcc	ggt	ttc	aaa	ttg	ctc	agt	tta	ttc	aag	cag	gtc	cgt	787	
Thr	Ser	Thr	Ser	Gly	Phe	Lys	Leu	Leu	Ser	Leu	Phe	Lys	Gln	Val	Arg		
	215					220					225						
tgg	ctc	gtc	gtc	gcg	gtc	atc	gcg	ttg	ttg	ctg	gtg	ggc	gta	gcc	gcc	835	
Trp	Leu	Val	Val	Ala	Val	Ile	Ala	Leu	Leu	Leu	Val	Gly	Val	Ala	Ala		
230					235					240					245		
gat	cta	gca	ttt	cca	aca	ctg	atg	cgc	gca	gcc	atc	gac	aac	ggt	gtg	883	
Asp	Leu	Ala	Phe	Pro	Thr	Leu	Met	Arg	Ala	Ala	Ile	Asp	Asn	Gly	Val		
				250					255					260			
caa	gca	caa	agc	acc	tcc	acg	ttg	tgg	tgg	atc	gcc	atc	gca	ggc	agc	931	
Gln	Ala	Gln	Ser	Thr	Ser	Thr	Leu	Trp	Trp	Ile	Ala	Ile	Ala	Gly	Ser		

265	270	275	
gta gta gtc ctt ctg tcc tgg gcc gcc gcc gcg atc aac acg att atc Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile 280 285 290			979
acg gca cgc acc ggt gaa cgg ctg ctt tac ggc ttg cgt ctg cgc tca Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser 295 300 305			1027
ttt gtg cat cta ttg cgc ctg tcc atg agc tat ttc gaa cgc acc atg Phe Val His Leu Leu Ser Met Ser Tyr Phe Glu Arg Thr Met 310 315 320 325			1075
tcc ggc cgc atc atg acg cgc atg acc acc gac atc gac aac ctc tcg Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser 330 335 340			1123
tcc ttc ctc caa tca ggt ctg gcg caa aca gtt gtc tct gtg ggc acg Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr 345 350 355			1171
ctc atc ggt gtg gtc acc atg ctc gcc atc acc gac gca caa cta gca Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr Asp Ala Gln Leu Ala 360 365 370			1219
ctc gtt gcg ctg tcc gtg gtg ccg atc atc atc gtg ctc act ctc att Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile Val Leu Thr Leu Ile 375 380 385			1267
ttc cga cgc atc agc tcc agg ctg tac acc gct tca cgc gag caa gcc Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala Ser Arg Glu Gln Ala 390 395 400 405			1315
agc cag gtc aac gcg gta ttc cac gag tcc atc gcc ggt tta cgc acc Ser Gln Val Asn Ala Val Phe His Glu Ser Ile Ala Gly Leu Arg Thr 410 415 420			1363
gcg cag atg cac cgc atg gaa gac caa gtc ttt gac aat tat gcg ggc Ala Gln Met His Arg Met Glu Asp Gln Val Phe Asp Asn Tyr Ala Gly 425 430 435			1411
gaa gca gag gaa ttc cga cgc ctg cgt gtg aaa tcc cag acg gcc atc Glu Ala Glu Glu Phe Arg Arg Leu Arg Val Lys Ser Gln Thr Ala Ile 440 445 450			1459
gcc atc tac ttc ccc gcc ctt gcc gcg ctc tct gaa atc gcc cag gca Ala Ile Tyr Phe Pro Gly Leu Gly Ala Leu Ser Glu Ile Ala Gln Ala 455 460 465			1507
ctc gtc ctc ggt ttc gcc gca ctg caa gta acg cgc ggc gac atc tcc Leu Val Leu Gly Phe Gly Ala Leu Gln Val Thr Arg Gly Asp Ile Ser 470 475 480 485			1555
acc ggc gta ctc gtg gca ttc gtg ctg tac atg ggc ctg atg ttc ggc Thr Gly Val Leu Val Ala Phe Val Leu Tyr Met Gly Leu Met Phe Gly 490 495 500			1603
ccc atc caa caa cta agc caa atc ttc gac tcc tac caa caa gcc gcc Pro Ile Gln Gln Leu Ser Gln Ile Phe Asp Ser Tyr Gln Gln Ala Ala 505 510 515			1651

gtc ggc ttc cgt cgc atc acc gaa ctg ctc gca acg cag ccc agc gtc 1699
 Val Gly Phe Arg Arg Ile Thr Glu Leu Leu Ala Thr Gln Pro Ser Val
 520 525 530
 cag atc tgg gca cca aca ggc acg cta ggc agg ctg cca cgc agc ctt 1747
 Gln Ile Trp Ala Pro Thr Gly Thr Leu Gly Arg Leu Pro Arg Ser Leu
 535 540 545
 tat tgc ttg acg acg tca cct tcg gct att cag acg atc cga tcc 1792
 Tyr Cys Leu Thr Thr Ser Pro Ser Ala Ile Gln Thr Ile Arg Ser
 550 555 560
 tagacaacgt caccgtccag atc 1815

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 <213> Corynebacterium glutamicum

<400> 362
 Met Gly Leu Asp Val Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu
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 Ala Gln Ala His Asp Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu
 20 25 30
 Val Ile Gly Glu Arg Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg
 35 40 45
 Ile Ala Leu Ala Arg Ala Phe Leu Ala His Pro Lys Val Leu Val Leu
 50 55 60
 Asp Asp Ala Thr Ser Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe
 65 70 75 80
 Gln Ala Leu Arg Glu Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala
 85 90 95
 His Arg His Ser Thr Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu
 100 105 110
 Asp Gly Arg Val Thr Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His
 115 120 125
 Ala Arg Phe Ser His Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp
 130 135 140
 Pro Glu Phe Thr Leu Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu
 145 150 155 160
 Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala
 165 170 175
 Pro Gly Arg Gly Arg Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu
 180 185 190
 Ala Gln Ile Glu Ala Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp
 195 200 205

Ala	Gly	Arg	Leu	Arg	Thr	Ser	Thr	Ser	Gly	Phe	Lys	Leu	Leu	Ser	Leu	210	215	220
Phe	Lys	Gln	Val	Arg	Trp	Leu	Val	Val	Ala	Val	Ile	Ala	Leu	Leu	Leu	225	230	235
Val	Gly	Val	Ala	Ala	Asp	Leu	Ala	Phe	Pro	Thr	Leu	Met	Arg	Ala	Ala	245	250	255
Ile	Asp	Asn	Gly	Val	Gln	Ala	Gln	Ser	Thr	Ser	Thr	Leu	Trp	Trp	Ile	260	265	270
Ala	Ile	Ala	Gly	Ser	Val	Val	Val	Leu	Leu	Ser	Trp	Ala	Ala	Ala	Ala	275	280	285
Ile	Asn	Thr	Ile	Ile	Thr	Ala	Arg	Thr	Gly	Glu	Arg	Leu	Leu	Tyr	Gly	290	295	300
Leu	Arg	Leu	Arg	Ser	Phe	Val	His	Leu	Leu	Arg	Leu	Ser	Met	Ser	Tyr	305	310	315
Phe	Glu	Arg	Thr	Met	Ser	Gly	Arg	Ile	Met	Thr	Arg	Met	Thr	Thr	Asp	325	330	335
Ile	Asp	Asn	Leu	Ser	Ser	Phe	Leu	Gln	Ser	Gly	Leu	Ala	Gln	Thr	Val	340	345	350
Val	Ser	Val	Gly	Thr	Leu	Ile	Gly	Val	Val	Thr	Met	Leu	Ala	Ile	Thr	355	360	365
Asp	Ala	Gln	Leu	Ala	Leu	Val	Ala	Leu	Ser	Val	Val	Pro	Ile	Ile	Ile	370	375	380
Val	Leu	Thr	Leu	Ile	Phe	Arg	Arg	Ile	Ser	Ser	Arg	Leu	Tyr	Thr	Ala	385	390	395
Ser	Arg	Glu	Gln	Ala	Ser	Gln	Val	Asn	Ala	Val	Phe	His	Glu	Ser	Ile	405	410	415
Ala	Gly	Leu	Arg	Thr	Ala	Gln	Met	His	Arg	Met	Glu	Asp	Gln	Val	Phe	420	425	430
Asp	Asn	Tyr	Ala	Gly	Glu	Ala	Glu	Glu	Phe	Arg	Arg	Leu	Arg	Val	Lys	435	440	445
Ser	Gln	Thr	Ala	Ile	Ala	Ile	Tyr	Phe	Pro	Gly	Leu	Gly	Ala	Leu	Ser	450	455	460
Glu	Ile	Ala	Gln	Ala	Leu	Val	Leu	Gly	Phe	Gly	Ala	Leu	Gln	Val	Thr	465	470	475
Arg	Gly	Asp	Ile	Ser	Thr	Gly	Val	Leu	Val	Ala	Phe	Val	Leu	Tyr	Met	485	490	495
Gly	Leu	Met	Phe	Gly	Pro	Ile	Gln	Gln	Leu	Ser	Gln	Ile	Phe	Asp	Ser	500	505	510
Tyr	Gln	Gln	Ala	Ala	Val	Gly	Phe	Arg	Arg	Ile	Thr	Glu	Leu	Leu	Ala	515	520	525
Thr	Gln	Pro	Ser	Val	Gln	Ile	Trp	Ala	Pro	Thr	Gly	Thr	Leu	Gly	Arg			

530 535 540

Leu Pro Arg Ser Leu Tyr Cys Leu Thr Thr Ser Pro Ser Ala Ile Gln
545 550 555 560

Thr Ile Arg Ser

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<211> 1203
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1180)
<223> RXN00412

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cttttgatccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115
Val Ser His Thr Ala 5
1

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln 20
10 15

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat 211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn 35
25 30

aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa 259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu 50
40 45

ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc 307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser 65
55 60

act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg 355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser 85
70 75 80

ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg 403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu 100
90 95

cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg 451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu 115
105 110

ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt 499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val 130
120 125

gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc 547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu 145
135 140

gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg 595
 Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu
 150 155 160 165

tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc 643
 Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr
 170 175 180

aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca 691
 Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro
 185 190 195

gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa 739
 Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu
 200 205 210

ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt 787
 Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg
 215 220 225

tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa 835
 Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu
 230 235 240 245

tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct 883
 Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala
 250 255 260

caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa 931
 Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu
 265 270 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu
 280 285 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln
 295 300 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg
 310 315 320 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala
 330 335 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu
 345 350 355

atc acc cga tgaacgagat gatcctcgca gct 1203
 Ile Thr Arg
 360

<210> 364

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln
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 Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys
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 Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val
 35 40 45
 Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser
 50 55 60
 Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser
 65 70 75 80
 Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met
 85 90 95
 Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe
 100 105 110
 Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu
 115 120 125
 Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg
 130 135 140
 Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn
 145 150 155 160
 Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala
 165 170 175
 Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr
 180 185 190
 Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg
 195 200 205
 Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu
 210 215 220
 Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser
 225 230 235 240
 Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro
 245 250 255
 Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr
 260 265 270
 Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu
 275 280 285
 Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala
 290 295 300
 Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val

305	310	315	320
Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr			
	325	330	335
Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr			
	340	345	350
Thr Thr Ile Lys Glu Ile Thr Arg			
	355	360	

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(775)
 <223> RXN00411

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 aaaccttgac caagaccacg accatcaagg agatcaccgc atg aac gag atg atc 115
 Met Asn Glu Met Ile
 1 5
 ctc gca gct gac tgg aac cgg cta gga ccc acc ttc caa aca gcc atc 163
 Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr Phe Gln Thr Ala Ile
 10 15 20
 att gac acc ctg ttg atg gtc atc atc acc atg gtg gtg gct ggc tta 211
 Ile Asp Thr Leu Leu Met Val Ile Ile Thr Met Val Val Ala Gly Leu
 25 30 35
 ctg ggt ctt gtc gtc ggc ctg ctg ctt tac acc acc cgc gct ggt gga 259
 Leu Gly Leu Val Val Gly Leu Leu Leu Tyr Thr Thr Arg Ala Gly Gly
 40 45 50
 atc ttg aag aac aag gtc atc tac acc att ttg aat gtg ctg gtg aac 307
 Ile Leu Lys Asn Lys Val Ile Tyr Thr Ile Leu Asn Val Leu Val Asn
 55 60 65
 ttt gtt cga ccc atc cca ttc att att ttg atc gcc gcc atc aag cca 355
 Phe Val Arg Pro Ile Pro Phe Ile Ile Leu Ile Ala Ala Ile Lys Pro
 70 75 80 85
 cta acg gtc gcc gtc atg ggc acc tcc atc ggc cga gat gcc ggc atc 403
 Leu Thr Val Ala Val Met Gly Thr Ser Ile Gly Arg Asp Ala Gly Ile
 90 95 100
 ttc gtc atg gtt gtc gca gcg att ttc tct gtg gct cga atc gtg gag 451
 Phe Val Met Val Val Ala Ala Ile Phe Ser Val Ala Arg Ile Val Glu
 105 110 115
 caa aac ttg gtc tcc att gat cct ggt gtc atc gag gca gct cgc tcc 499
 Gln Asn Leu Val Ser Ile Asp Pro Gly Val Ile Glu Ala Ala Arg Ser
 120 125 130

atg ggt gcg tcc ccg atg cgc atc atc gcc acc gtg atc att cca gaa 547
 Met Gly Ala Ser Pro Met Arg Ile Ile Ala Thr Val Ile Ile Pro Glu
 135 140 145
 gca ctt gga cca ttg gtt ctg ggt tac acc ttc ctg ttc atc gcg atc 595
 Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe Leu Phe Ile Ala Ile
 150 155 160 165
 gtc gat atg tcc gca atg gtc ggc tac atc ggt ggc ggt ggt ctt ggt 643
 Val Asp Met Ser Ala Met Val Gly Tyr Ile Gly Gly Gly Gly Leu Gly
 170 175 180
 gac ttc gcc att gtt tac ggc tac cgc gcc ttc gac aac gaa gtt atg 691
 Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Phe Asp Asn Glu Val Met
 185 190 195
 tac gtt gcc gtc ctg gtt atc gtc atc atc gtg cag gca gcc cag ctt 739
 Tyr Val Ala Val Leu Val Ile Val Ile Ile Val Gln Ala Ala Gln Leu
 200 205 210
 ctg ggc aat tgg ctg tcc aag aag atc atg cgc cgc taaacctctt 785
 Leu Gly Asn Trp Leu Ser Lys Lys Ile Met Arg Arg
 215 220 225
 gcatagaaaa acc 798

<210> 366

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

Met Asn Glu Met Ile Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr
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 Phe Gln Thr Ala Ile Ile Asp Thr Leu Leu Met Val Ile Ile Thr Met
 20 25 30
 Val Val Ala Gly Leu Leu Gly Leu Val Val Gly Leu Leu Tyr Thr
 35 40 45
 Thr Arg Ala Gly Gly Ile Leu Lys Asn Lys Val Ile Tyr Thr Ile Leu
 50 55 60
 Asn Val Leu Val Asn Phe Val Arg Pro Ile Pro Phe Ile Ile Leu Ile
 65 70 75 80
 Ala Ala Ile Lys Pro Leu Thr Val Ala Val Met Gly Thr Ser Ile Gly
 85 90 95
 Arg Asp Ala Gly Ile Phe Val Met Val Val Ala Ala Ile Phe Ser Val
 100 105 110
 Ala Arg Ile Val Glu Gln Asn Leu Val Ser Ile Asp Pro Gly Val Ile
 115 120 125
 Glu Ala Ala Arg Ser Met Gly Ala Ser Pro Met Arg Ile Ile Ala Thr
 130 135 140
 Val Ile Ile Pro Glu Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe

145	150	155	160
Leu Phe Ile Ala	Ile Val Asp Met Ser	Ala Met Val Gly Tyr	Ile Gly
	165	170	175
Gly Gly Gly Leu	Gly Asp Phe Ala	Ile Val Tyr Gly Tyr	Arg Ala Phe
	180	185	190
Asp Asn Glu Val	Met Tyr Val Ala	Val Leu Val Ile	Val Ile Ile Val
	195	200	205
Gln Ala Ala Gln	Leu Leu Gly Asn	Trp Leu Ser Lys	Lys Ile Met Arg
	210	215	220
Arg			
225			

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 <211> 852
 <212> DNA
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 <222> (101)..(829)
 <223> RXN02614

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 acaccttccg ctaccgaaac gcataagaaa gttgctcgcc atg act gcc aca ttg 115
 Met Thr Ala Thr Leu
 1 5
 tca ctc aaa ccc gca gcc act gtc cgt gga ttg cgc aaa tca tac gga 163
 Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu Arg Lys Ser Tyr Gly
 10 15 20
 act aaa gaa gtc ctc caa gga atc gac ctc acc atc aac tgc ggc gaa 211
 Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr Ile Asn Cys Gly Glu
 25 30 35
 gta acc gcg ctg atc gga cgc tca ggt tca gga aaa tcc acc atc ctg 259
 Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly Lys Ser Thr Ile Leu
 40 45 50
 cgc gtg ttg gcg ggc cta tct aaa gag cat tcc ggc tct gta gaa att 307
 Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser Gly Ser Val Glu Ile
 55 60 65
 tcc gga aac ccg gcc gtt gcc ttc caa gag cct cgc ctg ttg ccg tgg 355
 Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro Arg Leu Leu Pro Trp
 70 75 80 85
 aaa acg gtg ctc gat aat gtg acc ttt ggc ctc aac cgc act gat att 403
 Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu Asn Arg Thr Asp Ile
 90 95 100
 tcc tgg tca gaa gca caa gaa cgc gcc tcg gca ctg ctt gca gaa gtc 451
 Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala Leu Leu Ala Glu Val

105	110	115	
aaa ctt ccc gac tcc gac gcc gcc	tgg ccc ctc acg ctc tcc ggc ggc		499
Lys Leu Pro Asp Ser Asp Ala Ala	Trp Pro Leu Thr Leu Ser Gly Gly		
120	125	130	
caa gcc cag cgc gtc tcc ctt gcg cga gcg ctc atc tcc gag cca gag			547
Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu Ile Ser Glu Pro Glu			
135	140	145	
ctt ttg ctt ctc gac gaa ccc ttc ggc gcc ctc gat gct ctg aca aga			595
Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg			
150	155	160	165
ctg aca gcc caa gac ctg ctg ctc aaa acc gtg aac acc cga aac ttg			643
Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val Asn Thr Arg Asn Leu			
170	175	180	
gga gtt ctg ctg gtc acc cat gat gtt tcc gag gcc atc gcc ctg gcc			691
Gly Val Leu Leu Val Thr His Asp Val Ser Glu Ala Ile Ala Leu Ala			
185	190	195	
gac cac gtc ctt ctt ctt gac gac ggc gcc atc aca cac agt ttg act			739
Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr			
200	205	210	
gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac			787
Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr			
215	220	225	
acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc			829
Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala			
230	235	240	
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<210> 368

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

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Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr
20 25 30

Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly
35 40 45

Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser
50 55 60

Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro
65 70 75 80

Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu
85 90 95

Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala
 100 105 110
 Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu
 115 120 125
 Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu
 130 135 140
 Ile Ser Glu Pro Glu Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu
 145 150 155 160
 Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val
 165 170 175
 Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu
 180 185 190
 Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile
 195 200 205
 Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro
 210 215 220
 Ser Phe Ala Ser Tyr Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr
 225 230 235 240
 Thr Pro Ala

<210> 369
 <211> 1080
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1057)
 <223> RXN02613

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 tgagtggctc gaaatcacca cacctgccta gaaagaaatc atg aaa ttt aag aaa 115
 Met Lys Phe Lys Lys
 1 5
 atc gcc ctc gtt ctc gcc ttc ggt cta ggè ctt gca tcc tgc tca tca 163
 Ile Ala Leu Val Leu Ala Phe Gly Leu Gly Leu Ala Ser Cys Ser Ser
 10 15 20
 gct tct ggc gat ccc gcc acc aac gcc gat gga tcc atc gat ctg agc 211
 Ala Ser Gly Asp Pro Ala Thr Asn Ala Asp Gly Ser Ile Asp Leu Ser
 25 30 35
 aaa gta acc ctt aac atc ggt gat caa atc gcc gga aca gaa caa gtg 259
 Lys Val Thr Leu Asn Ile Gly Asp Gln Ile Ala Gly Thr Glu Gln Val
 40 45 50
 ctc caa gct tca ggg gag cta gat gat gtc cct tat aaa atc gaa tgg 307

Leu	Gln	Ala	Ser	Gly	Glu	Leu	Asp	Asp	Val	Pro	Tyr	Lys	Ile	Glu	Trp		
55						60					65						
tca	tca	ttt	acc	tct	gga	cca	ccc	caa	atc	gaa	gca	tta	aac	gca	ggt	355	
Ser	Ser	Phe	Thr	Ser	Gly	Pro	Pro	Gln	Ile	Glu	Ala	Leu	Asn	Ala	Gly		
70					75					80					85		
caa	att	gat	ttc	gcg	atc	acc	gga	aac	acc	cca	ccg	atc	atc	ggc	ggc	403	
Gln	Ile	Asp	Phe	Ala	Ile	Thr	Gly	Asn	Thr	Pro	Pro	Ile	Ile	ggy	ggy		
				90					95					100			
ccc	acc	aac	acc	aaa	gtg	gtc	tcc	gcc	tac	aac	aac	gat	gct	tta	ggt	451	
Pro	Thr	Asn	Thr	Lys	Val	Val	Ser	Ala	Tyr	Asn	Asn	Asp	Ala	Leu	Gly		
			105					110					115				
gat	gtc	atc	ttg	gtc	gcc	ccg	gat	tct	tca	ata	acc	tcg	gtg	gct	gac	499	
Asp	Val	Ile	Leu	Val	Ala	Pro	Asp	Ser	Ser	Ile	Thr	Ser	Val	Ala	Asp		
		120					125					130					
ctt	gct	gga	aag	aaa	gtg	gct	gtc	gcc	cgc	gga	tcc	agc	gcc	cac	gga	547	
Leu	Ala	Gly	Lys	Lys	Val	Ala	Val	Ala	Arg	Gly	Ser	Ser	Ala	His	Gly		
135					140					145							
cac	ctc	atc	caa	caa	cta	gaa	aaa	gca	ggc	gtg	agc	gtt	gac	gac	gta	595	
His	Leu	Ile	Gln	Gln	Leu	Glu	Lys	Ala	Gly	Val	Ser	Val	Asp	Asp	Val		
150					155					160					165		
gaa	atc	aac	ctc	ctc	caa	ccc	tcc	gac	gcc	aaa	gcc	gct	ttc	caa	aac	643	
Glu	Ile	Asn	Leu	Leu	Gln	Pro	Ser	Asp	Ala	Lys	Ala	Ala	Phe	Gln	Asn		
				170				175						180			
ggc	cag	gta	gat	gcg	tgg	gca	gtg	tgg	gat	ccc	tac	agc	tca	cag	gcg	691	
Gly	Gln	Val	Asp	Ala	Trp	Ala	Val	Trp	Asp	Pro	Tyr	Ser	Ser	Gln	Ala		
			185					190					195				
gaa	ctg	gaa	gga	gct	caa	gtt	ttg	gtc	agg	gga	gcg	gga	ctg	gtc	agt	739	
Glu	Leu	Glu	Gly	Ala	Gln	Val	Leu	Val	Arg	Gly	Ala	Gly	Leu	Val	Ser		
		200					205					210					
ggg	cat	gga	ttt	ggt	gtc	gca	agt	gat	gaa	gcg	ctc	gat	gac	ccc	gca	787	
Gly	His	Gly	Phe	Gly	Val	Ala	Ser	Asp	Glu	Ala	Leu	Asp	Asp	Pro	Ala		
	215					220					225						
aag	gaa	gcc	gcc	ttg	gca	gat	ttc	ctc	gat	cgc	gtg	gcc	gac	tct	tat	835	
Lys	Glu	Ala	Ala	Leu	Ala	Asp	Phe	Leu	Asp	Arg	Val	Ala	Asp	Ser	Tyr		
230					235					240					245		
gaa	tgg	gct	gaa	gac	aac	acc	gat	gaa	tgg	gcg	acg	att	ttc	agc	caa	883	
Glu	Trp	Ala	Glu	Asp	Asn	Thr	Asp	Glu	Trp	Ala	Thr	Ile	Phe	Ser	Gln		
				250					255					260			
gaa	tcc	ggc	ttt	gat	ccg	gag	gcc	tct	caa	ctg	aac	acc	cgc	agc	ctg	931	
Glu	Ser	Gly	Phe	Asp	Pro	Glu	Ala	Ser	Gln	Leu	Asn	Thr	Arg	Ser	Leu		
			265				270						275				
cgc	cat	cag	gtg	ccg	ctc	gac	gag	tcc	gtc	aac	acc	tat	cag	aac	gcg	979	
Arg	His	Gln	Val	Pro	Leu	Asp	Glu	Ser	Val	Asn	Thr	Tyr	Gln	Asn	Ala		
		280					285					290					
ctt	atc	gac	gct	ttc	gtc	tcc	gcg	ggt	ctc	gtt	gag	gac	ttt	aat	ttc	1027	
Leu	Ile	Asp	Ala	Phe	Val	Ser	Ala	Gly	Leu	Val	Glu	Asp	Phe	Asn	Phe		

295 300 305

gag gac acc gta gac acc cga ttt gag ggc taagtatgtc tgagtatggc 1077
 Glu Asp Thr Val Asp Thr Arg Phe Glu Gly
 310 315

aaa 1080

<210> 370
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 370
 Met Lys Phe Lys Lys Ile Ala Leu Val Leu Ala Phe Gly Leu Gly Leu
 1 5 10 15

Ala Ser Cys Ser Ser Ala Ser Gly Asp Pro Ala Thr Asn Ala Asp Gly
 20 25 30

Ser Ile Asp Leu Ser Lys Val Thr Leu Asn Ile Gly Asp Gln Ile Ala
 35 40 45

Gly Thr Glu Gln Val Leu Gln Ala Ser Gly Glu Leu Asp Asp Val Pro
 50 55 60

Tyr Lys Ile Glu Trp Ser Ser Phe Thr Ser Gly Pro Pro Gln Ile Glu
 65 70 75 80

Ala Leu Asn Ala Gly Gln Ile Asp Phe Ala Ile Thr Gly Asn Thr Pro
 85 90 95

Pro Ile Ile Gly Gly Pro Thr Asn Thr Lys Val Val Ser Ala Tyr Asn
 100 105 110

Asn Asp Ala Leu Gly Asp Val Ile Leu Val Ala Pro Asp Ser Ser Ile
 115 120 125

Thr Ser Val Ala Asp Leu Ala Gly Lys Lys Val Ala Val Ala Arg Gly
 130 135 140

Ser Ser Ala His Gly His Leu Ile Gln Gln Leu Glu Lys Ala Gly Val
 145 150 155 160

Ser Val Asp Asp Val Glu Ile Asn Leu Leu Gln Pro Ser Asp Ala Lys
 165 170 175

Ala Ala Phe Gln Asn Gly Gln Val Asp Ala Trp Ala Val Trp Asp Pro
 180 185 190

Tyr Ser Ser Gln Ala Glu Leu Glu Gly Ala Gln Val Leu Val Arg Gly
 195 200 205

Ala Gly Leu Val Ser Gly His Gly Phe Gly Val Ala Ser Asp Glu Ala
 210 215 220

Leu Asp Asp Pro Ala Lys Glu Ala Ala Leu Ala Asp Phe Leu Asp Arg
 225 230 235 240

Val Ala Asp Ser Tyr Glu Trp Ala Glu Asp Asn Thr Asp Glu Trp Ala

	245		250		255
Thr Ile Phe Ser Gln Glu Ser Gly Phe Asp Pro Glu Ala Ser Gln Leu					
	260		265		270
Asn Thr Arg Ser Leu Arg His Gln Val Pro Leu Asp Glu Ser Val Asn					
	275		280		285
Thr Tyr Gln Asn Ala Leu Ile Asp Ala Phe Val Ser Ala Gly Leu Val					
	290		295		300
Glu Asp Phe Asn Phe Glu Asp Thr Val Asp Thr Arg Phe Glu Gly					
	305		310		315

<210> 371
 <211> 1698
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1675)
 <223> RXN00368

<400> 371
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 Met Arg Leu Gly Val
 1 5
 tgg ctg att gtc gcg ggg ttg ttt atc act ccg ttg gcg ctg gtg gtg 163
 Trp Leu Ile Val Ala Gly Leu Phe Ile Thr Pro Leu Ala Leu Val Val
 10 15 20
 ggc ttg gcg ttg gga ggc aat cag ttt cct gct ctg ttg gat tcc gga 211
 Gly Leu Ala Leu Gly Gly Asn Gln Phe Pro Ala Leu Trp Asp Ser Gly
 25 30 35
 ttg ggc aaa gcc cta tgg aat tcc gcc tat aca aca gtg ctt tct gcg 259
 Leu Gly Lys Ala Leu Trp Asn Ser Ala Tyr Thr Thr Val Leu Ser Ala
 40 45 50
 gtg ggc gcg acc att atc ggc acg atc atg gct ctc acg ctg gac cga 307
 Val Gly Ala Thr Ile Ile Gly Thr Ile Met Ala Leu Thr Leu Asp Arg
 55 60 65
 act gat gtt ttc ggg cgc acc gcg ttg cgg tta ttt ttg tta tcc ccg 355
 Thr Asp Val Phe Gly Arg Thr Ala Leu Arg Leu Phe Leu Leu Ser Pro
 70 75 80 85
 ctg ttg atc cct ccg ttt att ggg gct att gcg ttg ttg cag ctg ttc 403
 Leu Leu Ile Pro Pro Phe Ile Gly Ala Ile Ala Trp Leu Gln Leu Phe
 90 95 100
 ggg aag aac cag ggc atc aac cgg ttt ttc ggc acg gaa gtg ttg gat 451
 Gly Lys Asn Gln Gly Ile Asn Arg Phe Phe Gly Thr Glu Val Trp Asp
 105 110 115
 att tac ggc gct gat ggt gtg aca ttt ttg ttg att gtg cac tcc tat 499

Ile	Tyr	Gly	Ala	Asp	Gly	Val	Thr	Phe	Leu	Leu	Ile	Val	His	Ser	Tyr		
		120					125					130					
ccc	act	gtg	tac	atc	att	gtt	tcg	gca	gct	ctg	agg	caa	ctt	cct	agt	547	
Pro	Thr	Val	Tyr	Ile	Ile	Val	Ser	Ala	Ala	Leu	Arg	Gln	Leu	Pro	Ser		
		135				140					145						
gat	ttg	gag	caa	gct	gca	cgg	atc	gcg	ggg	gcg	gat	act	ttt	acg	gtg	595	
Asp	Leu	Glu	Gln	Ala	Ala	Arg	Ile	Ala	Gly	Ala	Asp	Thr	Phe	Thr	Val		
		150			155				160						165		
ttg	cgc	acc	atc	aca	ctc	cca	ctg	ctc	aaa	cct	gca	ttg	ttg	tcg	gcg	643	
Leu	Arg	Thr	Ile	Thr	Leu	Pro	Leu	Leu	Lys	Pro	Ala	Leu	Leu	Ser	Ala		
				170					175						180		
ttt	act	ctt	acc	aca	gtg	gcg	aac	ctc	gcc	gac	ttt	ggc	att	cca	gct	691	
Phe	Thr	Leu	Thr	Thr	Val	Ala	Asn	Leu	Ala	Asp	Phe	Gly	Ile	Pro	Ala		
			185					190					195				
ctg	ttg	gga	tcg	cca	gcg	cgt	ttt	gaa	acc	tta	gcc	acc	atg	att	tat	739	
Leu	Leu	Gly	Ser	Pro	Ala	Arg	Phe	Glu	Thr	Leu	Ala	Thr	Met	Ile	Tyr		
		200					205					210					
cgc	ttc	atg	gaa	tcc	ggc	acc	gtg	agc	aat	cca	ttg	cag	gtg	gta	tcc	787	
Arg	Phe	Met	Glu	Ser	Gly	Thr	Val	Ser	Asn	Pro	Leu	Gln	Val	Val	Ser		
		215				220					225						
acc	att	ggc	atc	gtg	ttg	ttg	ttc	ctg	gga	atc	gca	gca	gta	acc	gcg	835	
Thr	Ile	Gly	Ile	Val	Leu	Phe	Leu	Gly	Ile	Ala	Ala	Ala	Val	Thr	Ala		
				235				240							245		
gat	tat	ctg	gtg	tct	ttg	tac	gcg	gca	tca	aag	ttg	caa	gac	gca	gga	883	
Asp	Tyr	Leu	Val	Ser	Leu	Tyr	Ala	Ala	Ser	Lys	Leu	Gln	Asp	Ala	Gly		
				250				255						260			
aca	ccg	cat	cgc	ttt	act	ctc	aac	aaa	tca	cga	atc	cca	gtc	agc	gtg	931	
Thr	Pro	His	Arg	Phe	Thr	Leu	Asn	Lys	Ser	Arg	Ile	Pro	Val	Ser	Val		
			265					270					275				
atc	acg	tgg	atc	atc	gcg	ttg	atc	atc	acc	gcc	gcc	ccg	ctg	ctg	ggg	979	
Ile	Thr	Trp	Ile	Ile	Ala	Leu	Ile	Ile	Thr	Ala	Ala	Pro	Leu	Leu	Gly		
		280					285					290					
ctg	gca	tac	aga	gca	tta	ctg	cct	gcc	cca	ggg	gtg	ccg	ttc	aac	cta	1027	
Leu	Ala	Tyr	Arg	Ala	Leu	Leu	Pro	Ala	Pro	Gly	Val	Pro	Phe	Asn	Leu		
		295				300					305						
gac	aac	atc	acg	ctc	aac	aac	ttt	gaa	gca	gca	ctg	agc	aac	cca	cga	1075	
Asp	Asn	Ile	Thr	Leu	Asn	Asn	Phe	Glu	Ala	Ala	Leu	Ser	Asn	Pro	Arg		
		310			315				320						325		
gta	atc	gaa	gga	ttc	agc	aac	tcc	ctc	atg	tta	tcc	ctg	ggg	gca	gcc	1123	
Val	Ile	Glu	Gly	Phe	Ser	Asn	Ser	Leu	Met	Leu	Ser	Leu	Gly	Ala	Ala		
				330				335						340			
cta	atc	tgt	ggg	gtg	ctg	gga	tgg	ctg	atc	gga	gtg	ctc	atc	acc	cga	1171	
Leu	Ile	Cys	Gly	Val	Leu	Gly	Trp	Leu	Ile	Gly	Val	Leu	Ile	Thr	Arg		
			345				350						355				
acc	cag	cat	ttc	gcc	aac	gta	ccg	ttg	aca	ctc	act	gtg	ctg	ctt	ccc	1219	
Thr	Gln	His	Phe	Ala	Asn	Val	Pro	Leu	Thr	Leu	Thr	Val	Leu	Leu	Pro		

360	365	370	
acc gca ctg ccg ggc atg atc atc ggc gtc ggc tgg ctc att ttg ggc			1267
Thr Ala Leu Pro Gly Met Ile Ile Gly Val Gly Trp Leu Ile Leu Gly			
375	380	385	
aga tac acc gga att tac aac aca cct tgg gtg att ttg ggt gca tat			1315
Arg Tyr Thr Gly Ile Tyr Asn Thr Pro Trp Val Ile Leu Gly Ala Tyr			
390	395	400	405
gtg tgt gct ttt acc gcg ctg gtt gtc caa gct gta cgc gga cca ctc			1363
Val Cys Ala Phe Thr Ala Leu Val Val Gln Ala Val Arg Gly Pro Leu			
410	415	420	
agt caa gca ccc gaa gca atc gaa gaa gcc gca cga atc agc ggc gca			1411
Ser Gln Ala Pro Glu Ala Ile Glu Glu Ala Ala Arg Ile Ser Gly Ala			
425	430	435	
ggc aga tta cga tcc atc atg gac acc acc gga gcg atg gca att ccc			1459
Gly Arg Leu Arg Ser Ile Met Asp Thr Thr Gly Ala Met Ala Ile Pro			
440	445	450	
gca gct ttc gcc ggc gca gtg ctg gtt gcg gta act gcg gtt cga gag			1507
Ala Ala Phe Ala Gly Ala Val Leu Val Ala Val Thr Ala Val Arg Glu			
455	460	465	
tta acc gtg tcc att ttg ctc atc gcg ccg ggc acc acc acc ctg ggt			1555
Leu Thr Val Ser Ile Leu Leu Ile Ala Pro Gly Thr Thr Thr Leu Gly			
470	475	480	485
gtg cag gtg ttc aat ttg cag cag gcg gga aat tac aat cag gca tcg			1603
Val Gln Val Phe Asn Leu Gln Gln Ala Gly Asn Tyr Asn Gln Ala Ser			
490	495	500	
gcg ttg tcg ttg atg ttt gcg att atc ggt atc gtg gcg ctc gcg ttg			1651
Ala Leu Ser Leu Met Phe Ala Ile Ile Gly Ile Val Ala Leu Ala Leu			
505	510	515	
acg gtg cgc agc cag aag gag ttt taggtgtcat cgatcaaatt gcg			1698
Thr Val Arg Ser Gln Lys Glu Phe			
520	525		

<210> 372

<211> 525

<212> PRT

<213> Corynebacterium glutamicum

<400> 372

Met Arg Leu Gly Val Trp Leu Ile Val Ala Gly Leu Phe Ile Thr Pro			
1	5	10	15
Leu Ala Leu Val Val Gly Leu Ala Leu Gly Gly Asn Gln Phe Pro Ala			
20	25	30	
Leu Trp Asp Ser Gly Leu Gly Lys Ala Leu Trp Asn Ser Ala Tyr Thr			
35	40	45	
Thr Val Leu Ser Ala Val Gly Ala Thr Ile Ile Gly Thr Ile Met Ala			
50	55	60	

Leu Thr Leu Asp Arg Thr Asp Val Phe Gly Arg Thr Ala Leu Arg Leu
 65 70 75 80
 Phe Leu Leu Ser Pro Leu Leu Ile Pro Pro Phe Ile Gly Ala Ile Ala
 85 90 95
 Trp Leu Gln Leu Phe Gly Lys Asn Gln Gly Ile Asn Arg Phe Phe Gly
 100 105 110
 Thr Glu Val Trp Asp Ile Tyr Gly Ala Asp Gly Val Thr Phe Leu Leu
 115 120 125
 Ile Val His Ser Tyr Pro Thr Val Tyr Ile Ile Val Ser Ala Ala Leu
 130 135 140
 Arg Gln Leu Pro Ser Asp Leu Glu Gln Ala Ala Arg Ile Ala Gly Ala
 145 150 155 160
 Asp Thr Phe Thr Val Leu Arg Thr Ile Thr Leu Pro Leu Leu Lys Pro
 165 170 175
 Ala Leu Leu Ser Ala Phe Thr Leu Thr Thr Val Ala Asn Leu Ala Asp
 180 185 190
 Phe Gly Ile Pro Ala Leu Leu Gly Ser Pro Ala Arg Phe Glu Thr Leu
 195 200 205
 Ala Thr Met Ile Tyr Arg Phe Met Glu Ser Gly Thr Val Ser Asn Pro
 210 215 220
 Leu Gln Val Val Ser Thr Ile Gly Ile Val Leu Leu Phe Leu Gly Ile
 225 230 235 240
 Ala Ala Val Thr Ala Asp Tyr Leu Val Ser Leu Tyr Ala Ala Ser Lys
 245 250 255
 Leu Gln Asp Ala Gly Thr Pro His Arg Phe Thr Leu Asn Lys Ser Arg
 260 265 270
 Ile Pro Val Ser Val Ile Thr Trp Ile Ile Ala Leu Ile Ile Thr Ala
 275 280 285
 Ala Pro Leu Leu Gly Leu Ala Tyr Arg Ala Leu Leu Pro Ala Pro Gly
 290 295 300
 Val Pro Phe Asn Leu Asp Asn Ile Thr Leu Asn Asn Phe Glu Ala Ala
 305 310 315 320
 Leu Ser Asn Pro Arg Val Ile Glu Gly Phe Ser Asn Ser Leu Met Leu
 325 330 335
 Ser Leu Gly Ala Ala Leu Ile Cys Gly Val Leu Gly Trp Leu Ile Gly
 340 345 350
 Val Leu Ile Thr Arg Thr Gln His Phe Ala Asn Val Pro Leu Thr Leu
 355 360 365
 Thr Val Leu Leu Pro Thr Ala Leu Pro Gly Met Ile Ile Gly Val Gly
 370 375 380
 Trp Leu Ile Leu Gly Arg Tyr Thr Gly Ile Tyr Asn Thr Pro Trp Val

385	390	395	400
Ile Leu Gly Ala Tyr Val Cys Ala Phe Thr Ala Leu Val Val Gln Ala	405	410	415
Val Arg Gly Pro Leu Ser Gln Ala Pro Glu Ala Ile Glu Glu Ala Ala	420	425	430
Arg Ile Ser Gly Ala Gly Arg Leu Arg Ser Ile Met Asp Thr Thr Gly	435	440	445
Ala Met Ala Ile Pro Ala Ala Phe Ala Gly Ala Val Leu Val Ala Val	450	455	460
Thr Ala Val Arg Glu Leu Thr Val Ser Ile Leu Leu Ile Ala Pro Gly	465	470	475
Thr Thr Thr Leu Gly Val Gln Val Phe Asn Leu Gln Gln Ala Gly Asn	485	490	495
Tyr Asn Gln Ala Ser Ala Leu Ser Leu Met Phe Ala Ile Ile Gly Ile	500	505	510
Val Ala Leu Ala Leu Thr Val Arg Ser Gln Lys Glu Phe	515	520	525

<210> 373

<211> 602

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(579)

<223> FRXA00368

<400> 373

tcc ctc atg tta tcc ctg ggt gca gcc cta atc tgt ggg gtg ctg gga	48
Ser Leu Met Leu Ser Leu Gly Ala Ala Leu Ile Cys Gly Val Leu Gly	
1 5 10 15	
tgg ctg atc gga gtg ctc atc acc cga acc cag cat ttc gcc aac gta	96
Trp Leu Ile Gly Val Leu Ile Thr Arg Thr Gln His Phe Ala Asn Val	
20 25 30	
ccg ttg aca ctc act gtg ctg ctt ccc acc gca ctg ccg ggc atg atc	144
Pro Leu Thr Leu Thr Val Leu Leu Pro Thr Ala Leu Pro Gly Met Ile	
35 40 45	
atc ggc gtc ggc tgg ctc att ttg ggc aga tac acc gga att tac aac	192
Ile Gly Val Gly Trp Leu Ile Leu Gly Arg Tyr Thr Gly Ile Tyr Asn	
50 55 60	
aca cct tgg gtg att ttg ggt gca tat gtg tgt gct ttt acc gcg ctg	240
Thr Pro Trp Val Ile Leu Gly Ala Tyr Val Cys Ala Phe Thr Ala Leu	
65 70 75 80	
gtt gtc caa gct gta cgc gga cca ctc agt caa gca ccc gaa gca atc	288
Val Val Gln Ala Val Arg Gly Pro Leu Ser Gln Ala Pro Glu Ala Ile	
85 90 95	

gaa gaa gcc gca cga atc agc ggc gca ggc aga tta cga tcc atc atg 336
 Glu Glu Ala Ala Arg Ile Ser Gly Ala Gly Arg Leu Arg Ser Ile Met
 100 105 110
 gac acc acc gga gcg atg gca att ccc gca gct ttc gcc ggc gca gtg 384
 Asp Thr Thr Gly Ala Met Ala Ile Pro Ala Ala Phe Ala Gly Ala Val
 115 120 125
 ctg gtt gcg gta act gcg gtt cga gag tta acc gtg tcc att ttg ctc 432
 Leu Val Ala Val Thr Ala Val Arg Glu Leu Thr Val Ser Ile Leu Leu
 130 135 140
 atc gcg ccg ggc acc acc acc ctg ggt gtg cag gtg ttc aat ttg cag 480
 Ile Ala Pro Gly Thr Thr Thr Leu Gly Val Gln Val Phe Asn Leu Gln
 145 150 155 160
 cag gcg gga aat tac aat cag gca tcg gcg ttg tcg ttg atg ttt gcg 528
 Gln Ala Gly Asn Tyr Asn Gln Ala Ser Ala Leu Ser Leu Met Phe Ala
 165 170 175
 att atc ggt atc gtg gcg ctc gcg ttg acg gtg cgc agc cag aag gag 576
 Ile Ile Gly Ile Val Ala Leu Ala Leu Thr Val Arg Ser Gln Lys Glu
 180 185 190
 ttt taggtgtcat cgatcaaatt gcg 602
 Phe

<210> 374
 <211> 193
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 374
 Ser Leu Met Leu Ser Leu Gly Ala Ala Leu Ile Cys Gly Val Leu Gly
 1 5 10 15
 Trp Leu Ile Gly Val Leu Ile Thr Arg Thr Gln His Phe Ala Asn Val
 20 25 30
 Pro Leu Thr Leu Thr Val Leu Leu Pro Thr Ala Leu Pro Gly Met Ile
 35 40 45
 Ile Gly Val Gly Trp Leu Ile Leu Gly Arg Tyr Thr Gly Ile Tyr Asn
 50 55 60
 Thr Pro Trp Val Ile Leu Gly Ala Tyr Val Cys Ala Phe Thr Ala Leu
 65 70 75 80
 Val Val Gln Ala Val Arg Gly Pro Leu Ser Gln Ala Pro Glu Ala Ile
 85 90 95
 Glu Glu Ala Ala Arg Ile Ser Gly Ala Gly Arg Leu Arg Ser Ile Met
 100 105 110
 Asp Thr Thr Gly Ala Met Ala Ile Pro Ala Ala Phe Ala Gly Ala Val
 115 120 125
 Leu Val Ala Val Thr Ala Val Arg Glu Leu Thr Val Ser Ile Leu Leu

130 135 140
 Ile Ala Pro Gly Thr Thr Thr Leu Gly Val Gln Val Phe Asn Leu Gln
 145 150 155 160
 Gln Ala Gly Asn Tyr Asn Gln Ala Ser Ala Leu Ser Leu Met Phe Ala
 165 170 175
 Ile Ile Gly Ile Val Ala Leu Ala Leu Thr Val Arg Ser Gln Lys Glu
 180 185 190
 Phe

<210> 375
 <211> 798
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(798)
 <223> FRXA00370

<400> 375
 ggc aaa gcc cta tgg aat tcc gcc tat aca aca gtg ctt tct gcg gtg 48
 Gly Lys Ala Leu Trp Asn Ser Ala Tyr Thr Thr Val Leu Ser Ala Val
 1 5 10 15
 ggc gcg acc att atc ggc acg atc atg gct ctc acg ctg gac cga act 96
 Gly Ala Thr Ile Ile Gly Thr Ile Met Ala Leu Thr Leu Asp Arg Thr
 20 25 30
 gat gtt ttc ggg cgc acc gcg ttg cgg tta ttt ttg tta tcc ccg ctg 144
 Asp Val Phe Gly Arg Thr Ala Leu Arg Leu Phe Leu Leu Ser Pro Leu
 35 40 45
 ttg atc cct ccg ttt att ggg gct att gcg tgg ttg cag ctg ttc ggg 192
 Leu Ile Pro Pro Phe Ile Gly Ala Ile Ala Trp Leu Gln Leu Phe Gly
 50 55 60
 aag aac cag ggc atc aac cgg ttt ttc ggc acg gaa gtg tgg gat att 240
 Lys Asn Gln Gly Ile Asn Arg Phe Phe Gly Thr Glu Val Trp Asp Ile
 65 70 75 80
 tac ggc gct gat ggt gtg aca ttt ttg ttg att gtg cac tcc tat ccc 288
 Tyr Gly Ala Asp Gly Val Thr Phe Leu Leu Ile Val His Ser Tyr Pro
 85 90 95
 act gtg tac atc att gtt tcg gca gct ctg agg caa ctt cct agt gat 336
 Thr Val Tyr Ile Ile Val Ser Ala Ala Leu Arg Gln Leu Pro Ser Asp
 100 105 110
 ttg gag caa gct gca cgg atc gcg ggg gcg gat act ttt acg gtg ttg 384
 Leu Glu Gln Ala Ala Arg Ile Ala Gly Ala Asp Thr Phe Thr Val Leu
 115 120 125
 cgc acc atc aca ctc cca ctg ctc aaa cct gca ttg ttg tcg gcg ttt 432
 Arg Thr Ile Thr Leu Pro Leu Leu Lys Pro Ala Leu Leu Ser Ala Phe
 130 135 140

act ctt acc aca gtg gcg aac ctc gcc gac ttt ggc att cca gct ctg 480
 Thr Leu Thr Thr Val Ala Asn Leu Ala Asp Phe Gly Ile Pro Ala Leu
 145 150 155 160

ttg gga tcg cca gcg cgt ttt gaa acc tta gcc acc atg att tat cgc 528
 Leu Gly Ser Pro Ala Arg Phe Glu Thr Leu Ala Thr Met Ile Tyr Arg
 165 170 175

ttc atg gaa tcc ggc acc gtg agc aat cca ttg cag gtg gta tcc acc 576
 Phe Met Glu Ser Gly Thr Val Ser Asn Pro Leu Gln Val Val Ser Thr
 180 185 190

att ggc atc gtg ttg ttg ttc ctg gga atc gca gca gta acc gcg gat 624
 Ile Gly Ile Val Leu Leu Phe Leu Gly Ile Ala Ala Val Thr Ala Asp
 195 200 205

tat ctg gtg tct ttg tac gcg gca tca aag ttg caa gac gca gga aca 672
 Tyr Leu Val Ser Leu Tyr Ala Ala Ser Lys Leu Gln Asp Ala Gly Thr
 210 215 220

ccg cat cgc ttt act ctc aac aaa tca cga atc cca gtc agc gtg atc 720
 Pro His Arg Phe Thr Leu Asn Lys Ser Arg Ile Pro Val Ser Val Ile
 225 230 235 240

acg tgg atc atc gcg ttg atc atc acc gcc gcc ccg ctg ctg ggt ctg 768
 Thr Trp Ile Ile Ala Leu Ile Ile Thr Ala Ala Pro Leu Leu Gly Leu
 245 250 255

gca tac aga gca tta ctg cct gcc cca ggt 798
 Ala Tyr Arg Ala Leu Leu Pro Ala Pro Gly
 260 265

<210> 376

<211> 266

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 376

Gly Lys Ala Leu Trp Asn Ser Ala Tyr Thr Thr Val Leu Ser Ala Val
 1 5 10 15

Gly Ala Thr Ile Ile Gly Thr Ile Met Ala Leu Thr Leu Asp Arg Thr
 20 25 30

Asp Val Phe Gly Arg Thr Ala Leu Arg Leu Phe Leu Leu Ser Pro Leu
 35 40 45

Leu Ile Pro Pro Phe Ile Gly Ala Ile Ala Trp Leu Gln Leu Phe Gly
 50 55 60

Lys Asn Gln Gly Ile Asn Arg Phe Phe Gly Thr Glu Val Trp Asp Ile
 65 70 75 80

Tyr Gly Ala Asp Gly Val Thr Phe Leu Leu Ile Val His Ser Tyr Pro
 85 90 95

Thr Val Tyr Ile Ile Val Ser Ala Ala Leu Arg Gln Leu Pro Ser Asp
 100 105 110

Leu Glu Gln Ala Ala Arg Ile Ala Gly Ala Asp Thr Phe Thr Val Leu
 115 120 125
 Arg Thr Ile Thr Leu Pro Leu Leu Lys Pro Ala Leu Leu Ser Ala Phe
 130 135 140
 Thr Leu Thr Thr Val Ala Asn Leu Ala Asp Phe Gly Ile Pro Ala Leu
 145 150 155 160
 Leu Gly Ser Pro Ala Arg Phe Glu Thr Leu Ala Thr Met Ile Tyr Arg
 165 170 175
 Phe Met Glu Ser Gly Thr Val Ser Asn Pro Leu Gln Val Val Ser Thr
 180 185 190
 Ile Gly Ile Val Leu Leu Phe Leu Gly Ile Ala Ala Val Thr Ala Asp
 195 200 205
 Tyr Leu Val Ser Leu Tyr Ala Ala Ser Lys Leu Gln Asp Ala Gly Thr
 210 215 220
 Pro His Arg Phe Thr Leu Asn Lys Ser Arg Ile Pro Val Ser Val Ile
 225 230 235 240
 Thr Trp Ile Ile Ala Leu Ile Ile Thr Ala Ala Pro Leu Leu Gly Leu
 245 250 255
 Ala Tyr Arg Ala Leu Leu Pro Ala Pro Gly
 260 265

<210> 377

<211> 749

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(726)

<223> RXN01285

<400> 377

ctc aac gtc acc atc ccc gac aac acc ttc acc gcc atc atc ggc ccc 48
 Leu Asn Val Thr Ile Pro Asp Asn Thr Phe Thr Ala Ile Ile Gly Pro
 1 5 10 15
 aac ggc tgc ggc aaa tcc acc ctg ctc cgc ggt ttc tcc cgc gtg ctc 96
 Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu
 20 25 30
 aat ccg cag cac ggc aaa gtg ctt ctc gac ggt cgg caa ctc gat tca 144
 Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser
 35 40 45
 ttc aag cct aaa gag atc gcc cga gaa cta ggc ctg ctg cca cag acc 192
 Phe Lys Pro Lys Glu Ile Ala Arg Glu Leu Gly Leu Leu Pro Gln Thr
 50 55 60
 tcc atc gcc cca gaa ggc atc cgg gtt tac gat ctc atc gcg cgc ggg 240
 Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile Ala Arg Gly
 65 70 75 80

cgc gct ccc tac caa agc ctc ata caa caa tgg cgc acc tcc gac gaa 288
 Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr Ser Asp Glu
 85 90 95

gac gcc gtc gcg caa gcg ctc gcc tcc acg aat ctc acc gaa ctt gca 336
 Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr Glu Leu Ala
 100 105 110

gct cgc ctc gtc gat gaa ctc tcc ggt ggc cag cgc caa cga gtg tgg 384
 Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Trp
 115 120 125

gtg gcc atg ttg ctc gcc cag caa aca ccg atc atg ctt ctc gac gag 432
 Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu Leu Asp Glu
 130 135 140

ccc acc acc ttc ctc gac atc gcc cac caa tac gaa ctc ttg gaa ttg 480
 Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu Leu Glu Leu
 145 150 155 160

ctg cgc gca ttc aac gag gcc ggg aaa act gtg gtc act gtg ctt cac 528
 Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr Val Leu His
 165 170 175

gat ctc aac caa gcc gcc cgc tac gcc gac cac ctc atc gtg atg aaa 576
 Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile Val Met Lys
 180 185 190

gat ggg cac gta cat gcc acg ggc aca ccg gag gaa gtc tta act gcc 624
 Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val Leu Thr Ala
 195 200 205

gag atg gtt caa gga gtt ttt ggc ctg ccc tgc atc atc tcc cca gac 672
 Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile Ser Pro Asp
 210 215 220

ccc gtc aca gga acc ccc acc gtc gtt ccc ctc agt cgg tct cgc gca 720
 Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg Ser Arg Ala
 225 230 235 240

gga gct taagtagcta cccctccaac gga 749
 Gly Ala

<210> 378

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 378

Leu Asn Val Thr Ile Pro Asp Asn Thr Phe Thr Ala Ile Ile Gly Pro
 1 5 10 15

Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu
 20 25 30

Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser
 35 40 45

585

gtt gcg gca ttg ggc gtc gtc acg ctt ggt att ttt gct ttt tct ttg	211
Val Ala Ala Leu Gly Val Val Thr Leu Gly Ile Phe Ala Phe Ser Leu	
25 30 35	
atg tgg ggc gag gtg ttt tat ggc cct gct cag gtg ctg aaa gtg ttg	259
Met Trp Gly Glu Val Phe Tyr Gly Pro Ala Gln Val Leu Lys Val Leu	
40 45 50	
tct gga cag cag gtt ccc ggc gcg agt tat tcc gtt ggc gtg ttg cgt	307
Ser Gly Gln Gln Val Pro Gly Ala Ser Tyr Ser Val Gly Val Leu Arg	
55 60 65	
ttg ccg cgc gcg gtg atg ggt ttg act gcg ggt ttg gcg ttt ggc gcg	355
Leu Pro Arg Ala Val Met Gly Leu Thr Ala Gly Leu Ala Phe Gly Ala	
70 75 80 85	
gcg ggc gtg att ttt cag acg gtg ttg cgt aat cag ttg gcg tcg ccg	403
Ala Gly Val Ile Phe Gln Thr Val Leu Arg Asn Gln Leu Ala Ser Pro	
90 95 100	
gat att atc ggc att tct tct ggc gcg tcg gcg gcg ggc gta att tgc	451
Asp Ile Ile Gly Ile Ser Ser Gly Ala Ser Ala Ala Gly Val Ile Cys	
105 110 115	
att gtg ttt ttc ggg atg tcg cag tct gca gtg tcg gcg att tct ttg	499
Ile Val Phe Phe Gly Met Ser Gln Ser Ala Val Ser Ala Ile Ser Leu	
120 125 130	
tgt gcg tcc ttg gct gtg gcg ttg ttg att tat ctg gtg gcg tat cgc	547
Cys Ala Ser Leu Ala Val Ala Leu Leu Ile Tyr Leu Val Ala Tyr Arg	
135 140 145	
ggt ggt ttt tcg gcc acg cgt ctg att ctt acc ggc att ggt att gct	595
Gly Gly Phe Ser Ala Thr Arg Leu Ile Leu Thr Gly Ile Gly Ile Ala	
150 155 160 165	
gcg atg ctg aat tca tta gtg tcg tat tcg ctg tcc aag gct gat tct	643
Ala Met Leu Asn Ser Leu Val Ser Tyr Ser Leu Ser Lys Ala Asp Ser	
170 175 180	
tgg gat ctg ccg acc gcg acg cgc tgg ctt acc ggc tcg ctc aat ggt	691
Trp Asp Leu Pro Thr Ala Thr Arg Trp Leu Thr Gly Ser Leu Asn Gly	
185 190 195	
gcg acg tgg gat cgt gcg atg ccg ctg att gtc acc act gtg gta ctc	739
Ala Thr Trp Asp Arg Ala Met Pro Leu Ile Val Thr Thr Val Val Leu	
200 205 210	
att ccg ctg ctg gtg gct aat gcg cgc aat gtg gat ctt atg cgt ttg	787
Ile Pro Leu Leu Val Ala Asn Ala Arg Asn Val Asp Leu Met Arg Leu	
215 220 225	
ggc aat gat tcc gcg gtg ggt ttg ggc gtt gct act aat cgc acg cgc	835
Gly Asn Asp Ser Ala Val Gly Leu Gly Val Ala Thr Asn Arg Thr Arg	
230 235 240 245	
gtc att gcg att att gcc gct gtt gcg ctc atc gcc gtt gct acc gct	883
Val Ile Ala Ile Ile Ala Ala Val Ala Leu Ile Ala Val Ala Thr Ala	
250 255 260	
gca tgc ggc ccg atc gca ttc gtg gcg ttt gtg tct ggc ccc att gcc	931

Ala Cys Gly Pro Ile Ala Phe Val Ala Phe Val Ser Gly Pro Ile Ala
 265 270 275

gcg cgc att tta ggc tcc ggc gga tcg ctc atc atc ccc tcc gca ctc 979
 Ala Arg Ile Leu Gly Ser Gly Gly Ser Leu Ile Ile Pro Ser Ala Leu
 280 285 290

atc ggc ggg ttg atc gtg ctc atc gcc gac cta att ggc caa tac ttc 1027
 Ile Gly Gly Leu Ile Val Leu Ile Ala Asp Leu Ile Gly Gln Tyr Phe
 295 300 305

ctc ggc acc cgc tac ccc gtc gga gtt gtc acc ggc gca ttc ggc gcc 1075
 Leu Gly Thr Arg Tyr Pro Val Gly Val Val Thr Gly Ala Phe Gly Ala
 310 315 320 325

cca ttc ctt atc tat tta ctc att cgt tcc aac cgc gcg gga gta acc 1123
 Pro Phe Leu Ile Tyr Leu Leu Ile Arg Ser Asn Arg Ala Gly Val Thr
 330 335 340

ctg tgaccaccaa ccatcaacta tcc 1149
 Leu

<210> 380
 <211> 342
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 380
 Met Ser Leu Ser His Gln Leu Lys Arg Gln Arg Ala Ser Arg Asn Ser
 1 5 10 15

Arg Arg Trp Leu Ile Val Ala Ala Leu Gly Val Val Thr Leu Gly Ile
 20 25 30

Phe Ala Phe Ser Leu Met Trp Gly Glu Val Phe Tyr Gly Pro Ala Gln
 35 40 45

Val Leu Lys Val Leu Ser Gly Gln Gln Val Pro Gly Ala Ser Tyr Ser
 50 55 60

Val Gly Val Leu Arg Leu Pro Arg Ala Val Met Gly Leu Thr Ala Gly
 65 70 75 80

Leu Ala Phe Gly Ala Ala Gly Val Ile Phe Gln Thr Val Leu Arg Asn
 85 90 95

Gln Leu Ala Ser Pro Asp Ile Ile Gly Ile Ser Ser Gly Ala Ser Ala
 100 105 110

Ala Gly Val Ile Cys Ile Val Phe Phe Gly Met Ser Gln Ser Ala Val
 115 120 125

Ser Ala Ile Ser Leu Cys Ala Ser Leu Ala Val Ala Leu Leu Ile Tyr
 130 135 140

Leu Val Ala Tyr Arg Gly Gly Phe Ser Ala Thr Arg Leu Ile Leu Thr
 145 150 155 160

Gly Ile Gly Ile Ala Ala Met Leu Asn Ser Leu Val Ser Tyr Ser Leu

165										170					175				
Ser	Lys	Ala	Asp	Ser	Trp	Asp	Leu	Pro	Thr	Ala	Thr	Arg	Trp	Leu	Thr				
			180						185					190					
Gly	Ser	Leu	Asn	Gly	Ala	Thr	Trp	Asp	Arg	Ala	Met	Pro	Leu	Ile	Val				
		195					200					205							
Thr	Thr	Val	Val	Leu	Ile	Pro	Leu	Leu	Val	Ala	Asn	Ala	Arg	Asn	Val				
		210				215					220								
Asp	Leu	Met	Arg	Leu	Gly	Asn	Asp	Ser	Ala	Val	Gly	Leu	Gly	Val	Ala				
225					230					235					240				
Thr	Asn	Arg	Thr	Arg	Val	Ile	Ala	Ile	Ile	Ala	Ala	Val	Ala	Leu	Ile				
			245					250						255					
Ala	Val	Ala	Thr	Ala	Ala	Cys	Gly	Pro	Ile	Ala	Phe	Val	Ala	Phe	Val				
			260					265					270						
Ser	Gly	Pro	Ile	Ala	Ala	Arg	Ile	Leu	Gly	Ser	Gly	Gly	Ser	Leu	Ile				
		275					280					285							
Ile	Pro	Ser	Ala	Leu	Ile	Gly	Gly	Leu	Ile	Val	Leu	Ile	Ala	Asp	Leu				
	290					295					300								
Ile	Gly	Gln	Tyr	Phe	Leu	Gly	Thr	Arg	Tyr	Pro	Val	Gly	Val	Val	Thr				
305					310					315					320				
Gly	Ala	Phe	Gly	Ala	Pro	Phe	Leu	Ile	Tyr	Leu	Leu	Ile	Arg	Ser	Asn				
			325					330						335					
Arg	Ala	Gly	Val	Thr	Leu														
			340																

<210> 381
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> RXN01142

<400> 381
 ctcccatcc accggcacag tcagcgagg caacgaagaa attaaaggac caggacctga 60
 ccgaggcatg gttttccaag accacgcct cctgccctga ttg acc gca cgc ggc 115
 Leu Thr Ala Arg Gly
 1 5
 aac atc gac ttc ggg ctc cgc tcc gcg cgc ccc tcc ttg agc aaa acc 163
 Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro Ser Leu Ser Lys Thr
 10 15 20
 gaa cgc gcc gac atc acc cgc acc cac ctc gaa caa gta ggc ctc acc 211
 Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr
 25 30 35

gac gcc gcc gaa cgg cgc ccc gcc cgc ctc tcc ggc ggc atg caa cag 259
 Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln
 40 45 50

cga gtc ggc atc gca cgc gcc ttc gcc atc gac cca cca atc atg ctt 307
 Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu
 55 60 65

ctc gac gaa ccc ttc ggc gcc ctc gac gcc ctc acc cgc cgc gaa ctc 355
 Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu
 70 75 80 85

cag ctc caa cta ctc aac att tgg gaa gcc tcc cgc cgc acc gtc gtc 403
 Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val
 90 95 100

atg gtc acc cac gac gtc gac gag gcc atc ctg ctc tcc gac cga gtt 451
 Met Val Thr His Asp Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val
 105 110 115

ctc gtg atg tcc aag agc ccc gaa gcc acc atc atc acc gat att cca 499
 Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro
 120 125 130

gtg aat ctt ccc cgc ccc aga cac gag ctg agt gaa gac gct tct gtt 547
 Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val
 135 140 145

gaa gcc gag acc aca gcc ctg cgt aag cgg atg ctg cat ctg ctg gag 595
 Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu
 150 155 160 165

cac tagtttctaa cacgtctttt aaa 621
 His

<210> 382

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Leu Thr Ala Arg Gly Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro
 1 5 10 15

Ser Leu Ser Lys Thr Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu
 20 25 30

Gln Val Gly Leu Thr Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser
 35 40 45

Gly Gly Met Gln Gln Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp
 50 55 60

Pro Pro Ile Met Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu
 65 70 75 80

Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser
 85 90 95

Arg Arg Thr Val Val Met Val Thr His Asp Val Asp Glu Ala Ile Leu
 100 105 110

Leu Ser Asp Arg Val Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile
 115 120 125

Ile Thr Asp Ile Pro Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser
 130 135 140

Glu Asp Ala Ser Val Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met
 145 150 155 160

Leu His Leu Leu Glu His
 165

<210> 383
 <211> 948
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(925)
 <223> RXN01141

<400> 383
 aaagaacact cggtatggca cctgatttaa ggatgctgca atcgtgacac atatcctctt 60

cgacagcagg cgttttctgc aactgggcgc ttttgcgctcc ttg agc acc gca ttg 115
 Leu Ser Thr Ala Leu
 1 5

gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat gaa cct gcg 163
 Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn Glu Pro Ala
 10 15 20

gat aac act ccc ctg acc att ggc tac gtg cct att gcg ggc tcg gcg 211
 Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala Gly Ser Ala
 25 30 35

ccg att gct atc gca gat gcg cta ggg ctg ttt aag aaa cac ggc gtg 259
 Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys His Gly Val
 40 45 50

aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg tgg acc gcc 307
 Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu Trp Thr Ala
 55 60 65

tat gca aca gag cag ctt gat gtt gcg cac atg ctg tcg ccg atg act 355
 Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met Leu Ser Pro Met Thr
 70 75 80 85

gtg gcg att aat gct gga gtg acc aac gcg tcg cgc ccg acg gag ctg 403
 Val Ala Ile Asn Ala Gly Val Thr Asn Ala Ser Arg Pro Thr Glu Leu
 90 95 100

tcg ttt acc cag aac acc aat ggg caa gca att acc ttg gcg tca aag 451
 Ser Phe Thr Gln Asn Thr Asn Gly Gln Ala Ile Thr Leu Ala Ser Lys
 105 110 115

cac tat ggt tcc gtc aat tca gcg gcg gat ctt aaa ggc atg gtg ctg 499
 His Tyr Gly Ser Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu
 120 125 130
 gga att cct ttt gaa tat tca gtc cat gcg ctg ctc ctg cgc gat tat 547
 Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr
 135 140 145
 ctc gtc tca aac gca gtt gat ccc atc gcc gat ctt gag ctt cgc ctg 595
 Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu
 150 155 160 165
 ctc cga cct gcc gat atg gtc gca caa ttg aca gtt gag ggc atc gat 643
 Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp
 170 175 180
 gga ttc att ggg cct ggg ccg ttt aat gaa cgc gcc atc agc aat ggc 691
 Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly
 185 190 195
 tcc ggc cgg att tgg ctg ctg acc aaa caa ctg tgg gac aaa cat cca 739
 Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro
 200 205 210
 tgc tgc gcc gtg gcg atg gcc aaa gag tgg aaa gct gaa cac ccc acg 787
 Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr
 215 220 225
 gcg gct cag ggt gtg ctt aat gcg ctg gag gaa gcc tcc gca att ttg 835
 Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu
 230 235 240 245
 agc aat ccg gca caa ttt gat tcc tcg gca cgc acg ctg tcg cag gaa 883
 Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu
 250 255 260
 aaa tac ctc aac cag cct gcc acg ttg ctg gat gga ccg tcg 925
 Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser
 265 270 275
 taatcatcgg catcaccggc tta 948

<210> 384

<211> 275

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 384

Leu Ser Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser
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Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro
 20 25 30

Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe
 35 40 45

Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser
 50 55 60

Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met
 65 70 75 80
 Leu Ser Pro Met Thr Val Ala Ile Asn Ala Gly Val Thr Asn Ala Ser
 85 90 95
 Arg Pro Thr Glu Leu Ser Phe Thr Gln Asn Thr Asn Gly Gln Ala Ile
 100 105 110
 Thr Leu Ala Ser Lys His Tyr Gly Ser Val Asn Ser Ala Ala Asp Leu
 115 120 125
 Lys Gly Met Val Leu Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu
 130 135 140
 Leu Leu Arg Asp Tyr Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp
 145 150 155 160
 Leu Glu Leu Arg Leu Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr
 165 170 175
 Val Glu Gly Ile Asp Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg
 180 185 190
 Ala Ile Ser Asn Gly Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu
 195 200 205
 Trp Asp Lys His Pro Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys
 210 215 220
 Ala Glu His Pro Thr Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu
 225 230 235 240
 Ala Ser Ala Ile Leu Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg
 245 250 255
 Thr Leu Ser Gln Glu Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp
 260 265 270
 Gly Pro Ser
 275

<210> 385
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXN01002

<400> 385
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 caactaattt ccctgtttcc aataactcaag gtgtgcgcat atg aat tct gat gct 115
 Met Asn Ser Asp Ala
 1 5
 tcg gct acc acc aac tcc tgg gct atc aac ttc gac cat gtg tcg gct 163

Ser	Ala	Thr	Thr	Asn	Ser	Trp	Ala	Ile	Asn	Phe	Asp	His	Val	Ser	Val	
				10					15					20		
acg	tat	ccc	aat	ggg	acg	aaa	gcc	ctc	gat	gat	gtt	tcc	ctc	acc	atc	211
Thr	Tyr	Pro	Asn	Gly	Thr	Lys	Ala	Leu	Asp	Asp	Val	Ser	Leu	Thr	Ile	
			25					30					35			
aat	ccc	ggg	gag	atg	gtt	gcc	atc	gtg	ggg	ctg	tca	gga	tcg	ggg	aaa	259
Asn	Pro	Gly	Glu	Met	Val	Ala	Ile	Val	Gly	Leu	Ser	Gly	Ser	Gly	Lys	
		40					45					50				
tcc	acg	ctg	att	cgc	acg	atc	aac	ggg	ctt	gtc	cgc	gct	acg	gaa	ggc	307
Ser	Thr	Leu	Ile	Arg	Thr	Ile	Asn	Gly	Leu	Val	Arg	Ala	Thr	Glu	Gly	
	55					60					65					
acc	gtg	acg	gtg	ggg	ccg	cat	cag	atc	aac	acc	ttg	aag	ggg	aaa	gca	355
Thr	Val	Thr	Val	Gly	Pro	His	Gln	Ile	Asn	Thr	Leu	Lys	Gly	Lys	Ala	
	70					75				80					85	
ctg	cgt	gat	gcc	cgt	ggg	cag	atc	ggc	atg	att	ttc	cag	ggg	ttc	aac	403
Leu	Arg	Asp	Ala	Arg	Gly	Gln	Ile	Gly	Met	Ile	Phe	Gln	Gly	Phe	Asn	
				90					95					100		
ctg	tcg	gaa	cgc	agc	agt	gtg	ttc	cag	aac	gtt	ttg	gtg	ggc	cgc	ttc	451
Leu	Ser	Glu	Arg	Ser	Ser	Val	Phe	Gln	Asn	Val	Leu	Val	Gly	Arg	Phe	
			105					110					115			
gcg	cac	aca	gcg	tgg	tgg	cgt	aac	ctc	ctc	ggg	ttt	ccc	acg	gag	cac	499
Ala	His	Thr	Ala	Trp	Trp	Arg	Asn	Leu	Leu	Gly	Phe	Pro	Thr	Glu	His	
		120					125					130				
gac	aag	cag	att	gct	ttt	cac	gcg	ttg	gag	tcc	gtg	ggc	att	ttg	cac	547
Asp	Lys	Gln	Ile	Ala	Phe	His	Ala	Leu	Glu	Ser	Val	Gly	Ile	Leu	His	
	135					140					145					
aaa	gtg	tgg	acc	cga	gct	ggg	gct	ttg	tcg	ggg	gga	cag	aaa	cag	cgc	595
Lys	Val	Trp	Thr	Arg	Ala	Gly	Ala	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	
	150					155				160					165	
gtt	gct	att	gcg	cgc	gcc	tta	tcg	caa	gat	ccg	tct	gtc	atg	ctg	gca	643
Val	Ala	Ile	Ala	Arg	Ala	Leu	Ser	Gln	Asp	Pro	Ser	Val	Met	Leu	Ala	
				170					175					180		
gat	gag	cct	gtg	gca	agc	ctt	gat	ccg	cca	acc	gcg	cat	tcc	gtg	atg	691
Asp	Glu	Pro	Val	Ala	Ser	Leu	Asp	Pro	Pro	Thr	Ala	His	Ser	Val	Met	
			185					190					195			
cgc	gat	cta	gaa	aac	atc	aac	aac	gtg	gaa	ggc	ctc	acc	gtg	ttg	gtg	739
Arg	Asp	Leu	Glu	Asn	Ile	Asn	Asn	Val	Glu	Gly	Leu	Thr	Val	Leu	Val	
		200					205					210				
aac	ttg	cac	ttg	att	gat	ttg	gct	cgt	caa	tac	acc	aca	agg	ctt	gtg	787
Asn	Leu	His	Leu	Ile	Asp	Leu	Ala	Arg	Gln	Tyr	Thr	Thr	Arg	Leu	Val	
	215					220					225					
ggg	ttg	cgt	gcc	ggc	aag	ctg	gtc	tat	gac	ggg	cct	atc	tct	gag	gcc	835
Gly	Leu	Arg	Ala	Gly	Lys	Leu	Val	Tyr	Asp	Gly	Pro	Ile	Ser	Glu	Ala	
	230				235					240					245	
acc	gat	aaa	gac	ttt	gaa	gct	atc	tat	ggg	cgc	ccc	atc	cag	gct	aaa	883
Thr	Asp	Lys	Asp	Phe	Glu	Ala	Ile	Tyr	Gly	Arg	Pro	Ile	Gln	Ala	Lys	

250 255 260 927

gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca ctt
Asp Leu Leu Gly Asp Arg Ala
265

<210> 386
<211> 268
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 386
Met Asn Ser Asp Ala Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe
1 5 10 15
Asp His Val Ser Val Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp
20 25 30
Val Ser Leu Thr Ile Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu
35 40 45
Ser Gly Ser Gly Lys Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val
50 55 60
Arg Ala Thr Glu Gly Thr Val Thr Val Gly Pro His Gln Ile Asn Thr
65 70 75 80
Leu Lys Gly Lys Ala Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile
85 90 95
Phe Gln Gly Phe Asn Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val
100 105 110
Leu Val Gly Arg Phe Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly
115 120 125
Phe Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser
130 135 140
Val Gly Ile Leu His Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly
145 150 155 160
Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro
165 170 175
Ser Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr
180 185 190
Ala His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly
195 200 205
Leu Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr
210 215 220
Thr Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly
225 230 235 240
Pro Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg
245 250 255

Pro Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
 260 265

<210> 387
 <211> 969
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(946)
 <223> RXN01000

<400> 387
 ctttctatgc ctacgcggat gtttccgtga tcattctgga aatcctcatc gtggtgattg 60
 tcattgaagt aatctccaac gcacttcgaa agaggctggt atg agc acc tta acc 115
 Met Ser Thr Leu Thr
 1 5
 tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac 163
 Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn
 10 15 20
 aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt 211
 Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu
 25 30 35
 ata gct acc ggc acg ctc aag atc gag tgg aat gag ctt ccg cag atg 259
 Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met
 40 45 50
 ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat 307
 Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp
 55 60 65
 tgg tcg aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc 355
 Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala
 70 75 80 85
 atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg 403
 Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu
 90 95 100
 gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt 451
 Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val
 105 110 115
 tta cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc 499
 Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile
 120 125 130
 gca att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg 547
 Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala
 135 140 145
 ctc gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat 595
 Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr
 150 155 160 165

gaa gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca 643
 Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala
 170 175 180

gcg ggt gga act acg ccg gag gtt ctg ccg tgg gcg ttg tgg cca cag 691
 Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln
 185 190 195

gtt gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac 739
 Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn
 200 205 210

atc cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt 787
 Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly
 215 220 225

agt atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc 835
 Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly
 230 235 240 245

atg ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc 883
 Met Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile
 250 255 260

tcc ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc 931
 Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val
 265 270 275

gtg gca cca agc aac tgacgctcca ccaagcatcc gca 969
 Val Ala Pro Ser Asn
 280

<210> 388

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

Met Ser Thr Leu Thr Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro
 1 5 10 15

Pro Ala Arg Pro Asn Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala
 20 25 30

Ala Leu Ile Val Leu Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn
 35 40 45

Glu Leu Pro Gln Met Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met
 50 55 60

Phe Ser Asp Pro Asp Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met
 65 70 75 80

Trp Arg Ser Ile Ala Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val
 85 90 95

Val Ser Val Pro Leu Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr
 100 105 110

Trp Leu Arg Thr Val Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe

115	120	125
Pro Glu Val Val Ile Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr 130	135	140
Pro Phe Thr Gly Ala Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln 145	150	155 160
Ala Lys Trp Thr Tyr Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser 165	170	175
Glu Ala Val Arg Ala Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp 180	185	190
Ala Leu Trp Pro Gln Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr 195	200	205
Arg Phe Glu Ile Asn Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly 210	215	220
Ala Gly Gly Ile Gly Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln 225	230	235 240
Trp Asp Thr Val Gly Met Leu Leu Ile Val Val Val Val Ala Thr Met 245	250	255
Ile Val Asp Leu Ile Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly 260	265	270
Ala Ser Asp Arg Val Val Ala Pro Ser Asn 275	280	

<210> 389

<211> 1173

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1150)

<223> RXN01732

<400> 389

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ctttcttgtc tcatgtcgct gaaaggtttt taaagatctc	atg ttc aag ctc tct	115
	Met Phe Lys Leu Ser	
	1 5	

aag cca tcc aag tcc atg cgt gtt gct gtt tct acg ctt gcg atc tct	163
Lys Pro Ser Lys Ser Met Arg Val Ala Val Ser Thr Leu Ala Ile Ser	
10 15 20	

acc ctt gct cta gtt ggt tgt tcc tct tcc gat gag tct tct tcc tca	211
Thr Leu Ala Leu Val Gly Cys Ser Ser Ser Asp Glu Ser Ser Ser Ser	
25 30 35	

tca tct gcg tct tct tct tcg gat gct gca agc cag tgg cct gag tcc	259
Ser Ser Ala Ser Ser Ser Ser Asp Ala Ala Ser Gln Trp Pro Glu Ser	
40 45 50	

att act ttg tct ctt gtt cct tct act gag ggt gag gat ttg gct gaa	307
Ile Thr Leu Ser Leu Val Pro Ser Thr Glu Gly Glu Asp Leu Ala Glu	
55 60 65	
gcg ttg gct cct ttg act gat tac ctg tct gag aac ctt ggt att gag	355
Ala Leu Ala Pro Leu Thr Asp Tyr Leu Ser Glu Asn Leu Gly Ile Glu	
70 75 80 85	
gtc aat ggt gtg gtg gcg tct gat tac gct gca acc gtt gag gct ttg	403
Val Asn Gly Val Val Ala Ser Asp Tyr Ala Ala Thr Val Glu Ala Leu	
90 95 100	
ggg gct gat cag gct cag gtg atc atc act gat gcg ggt tcc ctg tat	451
Gly Ala Asp Gln Ala Gln Val Ile Ile Thr Asp Ala Gly Ser Leu Tyr	
105 110 115	
aac gcg att gag cag tac gat gcg cag ctg att ctg cgt gat gtg cgt	499
Asn Ala Ile Glu Gln Tyr Asp Ala Gln Leu Ile Leu Arg Asp Val Arg	
120 125 130	
ttc ggt gcc acc tcg tac tct gct gtg gcg tac acc aac aat cct gat	547
Phe Gly Ala Thr Ser Tyr Ser Ala Val Ala Tyr Thr Asn Asn Pro Asp	
135 140 145	
aag tac tgc gac gat gcc cca gtg gct gcg tct tat gct gcg tcc gat	595
Lys Tyr Cys Asp Asp Ala Pro Val Ala Ala Ser Tyr Ala Ala Ser Asp	
150 155 160 165	
gta gac atg ctt tac tgc aac ggt att gaa act gag ggc cag gct gct	643
Val Asp Met Leu Tyr Cys Asn Gly Ile Glu Thr Glu Gly Gln Ala Ala	
170 175 180	
acc ggt gag ggc cca gca gct ctt gat gcg ctg gaa aag atc gag tcc	691
Thr Gly Glu Gly Pro Ala Ala Leu Asp Ala Leu Glu Lys Ile Glu Ser	
185 190 195	
ggg gac aag gta gcg ctg cag gct gca acc tct cct gcg ggt tac cag	739
Gly Asp Lys Val Ala Leu Gln Ala Ala Thr Ser Pro Ala Gly Tyr Gln	
200 205 210	
tac cct atc gtc gct atg cag gat ctg ggc atg gat acc gat tcc gct	787
Tyr Pro Ile Val Ala Met Gln Asp Leu Gly Met Asp Thr Asp Ser Ala	
215 220 225	
ttt gtt cag gtt cca gta gag ggc aac aac aac gct gtg ctg tct gtc	835
Phe Val Gln Val Pro Val Glu Gly Asn Asn Asn Ala Val Leu Ser Val	
230 235 240 245	
ctg aac ggt gac gcg gaa gtg tcc ttc ggt ttc tgg gat gcg cgt tcc	883
Leu Asn Gly Asp Ala Glu Val Ser Phe Gly Phe Trp Asp Ala Arg Ser	
250 255 260	
acc gtg ctg tct gag gct cct aac gca gct gag gat gtc gta gcg ttt	931
Thr Val Leu Ser Glu Ala Pro Asn Ala Ala Glu Asp Val Val Ala Phe	
265 270 275	
gcc tac acc gag atg atc cct aac ggt ggc gtc gca gcg tcc aag tcc	979
Ala Tyr Thr Glu Met Ile Pro Asn Gly Gly Val Ala Ala Ser Lys Ser	
280 285 290	

ctt cca tcc gac ctg gtg gaa aag ctc acc gag ttg atg gat gat tac 1027
 Leu Pro Ser Asp Leu Val Glu Lys Leu Thr Glu Leu Met Asp Asp Tyr
 295 300 305

gca gat tcc tcc gag gaa gcc aag gat gtc atg ttc gac atg gtt ggt 1075
 Ala Asp Ser Ser Glu Glu Ala Lys Asp Val Met Phe Asp Met Val Gly
 310 315 320 325

cta tct gac tgg act gct gat acc gca cag gat gaa atc act cgt tac 1123
 Leu Ser Asp Trp Thr Ala Asp Thr Ala Gln Asp Glu Ile Thr Arg Tyr
 330 335 340

ggc gag atc ctg aag aag ttc tcc aac taatttcct gttccaata 1170
 Gly Glu Ile Leu Lys Lys Phe Ser Asn
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ctc 1173

<210> 390

<211> 350

<212> PRT

<213> Corynebacterium glutamicum

<400> 390

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 20 25 30

Glu Ser Ser Ser Ser Ser Ser Ala Ser Ser Ser Ser Asp Ala Ala Ser
 35 40 45

Gln Trp Pro Glu Ser Ile Thr Leu Ser Leu Val Pro Ser Thr Glu Gly
 50 55 60

Glu Asp Leu Ala Glu Ala Leu Ala Pro Leu Thr Asp Tyr Leu Ser Glu
 65 70 75 80

Asn Leu Gly Ile Glu Val Asn Gly Val Val Ala Ser Asp Tyr Ala Ala
 85 90 95

Thr Val Glu Ala Leu Gly Ala Asp Gln Ala Gln Val Ile Ile Thr Asp
 100 105 110

Ala Gly Ser Leu Tyr Asn Ala Ile Glu Gln Tyr Asp Ala Gln Leu Ile
 115 120 125

Leu Arg Asp Val Arg Phe Gly Ala Thr Ser Tyr Ser Ala Val Ala Tyr
 130 135 140

Thr Asn Asn Pro Asp Lys Tyr Cys Asp Asp Ala Pro Val Ala Ala Ser
 145 150 155 160

Tyr Ala Ala Ser Asp Val Asp Met Leu Tyr Cys Asn Gly Ile Glu Thr
 165 170 175

Glu Gly Gln Ala Ala Thr Gly Glu Gly Pro Ala Ala Leu Asp Ala Leu
 180 185 190

Glu Lys Ile Glu Ser Gly Asp Lys Val Ala Leu Gln Ala Ala Thr Ser
 195 200 205
 Pro Ala Gly Tyr Gln Tyr Pro Ile Val Ala Met Gln Asp Leu Gly Met
 210 215 220
 Asp Thr Asp Ser Ala Phe Val Gln Val Pro Val Glu Gly Asn Asn Asn
 225 230 235 240
 Ala Val Leu Ser Val Leu Asn Gly Asp Ala Glu Val Ser Phe Gly Phe
 245 250 255
 Trp Asp Ala Arg Ser Thr Val Leu Ser Glu Ala Pro Asn Ala Ala Glu
 260 265 270
 Asp Val Val Ala Phe Ala Tyr Thr Glu Met Ile Pro Asn Gly Gly Val
 275 280 285
 Ala Ala Ser Lys Ser Leu Pro Ser Asp Leu Val Glu Lys Leu Thr Glu
 290 295 300
 Leu Met Asp Asp Tyr Ala Asp Ser Ser Glu Glu Ala Lys Asp Val Met
 305 310 315 320
 Phe Asp Met Val Gly Leu Ser Asp Trp Thr Ala Asp Thr Ala Gln Asp
 325 330 335
 Glu Ile Thr Arg Tyr Gly Glu Ile Leu Lys Lys Phe Ser Asn
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<210> 391

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN03080

<400> 391

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 Met Pro Gln Leu Val
 1 5
 gaa att cgt gat ctc aac gtt gaa ttc ccc tct cgc cat gca gtg aaa 163
 Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys
 10 15 20
 aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc 211
 Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly
 25 30 35
 cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg 259
 Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu
 40 45 50
 gtt gaa tcc acc ggc gag gta atg gtt ggt ggg agt ggg gtt gcg tcg 307

Val	Glu	Ser	Thr	Gly	Glu	Val	Met	Val	Gly	Gly	Ser	Gly	Val	Ala	Ser		
55						60					65						
aaa	agc	gct	aaa	gcc	cga	gcc	cgc	ctg	ctc	tca	ctc	gtg	ccg	caa	aac	355	
Lys	Ser	Ala	Lys	Ala	Arg	Ala	Arg	Leu	Leu	Ser	Leu	Val	Pro	Gln	Asn		
70					75					80					85		
acc	gag	ttg	cgc	att	ggt	ttt	agt	gca	cgc	gac	gtt	gtc	gcg	atg	ggc	403	
Thr	Glu	Leu	Arg	Ile	Gly	Phe	Ser	Ala	Arg	Asp	Val	Val	Ala	Met	Gly		
				90					95					100			
cgc	tac	ccg	cat	cgt	ggc	cgc	ttc	gcc	gtg	gag	acc	gac	gca	gat	cga	451	
Arg	Tyr	Pro	His	Arg	Gly	Arg	Phe	Ala	Val	Glu	Thr	Asp	Ala	Asp	Arg		
			105					110					115				
cgc	gcc	acc	gat	gac	gcc	ctg	cgc	gcc	atc	aac	gcg	ctc	gac	atc	gcc	499	
Arg	Ala	Thr	Asp	Asp	Ala	Leu	Arg	Ala	Ile	Asn	Ala	Leu	Asp	Ile	Ala		
		120					125					130					
gag	cag	ccc	gtc	aac	gaa	tta	tcg	ggc	ggc	cag	cag	cag	ctc	atc	cac	547	
Glu	Gln	Pro	Val	Asn	Glu	Leu	Ser	Gly	Gly	Gln	Gln	Gln	Leu	Ile	His		
	135					140						145					
atc	ggc	cga	gcg	ctc	gcc	caa	gac	acc	gcc	gtc	gtg	ctt	ctc	gac	gag	595	
Ile	Gly	Arg	Ala	Leu	Ala	Gln	Asp	Thr	Ala	Val	Val	Leu	Leu	Asp	Glu		
150					155					160					165		
ccc	gtc	tcc	gcc	ctt	gat	cta	cgg	cac	caa	gtt	gaa	gtc	ctt	caa	ctc	643	
Pro	Val	Ser	Ala	Leu	Asp	Leu	Arg	His	Gln	Val	Glu	Val	Leu	Gln	Leu		
				170					175					180			
ctg	cgc	gcc	cga	gct	aat	tcc	ggc	acc	acc	gtg	atc	gtc	gtc	ctt	cac	691	
Leu	Arg	Ala	Arg	Ala	Asn	Ser	Gly	Thr	Thr	Val	Ile	Val	Val	Leu	His		
			185					190					195				
gat	ctc	aac	cac	gtt	gcc	cgt	tgg	tgc	gac	cat	gca	gtg	ttg	atg	gcc	739	
Asp	Leu	Asn	His	Val	Ala	Arg	Trp	Cys	Asp	His	Ala	Val	Leu	Met	Ala		
		200					205					210					
gac	ggc	gaa	gtt	gtc	tcc	caa	ggt	gac	atc	cgc	gag	gtg	ctc	gaa	cct	787	
Asp	Gly	Glu	Val	Val	Ser	Gln	Gly	Asp	Ile	Arg	Glu	Val	Leu	Glu	Pro		
	215					220					225						
gcc	aca	ctg	tcc	acc	gtg	tac	gga	ctg	ccc	att	gcg	gtg	cgc	gat	gat	835	
Ala	Thr	Leu	Ser	Thr	Val	Tyr	Gly	Leu	Pro	Ile	Ala	Val	Arg	Asp	Asp		
230					235					240					245		
ccc	gaa	acc	agc	tca	ctt	cgc	gtg	atc	ccg	cat	cca	aat	ccc	ttt		880	
Pro	Glu	Thr	Ser	Ser	Leu	Arg	Val	Ile	Pro	His	Pro	Asn	Pro	Phe			
				250					255					260			
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<210> 392

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

Met Pro Gln Leu Val Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser

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Arg His Ala Val Lys Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val	20	25	30
Thr Ala Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser	35	40	45
Ala Ile Ala Gly Leu Val Glu Ser Thr Gly Glu Val Met Val Gly Gly	50	55	60
Ser Gly Val Ala Ser Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser	65	70	80
Leu Val Pro Gln Asn Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp	85	90	95
Val Val Ala Met Gly Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu	100	105	110
Thr Asp Ala Asp Arg Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn	115	120	125
Ala Leu Asp Ile Ala Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln	130	135	140
Gln Gln Leu Ile His Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val	145	150	155
Val Leu Leu Asp Glu Pro Val Ser Ala Leu Asp Leu Arg His Gln Val	165	170	175
Glu Val Leu Gln Leu Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val	180	185	190
Ile Val Val Leu His Asp Leu Asn His Val Ala Arg Trp Cys Asp His	195	200	205
Ala Val Leu Met Ala Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg	210	215	220
Glu Val Leu Glu Pro Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile	225	230	235
Ala Val Arg Asp Asp Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His	245	250	255
Pro Asn Pro Phe	260		

<210> 393

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXN03081

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atccaaatcc cttttgattg aaagtttgac ttaaaaaccc atg aaa aaa tca ctc 115
Met Lys Lys Ser Leu
1 5

atc gcc att gtt gcc agt gcg ctc gtg tta agc ggc tgc acc tct gat 163
Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser Gly Cys Thr Ser Asp
10 15 20

tct tct gac tct tcc ggc act tcc gga act gtg gaa acc act tcg att 211
Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val Glu Thr Thr Ser Ile
25 30 35

aca acc agc gtt gcc gca gct gac ggc gca ttc cca cgc acc gtc aca 259
Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe Pro Arg Thr Val Thr
40 45 50

ctc gac gat tcc tcc atc acc tta gaa tcc aaa cca gag cgc atc gcc 307
Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys Pro Glu Arg Ile Ala
55 60 65

gta ctc acc cca gag gca gca tcc ttg gtt ctc ccc atc aca ggc gcc 355
Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu Pro Ile Thr Gly Ala
70 75 80 85

gac cgc gtc gtg atg acc gcc gaa atg gac acc gct gac gaa gaa acc 403
Asp Arg Val Val Met Thr Ala Glu Met Asp Thr Ala Asp Glu Glu Thr
90 95 100

gca gct ctg gcc tcc caa gtg gaa tac caa gtc aaa aac ggt ggc agg 451
Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val Lys Asn Gly Gly Arg
105 110 115

ctc gac ccc gaa caa gtt gtc gcc ggc gac cca gat ttg gtg atc gtc 499
Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro Asp Leu Val Ile Val
120 125 130

agt gcg cgt ttc gat acc gaa caa ggc acc atc gac att ttg gaa ggc 547
Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile Asp Ile Leu Glu Gly
135 140 145

ctc aac gtc ccg tagttaactt cgattcagac gct 582
Leu Asn Val Pro
150

<210> 394

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser
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Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val
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Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe

35 40 45
 Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys
 50 55 60
 Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu
 65 70 75 80
 Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr
 85 90 95
 Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val
 100 105 110
 Lys Asn Gly Gly Arg Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro
 115 120 125
 Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile
 130 135 140
 Asp Ile Leu Glu Gly Leu Asn Val Pro
 145 150

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 <211> 444
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(421)
 <223> RXN03082

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 Met Val Met Pro Glu
 1 5
 tct gcc atg ctc acc ggc ctg atc cgc gaa gcc ggc ggc act cca gtg 163
 Ser Ala Met Leu Thr Gly Leu Ile Arg Glu Ala Gly Gly Thr Pro Val
 10 15 20
 gta gat tct ctc ggc gcg gta ggc acc atc act gca gac cca gaa caa 211
 Val Asp Ser Leu Gly Ala Val Gly Thr Ile Thr Ala Asp Pro Glu Gln
 25 30 35
 gtt gtt gcg atg gca cct gag atc atc atc att cag gac ttc caa ggt 259
 Val Val Ala Met Ala Pro Glu Ile Ile Ile Ile Gln Asp Phe Gln Gly
 40 45 50
 aaa ggc cga gag aac ttc gct aat ttc ctc tcc aac cca gcg cta gcc 307
 Lys Gly Arg Glu Asn Phe Ala Asn Phe Leu Ser Asn Pro Ala Leu Ala
 55 60 65
 aac gtt ccc gcc att gaa aac gac aag att ttc tac gcc gac act gtc 355
 Asn Val Pro Ala Ile Glu Asn Asp Lys Ile Phe Tyr Ala Asp Thr Val
 70 75 80 85

acc act gga gtt act gca ggt acc gat atc acc act ggt ctg cag caa 403
 Thr Thr Gly Val Thr Ala Gly Thr Asp Ile Thr Thr Gly Leu Gln Gln
 90 95 100

gtg gca gaa atg ctg agc tagttttgag atgttgaaac tag 444
 Val Ala Glu Met Leu Ser
 105

<210> 396

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Val Met Pro Glu Ser Ala Met Leu Thr Gly Leu Ile Arg Glu Ala
 1 5 10 15

Gly Gly Thr Pro Val Val Asp Ser Leu Gly Ala Val Gly Thr Ile Thr
 20 25 30

Ala Asp Pro Glu Gln Val Val Ala Met Ala Pro Glu Ile Ile Ile Ile
 35 40 45

Gln Asp Phe Gln Gly Lys Gly Arg Glu Asn Phe Ala Asn Phe Leu Ser
 50 55 60

Asn Pro Ala Leu Ala Asn Val Pro Ala Ile Glu Asn Asp Lys Ile Phe
 65 70 75 80

Tyr Ala Asp Thr Val Thr Thr Gly Val Thr Ala Gly Thr Asp Ile Thr
 85 90 95

Thr Gly Leu Gln Gln Val Ala Glu Met Leu Ser
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<210> 397

<211> 1479

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1456)

<223> RXA02261

<400> 397

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actccgctcg acagcatcac ttagctgaaa ggcctttaac atg gac ccc tca gat 115
 Met Asp Pro Ser Asp
 1 5

cta gcc tgg att ctc gca gct ttt gcg ttg gta agc ctg atg ttc ccc 163
 Leu Ala Trp Ile Leu Ala Ala Phe Ala Leu Val Ser Leu Met Phe Pro
 10 15 20

gga ttg tcc ctg ctc tac ggc ggc atg ctg ggt ggg caa cac gtt ctt 211
 Gly Leu Ser Leu Leu Tyr Gly Gly Met Leu Gly Gly Gln His Val Leu
 25 30 35

aac acg ttc atg atg gtt atg agc tca ctt gga atc atc agc ctt gtg	259
Asn Thr Phe Met Met Val Met Ser Ser Leu Gly Ile Ile Ser Leu Val	
40 45 50	
tac atc att tat gga cac gga ctt gtc tta gga aac tcc atc ggt ggg	307
Tyr Ile Ile Tyr Gly His Gly Leu Val Leu Gly Asn Ser Ile Gly Gly	
55 60 65	
tgg gga att atc gga aat ccc ctt gaa tac ttc ggc ttc cgc aac att	355
Trp Gly Ile Ile Gly Asn Pro Leu Glu Tyr Phe Gly Phe Arg Asn Ile	
70 75 80 85	
atg gaa gat gac ggc acc gga gac ctc atg tgg gcc ggc ttc tac att	403
Met Glu Asp Asp Gly Thr Gly Asp Leu Met Trp Ala Gly Phe Tyr Ile	
90 95 100	
ctg ttc gct gca atc tca ctc gca ctt gtt tca tct ggt gca gcg ggg	451
Leu Phe Ala Ala Ile Ser Leu Ala Leu Val Ser Ser Gly Ala Ala Gly	
105 110 115	
cgc atg cgc ttt gga gcg tgg ctg gtc ttc ggt gtc ctg tgg ttc acc	499
Arg Met Arg Phe Gly Ala Trp Leu Val Phe Gly Val Leu Trp Phe Thr	
120 125 130	
ttt gtg tac gcg cca ctg gca cac tgg gtt ttc gct atc gat gat cct	547
Phe Val Tyr Ala Pro Leu Ala His Trp Val Phe Ala Ile Asp Asp Pro	
135 140 145	
gag tcc ggc tac gtg ggt ggc tgg atg aaa aat gtg ctt gag ttc cac	595
Glu Ser Gly Tyr Val Gly Gly Trp Met Lys Asn Val Leu Glu Phe His	
150 155 160 165	
gac ttt gct ggt gga acg gca gtg cac atg aat gcg ggt gcg tct gga	643
Asp Phe Ala Gly Gly Thr Ala Val His Met Asn Ala Gly Ala Ser Gly	
170 175 180	
ctc gcg ctg gca ata gtg ctg gga cgc cgc cac tcc atg gct gtg cgt	691
Leu Ala Leu Ala Ile Val Leu Gly Arg Arg His Ser Met Ala Val Arg	
185 190 195	
cca cac aac ctt cca ctg att ttg att ggt gca gga ctg atc gtt gcg	739
Pro His Asn Leu Pro Leu Ile Leu Ile Gly Ala Gly Leu Ile Val Ala	
200 205 210	
ggc tgg ttc gga ttc aat ggt ggt acc gca ggt ggt gcc aac ttc ctc	787
Gly Trp Phe Gly Phe Asn Gly Gly Thr Ala Gly Gly Ala Asn Phe Leu	
215 220 225	
gca agc tac gtg gtc gtt acc tct ctc att gct gca gct ggc gga atg	835
Ala Ser Tyr Val Val Thr Ser Leu Ile Ala Ala Ala Gly Gly Met	
230 235 240 245	
atg ggc ttc atg ctc gtt gaa cgt gtg ttc agc gga aaa ccc act ttc	883
Met Gly Phe Met Leu Val Glu Arg Val Phe Ser Gly Lys Pro Thr Phe	
250 255 260	
ttt ggc tcg gca acc ggc aca atc gca ggc ctt gtg gct atc acc ccg	931
Phe Gly Ser Ala Thr Gly Thr Ile Ala Gly Leu Val Ala Ile Thr Pro	
265 270 275	

gcc gcg gat gca gtg agc ccg ctc gga gca ttc gcc gtc gga gcg ctc 979
 Ala Ala Asp Ala Val Ser Pro Leu Gly Ala Phe Ala Val Gly Ala Leu
 280 285 290

ggc gca gtt gtc tcc ttc tgg gca att agc tgg aag aag gga cac cga 1027
 Gly Ala Val Val Ser Phe Trp Ala Ile Ser Trp Lys Lys Gly His Arg
 295 300 305

gtc gat gat tcc ttc gat gtg ttc gca gtc cac gga atg gcc ggc att 1075
 Val Asp Asp Ser Phe Asp Val Phe Ala Val His Gly Met Ala Gly Ile
 310 315 320 325

gca ggt gca ctg ttt gtc atg ctc ttt ggc gat cca cta gca cca gcg 1123
 Ala Gly Ala Leu Phe Val Met Leu Phe Gly Asp Pro Leu Ala Pro Ala
 330 335 340

gga gtt tcc gga gtc ttc ttc ggt ggc gaa ctc tcc ctg ctg tgg agg 1171
 Gly Val Ser Gly Val Phe Phe Gly Gly Glu Leu Ser Leu Leu Trp Arg
 345 350 355

gaa cca ctg gcc atc atc gtg acc ctt aca tac gca ttc ggc gtg acc 1219
 Glu Pro Leu Ala Ile Ile Val Thr Leu Thr Tyr Ala Phe Gly Val Thr
 360 365 370

tgg ttg att gcc acg atc ttg aac aag ttc atg act ctg cgc atc acc 1267
 Trp Leu Ile Ala Thr Ile Leu Asn Lys Phe Met Thr Leu Arg Ile Thr
 375 380 385

tcc gaa gcc gaa tat gaa ggc att gac cgc gca gaa cac gca gaa tct 1315
 Ser Glu Ala Glu Tyr Glu Gly Ile Asp Arg Ala Glu His Ala Gly Ser
 390 395 400 405

gcc tac cac ctc aat tcc aac gga att ggg atg gca acc cgc acc aat 1363
 Ala Tyr His Leu Asn Ser Asn Gly Ile Gly Met Ala Thr Arg Thr Asn
 410 415 420

ttc gga cct gaa atc ccc gag gaa acc gtg ccc gac gcc gtg cag gtg 1411
 Phe Gly Pro Glu Ile Pro Glu Glu Thr Val Pro Asp Ala Val Gln Val
 425 430 435

ggc gtc gat aag caa aaa atc gct gat act cga aag gcc tca aaa 1456
 Gly Val Asp Lys Gln Lys Ile Ala Asp Thr Arg Lys Ala Ser Lys
 440 445 450

tgaccgcaac ctacaccact gaa 1479

<210> 398

<211> 452

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

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Ser Leu Met Phe Pro Gly Leu Ser Leu Leu Tyr Gly Gly Met Leu Gly
 20 25 30

Gly Gln His Val Leu Asn Thr Phe Met Met Val Met Ser Ser Leu Gly
 35 40 45

Ile Ile Ser Leu Val Tyr Ile Ile Tyr Gly His Gly Leu Val Leu Gly
 50 55 60
 Asn Ser Ile Gly Gly Trp Gly Ile Ile Gly Asn Pro Leu Glu Tyr Phe
 65 70 75 80
 Gly Phe Arg Asn Ile Met Glu Asp Asp Gly Thr Gly Asp Leu Met Trp
 85 90 95
 Ala Gly Phe Tyr Ile Leu Phe Ala Ala Ile Ser Leu Ala Leu Val Ser
 100 105 110
 Ser Gly Ala Ala Gly Arg Met Arg Phe Gly Ala Trp Leu Val Phe Gly
 115 120 125
 Val Leu Trp Phe Thr Phe Val Tyr Ala Pro Leu Ala His Trp Val Phe
 130 135 140
 Ala Ile Asp Asp Pro Glu Ser Gly Tyr Val Gly Gly Trp Met Lys Asn
 145 150 155 160
 Val Leu Glu Phe His Asp Phe Ala Gly Gly Thr Ala Val His Met Asn
 165 170 175
 Ala Gly Ala Ser Gly Leu Ala Leu Ala Ile Val Leu Gly Arg Arg His
 180 185 190
 Ser Met Ala Val Arg Pro His Asn Leu Pro Leu Ile Leu Ile Gly Ala
 195 200 205
 Gly Leu Ile Val Ala Gly Trp Phe Gly Phe Asn Gly Gly Thr Ala Gly
 210 215 220
 Gly Ala Asn Phe Leu Ala Ser Tyr Val Val Val Thr Ser Leu Ile Ala
 225 230 235 240
 Ala Ala Gly Gly Met Met Gly Phe Met Leu Val Glu Arg Val Phe Ser
 245 250 255
 Gly Lys Pro Thr Phe Phe Gly Ser Ala Thr Gly Thr Ile Ala Gly Leu
 260 265 270
 Val Ala Ile Thr Pro Ala Ala Asp Ala Val Ser Pro Leu Gly Ala Phe
 275 280 285
 Ala Val Gly Ala Leu Gly Ala Val Val Ser Phe Trp Ala Ile Ser Trp
 290 295 300
 Lys Lys Gly His Arg Val Asp Asp Ser Phe Asp Val Phe Ala Val His
 305 310 315 320
 Gly Met Ala Gly Ile Ala Gly Ala Leu Phe Val Met Leu Phe Gly Asp
 325 330 335
 Pro Leu Ala Pro Ala Gly Val Ser Gly Val Phe Phe Gly Gly Glu Leu
 340 345 350
 Ser Leu Leu Trp Arg Glu Pro Leu Ala Ile Ile Val Thr Leu Thr Tyr
 355 360 365

Ala Phe Gly Val Thr Trp Leu Ile Ala Thr Ile Leu Asn Lys Phe Met
 370 375 380

Thr Leu Arg Ile Thr Ser Glu Ala Glu Tyr Glu Gly Ile Asp Arg Ala
 385 390 395 400

Glu His Ala Glu Ser Ala Tyr His Leu Asn Ser Asn Gly Ile Gly Met
 405 410 415

Ala Thr Arg Thr Asn Phe Gly Pro Glu Ile Pro Glu Glu Thr Val Pro
 420 425 430

Asp Ala Val Gln Val Gly Val Asp Lys Gln Lys Ile Ala Asp Thr Arg
 435 440 445

Lys Ala Ser Lys
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<210> 399
 <211> 1111
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1111)
 <223> RXA02020

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cattttcata accagtgccca tgtgggttta cggttgatac atg gct aaa tct aat 115
 Met Ala Lys Ser Asn
 1 5

gaa ggg ctg gga acc gga ctt cgg acc cgc cac ctc aca atg atg gga 163
 Glu Gly Leu Gly Thr Gly Leu Arg Thr Arg His Leu Thr Met Met Gly
 10 15 20

ctc ggc tcc gca att ggt gcc gga ctg ttc ctc ggc acc ggc gtt ggt 211
 Leu Gly Ser Ala Ile Gly Ala Gly Leu Phe Leu Gly Thr Gly Val Gly
 25 30 35

atc cgc gca gcc ggc ccc gca gtg ctc ctg gcg tac atc atc gcc gga 259
 Ile Arg Ala Ala Gly Pro Ala Val Leu Leu Ala Tyr Ile Ile Ala Gly
 40 45 50

gcc atc gtt gtg ctt gtt atg caa atg ctc ggc gag atg gct gct gcc 307
 Ala Ile Val Val Leu Val Met Gln Met Leu Gly Glu Met Ala Ala Ala
 55 60 65

cgt ccc gcc tcc gga tcg ttt tca cgt tac ggc gag gat gct ttc ggc 355
 Arg Pro Ala Ser Gly Ser Phe Ser Arg Tyr Gly Glu Asp Ala Phe Gly
 70 75 80 85

cac tgg gct ggt ttc tcc ctc ggt tgg ttg tac tgg ttc atg ctg att 403
 His Trp Ala Gly Phe Ser Leu Gly Trp Leu Tyr Trp Phe Met Leu Ile
 90 95 100

atg gtg atg ggc gcc gaa atg act ggc gct gct gcc atc atg ggt gca 451

Met Val Met Gly Ala Glu Met Thr Gly Ala Ala Ala Ile Met Gly Ala	
105 110 115	
tgg ttc ggc gtc gaa ccg tgg att cct tcg ctt gtc tgc gtg gtc ttc	499
Trp Phe Gly Val Glu Pro Trp Ile Pro Ser Leu Val Cys Val Val Phe	
120 125 130	
ttc gct gtg gtg aac ctc gtc gcg gtt cgc ggt ttc ggt gaa ttc gag	547
Phe Ala Val Val Asn Leu Val Ala Val Arg Gly Phe Gly Glu Phe Glu	
135 140 145	
tac tgg ttc gca ttc att aag gtc gcg gtg atc atc gct ttc ctc atc	595
Tyr Trp Phe Ala Phe Ile Lys Val Ala Val Ile Ile Ala Phe Leu Ile	
150 155 160 165	
att ggt att gct ctt att ttc gga tgg ctt ccc gga tcc acc ttt gtt	643
Ile Gly Ile Ala Leu Ile Phe Gly Trp Leu Pro Gly Ser Thr Phe Val	
170 175 180	
gga acc tca aac ttc atc ggt gat cac gga ttc atg ccc aat ggt att	691
Gly Thr Ser Asn Phe Ile Gly Asp His Gly Phe Met Pro Asn Gly Ile	
185 190 195	
tct ggt gtt gct gct ggt ttg ctc gcg gtg gct ttt gcc ttt ggt ggc	739
Ser Gly Val Ala Ala Gly Leu Leu Ala Val Ala Phe Ala Phe Gly Gly	
200 205 210	
att gaa att gtc acc att gca gct gca gag tcc gat aag cca cgt gaa	787
Ile Glu Ile Val Thr Ile Ala Ala Ala Glu Ser Asp Lys Pro Arg Glu	
215 220 225	
gct att tcc ctg gcg gtg cgt gcc gtg att tgg cgt att tca gtc ttt	835
Ala Ile Ser Leu Ala Val Arg Ala Val Ile Trp Arg Ile Ser Val Phe	
230 235 240 245	
tac ttg ggc tct gtt ttg gtc atc act ttc ctc atg cct tat gag tcg	883
Tyr Leu Gly Ser Val Leu Val Ile Thr Phe Leu Met Pro Tyr Glu Ser	
250 255 260	
atc aat ggt gcc gac acc gct gcg gaa tcc ccc ttc acc caa atc ctg	931
Ile Asn Gly Ala Asp Thr Ala Ala Glu Ser Pro Phe Thr Gln Ile Leu	
265 270 275	
gcg atg gca aac atc cct ggc acg gtt ggt ttc atg gaa gcg atc atc	979
Ala Met Ala Asn Ile Pro Gly Thr Val Gly Phe Met Glu Ala Ile Ile	
280 285 290	
gtt cta gca ctg ctt tcc gct ttc aac gcc caa atc tat gcc act tct	1027
Val Leu Ala Leu Leu Ser Ala Phe Asn Ala Gln Ile Tyr Ala Thr Ser	
295 300 305	
cgt ttg gta ttt tcc atg gcg aat cga caa gac gct ccg cga gtt ttc	1075
Arg Leu Val Phe Ser Met Ala Asn Arg Gln Asp Ala Pro Arg Val Phe	
310 315 320 325	
agt aag ctc agc acc agc cac gtc ccc acc aat gcg	1111
Ser Lys Leu Ser Thr Ser His Val Pro Thr Asn Ala	
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<210> 400

<211> 337

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 400

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Leu Thr Met Met Gly Leu Gly Ser Ala Ile Gly Ala Gly Leu Phe Leu
      20              25              30

Gly Thr Gly Val Gly Ile Arg Ala Ala Gly Pro Ala Val Leu Leu Ala
      35              40              45

Tyr Ile Ile Ala Gly Ala Ile Val Val Leu Val Met Gln Met Leu Gly
      50              55              60

Glu Met Ala Ala Ala Arg Pro Ala Ser Gly Ser Phe Ser Arg Tyr Gly
      65              70              75              80

Glu Asp Ala Phe Gly His Trp Ala Gly Phe Ser Leu Gly Trp Leu Tyr
      85              90              95

Trp Phe Met Leu Ile Met Val Met Gly Ala Glu Met Thr Gly Ala Ala
      100             105             110

Ala Ile Met Gly Ala Trp Phe Gly Val Glu Pro Trp Ile Pro Ser Leu
      115             120             125

Val Cys Val Val Phe Phe Ala Val Val Asn Leu Val Ala Val Arg Gly
      130             135             140

Phe Gly Glu Phe Glu Tyr Trp Phe Ala Phe Ile Lys Val Ala Val Ile
      145             150             155             160

Ile Ala Phe Leu Ile Ile Gly Ile Ala Leu Ile Phe Gly Trp Leu Pro
      165             170             175

Gly Ser Thr Phe Val Gly Thr Ser Asn Phe Ile Gly Asp His Gly Phe
      180             185             190

Met Pro Asn Gly Ile Ser Gly Val Ala Ala Gly Leu Leu Ala Val Ala
      195             200             205

Phe Ala Phe Gly Gly Ile Glu Ile Val Thr Ile Ala Ala Ala Glu Ser
      210             215             220

Asp Lys Pro Arg Glu Ala Ile Ser Leu Ala Val Arg Ala Val Ile Trp
      225             230             235             240

Arg Ile Ser Val Phe Tyr Leu Gly Ser Val Leu Val Ile Thr Phe Leu
      245             250             255

Met Pro Tyr Glu Ser Ile Asn Gly Ala Asp Thr Ala Ala Glu Ser Pro
      260             265             270

Phe Thr Gln Ile Leu Ala Met Ala Asn Ile Pro Gly Thr Val Gly Phe
      275             280             285

Met Glu Ala Ile Ile Val Leu Ala Leu Leu Ser Ala Phe Asn Ala Gln
      290             295             300

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Ile Tyr Ala Thr Ser Arg Leu Val Phe Ser Met Ala Asn Arg Gln Asp
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Ala Pro Arg Val Phe Ser Lys Leu Ser Thr Ser His Val Pro Thr Asn
 325 330 335

Ala

<210> 401

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> RXA00281

<400> 401

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actgaacaca acagagtagg tttatgcgac actggtgcgc atg atc aac gtt gaa 115
                                         Met Ile Asn Val Glu
                                         1 5

ggc ctc acc aaa caa tat ggt cag gtc cgc gca gtc gat gat ctg agc 163
Gly Leu Thr Lys Gln Tyr Gly Gln Val Arg Ala Val Asp Asp Leu Ser
                        10 15 20

ttc gaa gta aaa ccc gga ata gtc acc gga ttt ctc ggc ccc aac ggc 211
Phe Glu Val Lys Pro Gly Ile Val Thr Gly Phe Leu Gly Pro Asn Gly
                        25 30 35

gcc gga aaa tcc acc acg atg cgg ctg atc ctt ggc tta gat aat cca 259
Ala Gly Lys Ser Thr Thr Met Arg Leu Ile Leu Gly Leu Asp Asn Pro
                        40 45 50

act gca ggg cat gcc acg atc gaa gga caa ccc tac cga tcg ctc aaa 307
Thr Ala Gly His Ala Thr Ile Glu Gly Gln Pro Tyr Arg Ser Leu Lys
                        55 60 65

aat ccc ctg acc aaa gtg gga gca ctg ctt gat gcc aaa gca aca cac 355
Asn Pro Leu Thr Lys Val Gly Ala Leu Leu Asp Ala Lys Ala Thr His
                        70 75 80 85

cca aat aga aca gca gaa aac cac ctc aag tgg atc gcc cgt gca aat 403
Pro Asn Arg Thr Ala Glu Asn His Leu Lys Trp Ile Ala Arg Ala Asn
                        90 95 100

ggg ctg tcc acc aaa aga gtc gat gaa gtt ctc acc ctc gtg gga ctg 451
Gly Leu Ser Thr Lys Arg Val Asp Glu Val Leu Thr Leu Val Gly Leu
                        105 110 115

act ggt gtt ggg tca aag aag acc ggt ggg ttt tca cta ggc atg ggc 499
Thr Gly Val Gly Ser Lys Lys Thr Gly Gly Phe Ser Leu Gly Met Gly
                        120 125 130

caa cgt cta gga ctt gct gca gca ttg ctc ggc gat ccg gaa tac tta 547

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Gln Arg Leu Gly Leu Ala Ala Ala Leu Leu Gly Asp Pro Glu Tyr Leu
 135 140 145
 att ctc gac gaa ccc gtc aac ggc ctt gac cca gaa ggc att cac tgg 595
 Ile Leu Asp Glu Pro Val Asn Gly Leu Asp Pro Glu Gly Ile His Trp
 150 155 160 165
 gtg cgc acc ttg ttg caa aac atc gcc aag cag ggc aga acc gtg ctc 643
 Val Arg Thr Leu Leu Gln Asn Ile Ala Lys Gln Gly Arg Thr Val Leu
 170 175 180
 gtg agt tcc cac ctg ctg tcc gag atg gcg caa act gcg gaa cat ttg 691
 Val Ser Ser His Leu Leu Ser Glu Met Ala Gln Thr Ala Glu His Leu
 185 190 195
 atc gtg att ggg cgt ggc aag ctg gtc gcc gat atg ccc atg cat gag 739
 Ile Val Ile Gly Arg Gly Lys Leu Val Ala Asp Met Pro Met His Glu
 200 205 210
 ttt gtg cgc tcc cat tcc gct tcc aca gtt gtg gtg cgg gca gca 784
 Phe Val Arg Ser His Ser Ala Ser Thr Val Val Val Arg Ala Ala
 215 220 225
 <210> 402
 <211> 228
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 <213> Corynebacterium glutamicum
 <400> 402
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 20 25 30
 Leu Gly Pro Asn Gly Ala Gly Lys Ser Thr Thr Met Arg Leu Ile Leu
 35 40 45
 Gly Leu Asp Asn Pro Thr Ala Gly His Ala Thr Ile Glu Gly Gln Pro
 50 55 60
 Tyr Arg Ser Leu Lys Asn Pro Leu Thr Lys Val Gly Ala Leu Leu Asp
 65 70 75 80
 Ala Lys Ala Thr His Pro Asn Arg Thr Ala Glu Asn His Leu Lys Trp
 85 90 95
 Ile Ala Arg Ala Asn Gly Leu Ser Thr Lys Arg Val Asp Glu Val Leu
 100 105 110
 Thr Leu Val Gly Leu Thr Gly Val Gly Ser Lys Lys Thr Gly Gly Phe
 115 120 125
 Ser Leu Gly Met Gly Gln Arg Leu Gly Leu Ala Ala Ala Leu Leu Gly
 130 135 140
 Asp Pro Glu Tyr Leu Ile Leu Asp Glu Pro Val Asn Gly Leu Asp Pro
 145 150 155 160
 Glu Gly Ile His Trp Val Arg Thr Leu Leu Gln Asn Ile Ala Lys Gln

	165		170		175
Gly Arg Thr Val Leu Val Ser Ser His Leu Leu Ser Glu Met Ala Gln					
	180		185		190
Thr Ala Glu His Leu Ile Val Ile Gly Arg Gly Lys Leu Val Ala Asp					
	195		200		205
Met Pro Met His Glu Phe Val Arg Ser His Ser Ala Ser Thr Val Val					
	210		215		220
Val Arg Ala Ala					
225					

<210> 403

<211> 852

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(852)

<223> RXN00570

<400> 403

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Thr Arg Pro Arg Pro Gln Glu Ile Gly Asn Gly Leu Val Ala Leu Ile	
1 5 10 15	
ttc tcc gca tcc gga ccc atc gca gtg atc ctg gct gct gct gca gcg	96
Phe Ser Ala Ser Gly Pro Ile Ala Val Ile Leu Ala Ala Ala Ala	
20 25 30	
gga aac ctt tcg cct gat caa aca tct tca tgg atc ttc gga gca ttt	144
Gly Asn Leu Ser Pro Asp Gln Thr Ser Ser Trp Ile Phe Gly Ala Phe	
35 40 45	
tta ggc aac gga ctg ctc acg ctg tgg ctt acc tat atg tac cgc agc	192
Leu Gly Asn Gly Leu Leu Thr Leu Trp Leu Thr Tyr Met Tyr Arg Ser	
50 55 60	
ccg cag gca tac ttc tgg acg att ccc gga acc gtc atc gtg ggc gac	240
Pro Gln Ala Tyr Phe Trp Thr Ile Pro Gly Thr Val Ile Val Gly Asp	
65 70 75 80	
tca ctt acc cac tta agt ttc gct gaa gtt atc ggc gca tac ctt gtt	288
Ser Leu Thr His Leu Ser Phe Ala Glu Val Ile Gly Ala Tyr Leu Val	
85 90 95	
acc ggc gtt gtg gtg ttt gcg ctc gga tgg acc ggt ctc atc gga cgg	336
Thr Gly Val Val Val Phe Ala Leu Gly Trp Thr Gly Leu Ile Gly Arg	
100 105 110	
atc atg gcg gta ctg cca cca acc atc gtg atg gcc atg gtc gca ggc	384
Ile Met Ala Val Leu Pro Pro Thr Ile Val Met Ala Met Val Ala Gly	
115 120 125	
att ttc ctc cgc ttc gga ctc gac ctc atc gac gcc agc gtg acc gac	432
Ile Phe Leu Arg Phe Gly Leu Asp Leu Ile Asp Ala Ser Val Thr Asp	
130 135 140	

ccg ctc att gca ctt ccc atg gtc ata gtt ttt gtg gca ttg agc atg 480
 Pro Leu Ile Ala Leu Pro Met Val Ile Val Phe Val Ala Leu Ser Met
 145 150 155 160
 agt ccc cgc ttg gca agc atc gcc cca ccc gtt gca gta gcc gca gta 528
 Ser Pro Arg Leu Ala Ser Ile Ala Pro Pro Val Ala Val Ala Ala Val
 165 170 175
 gtg gga acc atc gtt gcc atc gca tcc ggc aaa cta gcg tcc gga att 576
 Val Gly Thr Ile Val Ala Ile Ala Ser Gly Lys Leu Ala Ser Gly Ile
 180 185 190
 cta gac aac gga att atc tcc cgc ccc gtc ttt acc gcc cca gaa ttt 624
 Leu Asp Asn Gly Ile Ile Ser Arg Pro Val Phe Thr Ala Pro Glu Phe
 195 200 205
 tcc ttc gcc gcc atc atg gaa ctc gtt gtt ccc ttg gcg atc acc gta 672
 Ser Phe Ala Ala Ile Met Glu Leu Val Val Pro Leu Ala Ile Thr Val
 210 215 220
 gtc att gtc caa aac ggc caa ggc gtc gca gtg ctt aaa gca gca ggt 720
 Val Ile Val Gln Asn Gly Gln Gly Val Ala Val Leu Lys Ala Ala Gly
 225 230 235 240
 cac cgc ccc gga gta aac ctt gcc gcc gcg gcc tcc gga ctg tgg tcc 768
 His Arg Pro Gly Val Asn Leu Ala Ala Ala Ala Ser Gly Leu Trp Ser
 245 250 255
 cta ccc atg gcg ttg atc ggc aac atc acc acc tgc ctc acc gcc ccc 816
 Leu Pro Met Ala Leu Ile Gly Asn Ile Thr Thr Cys Leu Thr Gly Pro
 260 265 270
 acc aac gcg ctg atc gtc gcc gga gca aaa tca cac 852
 Thr Asn Ala Leu Ile Val Ala Gly Ala Lys Ser His
 275 280

<210> 404

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

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 Phe Ser Ala Ser Gly Pro Ile Ala Val Ile Leu Ala Ala Ala Ala Ala
 20 25 30
 Gly Asn Leu Ser Pro Asp Gln Thr Ser Ser Trp Ile Phe Gly Ala Phe
 35 40 45
 Leu Gly Asn Gly Leu Leu Thr Leu Trp Leu Thr Tyr Met Tyr Arg Ser
 50 55 60
 Pro Gln Ala Tyr Phe Trp Thr Ile Pro Gly Thr Val Ile Val Gly Asp
 65 70 75 80
 Ser Leu Thr His Leu Ser Phe Ala Glu Val Ile Gly Ala Tyr Leu Val
 85 90 95

Thr Gly Val Val Val Phe Ala Leu Gly Trp Thr Gly Leu Ile Gly Arg
 100 105 110
 Ile Met Ala Val Leu Pro Pro Thr Ile Val Met Ala Met Val Ala Gly
 115 120 125
 Ile Phe Leu Arg Phe Gly Leu Asp Leu Ile Asp Ala Ser Val Thr Asp
 130 135 140
 Pro Leu Ile Ala Leu Pro Met Val Ile Val Phe Val Ala Leu Ser Met
 145 150 155 160
 Ser Pro Arg Leu Ala Ser Ile Ala Pro Pro Val Ala Val Ala Val
 165 170 175
 Val Gly Thr Ile Val Ala Ile Ala Ser Gly Lys Leu Ala Ser Gly Ile
 180 185 190
 Leu Asp Asn Gly Ile Ile Ser Arg Pro Val Phe Thr Ala Pro Glu Phe
 195 200 205
 Ser Phe Ala Ala Ile Met Glu Leu Val Val Pro Leu Ala Ile Thr Val
 210 215 220
 Val Ile Val Gln Asn Gly Gln Gly Val Ala Val Leu Lys Ala Ala Gly
 225 230 235 240
 His Arg Pro Gly Val Asn Leu Ala Ala Ala Ser Gly Leu Trp Ser
 245 250 255
 Leu Pro Met Ala Leu Ile Gly Asn Ile Thr Thr Cys Leu Thr Gly Pro
 260 265 270
 Thr Asn Ala Leu Ile Val Ala Gly Ala Lys Ser His
 275 280

<210> 405

<211> 498

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(498)

<223> FRXA00570

<400> 405

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 Pro Thr Ile Val Met Ala Met Val Ala Gly Ile Phe Leu Arg Phe Gly
 1 5 10 15

ctc gac ctc atc gac gcc agc gtg acc gac ccg ctc att gca ctt ccc 96
 Leu Asp Leu Ile Asp Ala Ser Val Thr Asp Pro Leu Ile Ala Leu Pro
 20 25 30

atg gtc ata gtt ttt gtg gca ttg agc atg agt ccc cgc ttg gca agc 144
 Met Val Ile Val Phe Val Ala Leu Ser Met Ser Pro Arg Leu Ala Ser
 35 40 45

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atc gcc cca ccc gtt gca gta gcc gca gta gtg gga acc atc gtt gcc 192
Ile Ala Pro Pro Val Ala Val Ala Ala Val Val Gly Thr Ile Val Ala
    50                      55                      60

atc gca tcc ggc aaa cta gcg tcc gga att cta gac aac gga att atc 240
Ile Ala Ser Gly Lys Leu Ala Ser Gly Ile Leu Asp Asn Gly Ile Ile
    65                      70                      75                      80

tcc cgc ccc gtc ttt acc gcc cca gaa ttt tcc ttc gcc gcc atc atg 288
Ser Arg Pro Val Phe Thr Ala Pro Glu Phe Ser Phe Ala Ala Ile Met
                      85                      90                      95

gaa ctc gtt gtt ccc ttg gcg atc acc gta gtc att gtc caa aac ggc 336
Glu Leu Val Val Pro Leu Ala Ile Thr Val Val Ile Val Gln Asn Gly
    100                      105                      110

caa ggc gtc gca gtg ctt aaa gca gca ggt cac cgc ccc gga gta aac 384
Gln Gly Val Ala Val Leu Lys Ala Ala Gly His Arg Pro Gly Val Asn
    115                      120                      125

ctt gcc gcc gcg gcc tcc gga ctg tgg tcc cta ccc atg gcg ttg atc 432
Leu Ala Ala Ala Ala Ser Gly Leu Trp Ser Leu Pro Met Ala Leu Ile
    130                      135                      140

ggc aac atc acc acc tgc ctc acc ggc ccc acc aac gcg ctg atc gtc 480
Gly Asn Ile Thr Thr Cys Leu Thr Gly Pro Thr Asn Ala Leu Ile Val
    145                      150                      155                      160

gcc gga gca aaa tca cac 498
Ala Gly Ala Lys Ser His
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<210> 406

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 406

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    20                      25                      30

Met Val Ile Val Phe Val Ala Leu Ser Met Ser Pro Arg Leu Ala Ser
    35                      40                      45

Ile Ala Pro Pro Val Ala Val Ala Ala Val Val Gly Thr Ile Val Ala
    50                      55                      60

Ile Ala Ser Gly Lys Leu Ala Ser Gly Ile Leu Asp Asn Gly Ile Ile
    65                      70                      75                      80

Ser Arg Pro Val Phe Thr Ala Pro Glu Phe Ser Phe Ala Ala Ile Met
    85                      90                      95

Glu Leu Val Val Pro Leu Ala Ile Thr Val Val Ile Val Gln Asn Gly
    100                      105                      110

Gln Gly Val Ala Val Leu Lys Ala Ala Gly His Arg Pro Gly Val Asn

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115 120 125
 Leu Ala Ala Ala Ala Ser Gly Leu Trp Ser Leu Pro Met Ala Leu Ile
 130 135 140
 Gly Asn Ile Thr Thr Cys Leu Thr Gly Pro Thr Asn Ala Leu Ile Val
 145 150 155 160
 Ala Gly Ala Lys Ser His
 165

<210> 407
 <211> 1280
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1257)
 <223> RXN00571

<400> 407
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 tca gct gta cat gaa gat cca acc cag atc ggt gcg ctc agc cca gca 96
 Ser Ala Val His Glu Asp Pro Thr Gln Ile Gly Ala Leu Ser Pro Ala
 20 25 30
 gtc gcc ggc acc ctt ggt tcc tac gcc atg atc ggc gtg atg atc ggt 144
 Val Ala Gly Thr Leu Gly Ser Tyr Ala Met Ile Gly Val Met Ile Gly
 35 40 45
 gct cta tct gca ggt gcc gtt ggt gac cgc ctt ggt cgt cgc aaa gtt 192
 Ala Leu Ser Ala Gly Ala Val Gly Asp Arg Leu Gly Arg Arg Lys Val
 50 55 60
 atg ctc acc gca atc gtc tgg ttc tct gtg ggc atg gcg ctg acc gcg 240
 Met Leu Thr Ala Ile Val Trp Phe Ser Val Gly Met Ala Leu Thr Ala
 65 70 75 80
 ttc gcg tcc tcg att gcg ctg ttc ggt ttc ttg cgc ttc ctc acc gga 288
 Phe Ala Ser Ser Ile Ala Leu Phe Gly Phe Leu Arg Phe Leu Thr Gly
 85 90 95
 ctt ggc gtg ggc atg atc gtt gca acc ggc ggc gca atc atc gcg gag 336
 Leu Gly Val Gly Met Ile Val Ala Thr Gly Gly Ala Ile Ile Ala Glu
 100 105 110
 ttc gct cca gcg aat agg cgc aac ttg ttc aac gca atc gtg tac tcc 384
 Phe Ala Pro Ala Asn Arg Arg Asn Leu Phe Asn Ala Ile Val Tyr Ser
 115 120 125
 ggt gtc cca gcc ggt ggc gtg ctg gct tct atc ctt gca ctg ctc ttt 432
 Gly Val Pro Ala Gly Gly Leu Ala Ser Ile Leu Ala Leu Leu Phe
 130 135 140
 gaa gat gtc atc ggc tgg cgc gga ctc ttc ctc atc ggt gga tcc cca 480
 Glu Asp Val Ile Gly Trp Arg Gly Leu Phe Leu Ile Gly Gly Ser Pro

145	150	155	160	
cta ctg ttc ctc ctg cca ctt gca tac ttc ttc ctc cca gag tcc ccg Leu Leu Phe Leu Leu Pro Leu Ala Tyr Phe Phe Leu Pro Glu Ser Pro	165	170	175	528
cgc tgg ctc acc tcc cgc ggc cgt gct gcg gac gcc aaa gcc ctc tgc Arg Trp Leu Thr Ser Arg Gly Arg Ala Ala Asp Ala Lys Ala Leu Cys	180	185	190	576
gca cgc tat ggg ctg ccg acg gag gaa ttt gtc gtc gaa aag cag cag Ala Arg Tyr Gly Leu Pro Thr Glu Glu Phe Val Val Glu Lys Gln Gln	195	200	205	624
gaa aca aag ggc acc gga ttc gct gga att ttc tcc tcc aag tac ctc Glu Thr Lys Gly Thr Gly Phe Ala Gly Ile Phe Ser Ser Lys Tyr Leu	210	215	220	672
atg ggc acc att ctc atc ggc gca atg agc ttc atc ggg ctg ctt tcg Met Gly Thr Ile Leu Ile Gly Ala Met Ser Phe Ile Gly Leu Leu Ser	225	230	235	720
acc tac ggc ctg aac acc tgg ttg cca aag atc atg gaa tcc aac ggc Thr Tyr Gly Leu Asn Thr Trp Leu Pro Lys Ile Met Glu Ser Asn Gly	245	250	255	768
gca acc tca cat gat tcc ctg tac tcc ctg ctg ttc ctc aac ggc ggc Ala Thr Ser His Asp Ser Leu Tyr Ser Leu Leu Phe Leu Asn Gly Gly	260	265	270	816
gca gtg ttc ggt ggc ctc atc gca tcc tgg ttc gct gac cgc atc ggc Ala Val Phe Gly Gly Leu Ile Ala Ser Trp Phe Ala Asp Arg Ile Gly	275	280	285	864
gcg aag acc gtg atc acc tcc acc ttc gct ctc gcc gcg atc tgc ctc Ala Lys Thr Val Ile Thr Ser Thr Phe Ala Leu Ala Ala Ile Cys Leu	290	295	300	912
gga gtc ctg cca aac atc tcc tcc tgg cca atg atg tac acc gca atc Gly Val Leu Pro Asn Ile Ser Ser Trp Pro Met Met Tyr Thr Ala Ile	305	310	315	960
gca ttc gca ggc gtc ggc gtc ctg ggc acc cag gtt ctc acc tac ggc Ala Phe Ala Gly Val Gly Val Leu Gly Thr Gln Val Leu Thr Tyr Gly	325	330	335	1008
ctg acc tcg aac ttc ttc gga acc gaa tgc cgc gca gcg gga gtt gca Leu Thr Ser Asn Phe Phe Gly Thr Glu Cys Arg Ala Ala Gly Val Ala	340	345	350	1056
tgg tgt gca gga ttc ggc cga ctc ggc gga atc gtc gga cca gca atc Trp Cys Ala Gly Phe Gly Arg Leu Gly Gly Ile Val Gly Pro Ala Ile	355	360	365	1104
ggt ggc ctg atc atc ggc gca gga ttc gga cca agc tcc gca ttc ctc Gly Gly Leu Ile Ile Gly Ala Gly Phe Gly Pro Ser Ser Ala Phe Leu	370	375	380	1152
atc ttc gca gca gct gcc gca atc ggc gcg gtc tgc acc ttg ctg atc Ile Phe Ala Ala Ala Ala Ala Ile Gly Ala Val Cys Thr Leu Leu Ile	385	390	395	1200
			400	

ccg cgc tcc cca gca gaa gta gag gtc aag gtc gcg cag gaa cca ctt 1248
 Pro Arg Ser Pro Ala Glu Val Glu Val Lys Val Ala Gln Glu Pro Leu
 405 410 415

gca cgt gtc taacccaat taattcgaaa caa 1280
 Ala Arg Val

<210> 408

<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 408

Thr Leu Val Pro Gln Val Tyr Glu Ile Val Ile Tyr Gly Ala Val Leu
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Ser Ala Val His Glu Asp Pro Thr Gln Ile Gly Ala Leu Ser Pro Ala
 20 25 30

Val Ala Gly Thr Leu Gly Ser Tyr Ala Met Ile Gly Val Met Ile Gly
 35 40 45

Ala Leu Ser Ala Gly Ala Val Gly Asp Arg Leu Gly Arg Arg Lys Val
 50 55 60

Met Leu Thr Ala Ile Val Trp Phe Ser Val Gly Met Ala Leu Thr Ala
 65 70 75 80

Phe Ala Ser Ser Ile Ala Leu Phe Gly Phe Leu Arg Phe Leu Thr Gly
 85 90 95

Leu Gly Val Gly Met Ile Val Ala Thr Gly Gly Ala Ile Ile Ala Glu
 100 105 110

Phe Ala Pro Ala Asn Arg Arg Asn Leu Phe Asn Ala Ile Val Tyr Ser
 115 120 125

Gly Val Pro Ala Gly Gly Val Leu Ala Ser Ile Leu Ala Leu Leu Phe
 130 135 140

Glu Asp Val Ile Gly Trp Arg Gly Leu Phe Leu Ile Gly Gly Ser Pro
 145 150 155 160

Leu Leu Phe Leu Leu Pro Leu Ala Tyr Phe Phe Leu Pro Glu Ser Pro
 165 170 175

Arg Trp Leu Thr Ser Arg Gly Arg Ala Ala Asp Ala Lys Ala Leu Cys
 180 185 190

Ala Arg Tyr Gly Leu Pro Thr Glu Glu Phe Val Val Glu Lys Gln Gln
 195 200 205

Glu Thr Lys Gly Thr Gly Phe Ala Gly Ile Phe Ser Ser Lys Tyr Leu
 210 215 220

Met Gly Thr Ile Leu Ile Gly Ala Met Ser Phe Ile Gly Leu Leu Ser
 225 230 235 240

Ser Val Gly Met Ala Leu Thr Ala Phe Ala Ser Ser Ile Ala Leu Phe	
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ggt ttc ttg cgc ttc ctc acc gga ctt ggc gtg ggc atg atc gtt gca	240
Gly Phe Leu Arg Phe Leu Thr Gly Leu Gly Val Gly Met Ile Val Ala	
65 70 75 80	
acc ggc ggc gca atc atc gcg gag ttc gct cca gcg aat agg cgc aac	288
Thr Gly Gly Ala Ile Ile Ala Glu Phe Ala Pro Ala Asn Arg Arg Asn	
85 90 95	
ttg ttc aac gca atc gtg tac tcc ggt gtc cca gcc ggt ggc gtg ctg	336
Leu Phe Asn Ala Ile Val Tyr Ser Gly Val Pro Ala Gly Gly Val Leu	
100 105 110	
gct tct atc ctt gca ctg ctc ttt gaa gat gtc atc ggc tgg cgc gga	384
Ala Ser Ile Leu Ala Leu Leu Phe Glu Asp Val Ile Gly Trp Arg Gly	
115 120 125	
ctc ttc ctc atc ggt gga tcc cca cta ctg ttc ctc ctg cca ctt gca	432
Leu Phe Leu Ile Gly Gly Ser Pro Leu Leu Phe Leu Leu Pro Leu Ala	
130 135 140	
tac ttc ttc ctc cca gag tcc ccg cgc tgg ctc acc tcc cgc ggc cgt	480
Tyr Phe Phe Leu Pro Glu Ser Pro Arg Trp Leu Thr Ser Arg Gly Arg	
145 150 155 160	
gct gcg gac gcc aaa gcc ctc tgc gca cgc tat ggg ctg ccg acg gag	528
Ala Ala Asp Ala Lys Ala Leu Cys Ala Arg Tyr Gly Leu Pro Thr Glu	
165 170 175	
gaa ttt gtc gtc gaa aag cag cag gaa aca aag ggc acc gga ttc gct	576
Glu Phe Val Val Glu Lys Gln Gln Glu Thr Lys Gly Thr Gly Phe Ala	
180 185 190	
gga att ttc tcc tcc aag tac ctc atg ggc acc att ctc atc ggc gca	624
Gly Ile Phe Ser Ser Lys Tyr Leu Met Gly Thr Ile Leu Ile Gly Ala	
195 200 205	
atg agc ttc atc ggg ctg ctt tcg acc tac ggc ctg aac acc tgg ttg	672
Met Ser Phe Ile Gly Leu Leu Ser Thr Tyr Gly Leu Asn Thr Trp Leu	
210 215 220	
cca aag atc atg gaa tcc aac ggc gca acc tca cat gat tcc ctg tac	720
Pro Lys Ile Met Glu Ser Asn Gly Ala Thr Ser His Asp Ser Leu Tyr	
225 230 235 240	
tcc ctg ctg ttc ctc aac ggc ggc gca gtg ttc ggt ggc ctc atc gca	768
Ser Leu Leu Phe Leu Asn Gly Gly Ala Val Phe Gly Gly Leu Ile Ala	
245 250 255	
tcc tgg ttc gct gac cgc atc ggc gcg aag acc gtg atc acc tcc acc	816
Ser Trp Phe Ala Asp Arg Ile Gly Ala Lys Thr Val Ile Thr Ser Thr	
260 265 270	
ttc gct ctc gcc gcg atc tgc ctc gga gtc ctg cca aac atc tcc tcc	864
Phe Ala Leu Ala Ala Ile Cys Leu Gly Val Leu Pro Asn Ile Ser Ser	
275 280 285	
tgg cca atg atg tac acc gca atc gca ttc gca ggc gtc ggc gtc ctg	912
Trp Pro Met Met Tyr Thr Ala Ile Ala Phe Ala Gly Val Gly Val Leu	

290	295	300	
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Gly Thr Gln Val Leu Thr Tyr Gly Leu Thr Ser Asn Phe Phe Gly Thr			
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gaa tgc cgc gca gcg gga gtt gca tgg tgt gca gga ttc ggc cga ctc			1008
Glu Cys Arg Ala Ala Gly Val Ala Trp Cys Ala Gly Phe Gly Arg Leu			
	325	330	335
ggc gga atc gtc gga cca gca atc ggt ggc ctg atc atc ggc gca gga			1056
Gly Gly Ile Val Gly Pro Ala Ile Gly Gly Leu Ile Ile Gly Ala Gly			
	340	345	350
ttc gga cca agc tcc gca ttc ctc atc ttc gca gca gct gcc gca atc			1104
Phe Gly Pro Ser Ser Ala Phe Leu Ile Phe Ala Ala Ala Ala Ala Ile			
	355	360	365
ggc gcg gtc tgc acc ttg ctg atc ccg cgc tcc cca gca gaa gta gag			1152
Gly Ala Val Cys Thr Leu Leu Ile Pro Arg Ser Pro Ala Glu Val Glu			
	370	375	380
gtc aag gtc gcg cag gaa cca ctt gca cgt gtc taaccccaat taattcgaaa			1205
Val Lys Val Ala Gln Glu Pro Leu Ala Arg Val			
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<210> 410

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 410

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Ala	Met	Ile	Gly	Val	Met	Ile	Gly	Ala	Leu	Ser	Ala	Gly	Ala	Val	Gly
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Asp	Arg	Leu	Gly	Arg	Arg	Lys	Val	Met	Leu	Thr	Ala	Ile	Val	Trp	Phe
		35					40					45			

Ser	Val	Gly	Met	Ala	Leu	Thr	Ala	Phe	Ala	Ser	Ser	Ile	Ala	Leu	Phe
	50					55					60				

Gly	Phe	Leu	Arg	Phe	Leu	Thr	Gly	Leu	Gly	Val	Gly	Met	Ile	Val	Ala
65					70					75					80

Thr	Gly	Gly	Ala	Ile	Ile	Ala	Glu	Phe	Ala	Pro	Ala	Asn	Arg	Arg	Asn
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Leu	Phe	Asn	Ala	Ile	Val	Tyr	Ser	Gly	Val	Pro	Ala	Gly	Gly	Val	Leu
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Ala	Ser	Ile	Leu	Ala	Leu	Leu	Phe	Glu	Asp	Val	Ile	Gly	Trp	Arg	Gly
		115					120					125			

Leu	Phe	Leu	Ile	Gly	Gly	Ser	Pro	Leu	Leu	Phe	Leu	Leu	Pro	Leu	Ala
130						135					140				

Tyr Phe Phe Leu Pro Glu Ser Pro Arg Trp Leu Thr Ser Arg Gly Arg
 145 150 155 160
 Ala Ala Asp Ala Lys Ala Leu Cys Ala Arg Tyr Gly Leu Pro Thr Glu
 165 170 175
 Glu Phe Val Val Glu Lys Gln Gln Glu Thr Lys Gly Thr Gly Phe Ala
 180 185 190
 Gly Ile Phe Ser Ser Lys Tyr Leu Met Gly Thr Ile Leu Ile Gly Ala
 195 200 205
 Met Ser Phe Ile Gly Leu Leu Ser Thr Tyr Gly Leu Asn Thr Trp Leu
 210 215 220
 Pro Lys Ile Met Glu Ser Asn Gly Ala Thr Ser His Asp Ser Leu Tyr
 225 230 235 240
 Ser Leu Leu Phe Leu Asn Gly Gly Ala Val Phe Gly Gly Leu Ile Ala
 245 250 255
 Ser Trp Phe Ala Asp Arg Ile Gly Ala Lys Thr Val Ile Thr Ser Thr
 260 265 270
 Phe Ala Leu Ala Ala Ile Cys Leu Gly Val Leu Pro Asn Ile Ser Ser
 275 280 285
 Trp Pro Met Met Tyr Thr Ala Ile Ala Phe Ala Gly Val Gly Val Leu
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 Gly Thr Gln Val Leu Thr Tyr Gly Leu Thr Ser Asn Phe Phe Gly Thr
 305 310 315 320
 Glu Cys Arg Ala Ala Gly Val Ala Trp Cys Ala Gly Phe Gly Arg Leu
 325 330 335
 Gly Gly Ile Val Gly Pro Ala Ile Gly Gly Leu Ile Ile Gly Ala Gly
 340 345 350
 Phe Gly Pro Ser Ser Ala Phe Leu Ile Phe Ala Ala Ala Ala Ile
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 Gly Ala Val Cys Thr Leu Leu Ile Pro Arg Ser Pro Ala Glu Val Glu
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 Val Lys Val Ala Gln Glu Pro Leu Ala Arg Val
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<211> 689

<212> DNA

<213> Corynebacterium glutamicum

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<222> (1)..(666)

<223> RXA00962

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cca gca ggt ttc aag gat ctg ctt gtc gat cgc tac cgc tgg atc tcc	96
Pro Ala Gly Phe Lys Asp Leu Leu Val Asp Arg Tyr Arg Trp Ile Ser	
20 25 30	
att tgg ttc gcg ctc gcc aca ttt gtc acc ctg ctc gcg tgg tac gga	144
Ile Trp Phe Ala Leu Ala Thr Phe Val Thr Leu Leu Ala Trp Tyr Gly	
35 40 45	
ctg ggc aca tgg ttg cct cgc ctc atg gaa act gca ggt tat gag ttc	192
Leu Gly Thr Trp Leu Pro Arg Leu Met Glu Thr Ala Gly Tyr Glu Phe	
50 55 60	
ggc cat gca ttg atg ttc acc ctg gct ctg aac ctc ggt gca gtg atc	240
Gly His Ala Leu Met Phe Thr Leu Ala Leu Asn Leu Gly Ala Val Ile	
65 70 75 80	
gga tcc gtg gtt act gcg tgg gcc ggc gat cgc ttc ggg cca atc cgt	288
Gly Ser Val Val Thr Ala Trp Ala Gly Asp Arg Phe Gly Pro Ile Arg	
85 90 95	
tcc ggt gtc atc gct gca ggt atc gcc ggt att gca ctg ctc ctg ctg	336
Ser Gly Val Ile Ala Ala Gly Ile Ala Gly Ile Ala Leu Leu Leu Leu	
100 105 110	
ctc act tac ccg cct gtc acc gcg gtt tat gtc att ctc att ttg gct	384
Leu Thr Tyr Pro Pro Val Thr Ala Val Tyr Val Ile Leu Ile Leu Ala	
115 120 125	
ggc gtg ggc acc cac ggc act cag atc ctc atc att gca gct gtc gcc	432
Gly Val Gly Thr His Gly Thr Gln Ile Leu Ile Ile Ala Ala Val Ala	
130 135 140	
aac ttc tac cca agc aac ctg cgt ggc aca gca ctg ggc tgg gcg cta	480
Asn Phe Tyr Pro Ser Asn Leu Arg Gly Thr Ala Leu Gly Trp Ala Leu	
145 150 155 160	
ggc gta ggt cgt att ggt gct gtt gtg gcc ccg cag ctc gct ggc ctg	528
Gly Val Gly Arg Ile Gly Ala Val Val Ala Pro Gln Leu Ala Gly Leu	
165 170 175	
ctg ctg gca tgg aac ttg ggc gtg aac tcc aac ttc atc atg ttc ggc	576
Leu Leu Ala Trp Asn Leu Gly Val Asn Ser Asn Phe Ile Met Phe Gly	
180 185 190	
acc gct gcg ctg ctc tct gcg ctg gct ctc agc gtg ttg ctg cgc ctg	624
Thr Ala Ala Leu Leu Ser Ala Leu Ala Leu Ser Val Leu Leu Arg Leu	
195 200 205	
cag aaa acc tac agc gtc acc cac aaa gtc gaa atc caa ggc	666
Gln Lys Thr Tyr Ser Val Thr His Lys Val Glu Ile Gln Gly	
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<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

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 20 25 30

Ile Trp Phe Ala Leu Ala Thr Phe Val Thr Leu Leu Ala Trp Tyr Gly
 35 40 45

Leu Gly Thr Trp Leu Pro Arg Leu Met Glu Thr Ala Gly Tyr Glu Phe
 50 55 60

Gly His Ala Leu Met Phe Thr Leu Ala Leu Asn Leu Gly Ala Val Ile
 65 70 75 80

Gly Ser Val Val Thr Ala Trp Ala Gly Asp Arg Phe Gly Pro Ile Arg
 85 90 95

Ser Gly Val Ile Ala Ala Gly Ile Ala Gly Ile Ala Leu Leu Leu Leu
 100 105 110

Leu Thr Tyr Pro Pro Val Thr Ala Val Tyr Val Ile Leu Ile Leu Ala
 115 120 125

Gly Val Gly Thr His Gly Thr Gln Ile Leu Ile Ile Ala Ala Val Ala
 130 135 140

Asn Phe Tyr Pro Ser Asn Leu Arg Gly Thr Ala Leu Gly Trp Ala Leu
 145 150 155 160

Gly Val Gly Arg Ile Gly Ala Val Val Ala Pro Gln Leu Ala Gly Leu
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Leu Leu Ala Trp Asn Leu Gly Val Asn Ser Asn Phe Ile Met Phe Gly
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Leu Gly Ala Ser Asn Ser Ser Gln Thr Ile Glu Asn Lys Gly Leu Thr						
	10				20	
atc ttg ggc atc agc ggc cga cgc ttg gct gcg gtg ctc att ggc tgg						211
Ile Leu Gly Ile Ser Gly Arg Arg Leu Ala Ala Val Leu Ile Gly Trp						
	25				35	
ttt ttt gtc att ttc gac ggc tac gac ctc att gtg tac ggc acc gtc						259
Phe Phe Val Ile Phe Asp Gly Tyr Asp Leu Ile Val Tyr Gly Thr Val						
	40				50	
caa tcg gcc ctg gct aag gag tgg aac tta agc tct gca acg ctg ggc						307
Gln Ser Ala Leu Ala Lys Glu Trp Asn Leu Ser Ser Ala Thr Leu Gly						
	55				65	
acc atc ggc tcc acc gcg ttc ttt ggc atg gcg atc ggc gct gtg ttc						355
Thr Ile Gly Ser Thr Ala Phe Phe Gly Met Ala Ile Gly Ala Val Phe						
	70				80	85
att ggt cga ctg tca gac cgc gtg ggc cga aaa gca gcg gtg att gga						403
Ile Gly Arg Leu Ser Asp Arg Val Gly Arg Lys Ala Ala Val Ile Gly						
	90				95	100
tcc gtg ctg att ctc tct gtc ttc acc atg ctg tgt gca ttt gct cca						451
Ser Val Leu Ile Leu Ser Val Phe Thr Met Leu Cys Ala Phe Ala Pro						
	105				110	115
aac cca tgg gtg ttc ggc gct ttc cgt ttc atc						484
Asn Pro Trp Val Phe Gly Ala Phe Arg Phe Ile						
	120				125	

<210> 414

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

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Asn	Lys	Gly	Leu	Thr	Ile	Leu	Gly	Ile	Ser	Gly	Arg	Arg	Leu	Ala	Ala
		20					25						30		

Val	Leu	Ile	Gly	Trp	Phe	Phe	Val	Ile	Phe	Asp	Gly	Tyr	Asp	Leu	Ile
	35						40					45			

Val	Tyr	Gly	Thr	Val	Gln	Ser	Ala	Leu	Ala	Lys	Glu	Trp	Asn	Leu	Ser
	50					55					60				

Ser	Ala	Thr	Leu	Gly	Thr	Ile	Gly	Ser	Thr	Ala	Phe	Phe	Gly	Met	Ala
	65				70					75				80	

Ile	Gly	Ala	Val	Phe	Ile	Gly	Arg	Leu	Ser	Asp	Arg	Val	Gly	Arg	Lys
			85					90						95	

Ala	Ala	Val	Ile	Gly	Ser	Val	Leu	Ile	Leu	Ser	Val	Phe	Thr	Met	Leu
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Thr	Arg	Ala	Thr	Lys	Ser	Val	Gly	Thr	Val	Leu	Ala	Leu	Leu	Trp	Phe	
1				5					10					15		
gca	att	gtc	ctc	gac	ggc	ttt	gac	cta	gtc	gtc	ctg	ggt	gca	aca	atc	96
Ala	Ile	Val	Leu	Asp	Gly	Phe	Asp	Leu	Val	Val	Leu	Gly	Ala	Thr	Ile	
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ccg	tcc	atg	ctg	gag	gat	ccc	gcg	tgg	gat	ctc	act	gct	gga	cag	gcc	144
Pro	Ser	Met	Leu	Glu	Asp	Pro	Ala	Trp	Asp	Leu	Thr	Ala	Gly	Gln	Ala	
		35					40					45				
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Thr	Gln	Ile	Ser	Thr	Ile	Gly	Leu	Val	Gly	Met	Thr	Ile	Gly	Ala	Leu	
	50					55					60					
acc	atc	ggt	ttc	tta	acg	gac	cgt	ctg	ggt	cga	cgc	cgt	gtc	atg	ctg	240
Thr	Ile	Gly	Phe	Leu	Thr	Asp	Arg	Leu	Gly	Arg	Arg	Arg	Val	Met	Leu	
	65					70					75				80	
ttc	tct	gtg	gca	gta	ttt	tct	gta	ttc	act	ctc	ctg	ctg	gca	ttc	acc	288
Phe	Ser	Val	Ala	Val	Phe	Ser	Val	Phe	Thr	Leu	Leu	Leu	Ala	Phe	Thr	
				85					90					95		
acc	aac	gtc	cag	ctc	ttc	agc	ctg	tgg	cgt	ttc	ctc	gca	ggt	gtt	ggc	336
Thr	Asn	Val	Gln	Leu	Phe	Ser	Leu	Trp	Arg	Phe	Leu	Ala	Gly	Val	Gly	
			100					105					110			
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Leu	Gly	Gly	Ala	Leu	Pro	Thr	Ala	Ile	Ala	Met	Val	Thr	Glu	Phe	Arg	
		115					120					125				
ccc	ggc	acc	aaa	gcg	ggc	tct	gca	tcc	acc	acc	ttg	atg	acc	ggc	tac	432
Pro	Gly	Thr	Lys	Ala	Gly	Ser	Ala	Ser	Thr	Thr	Leu	Met	Thr	Gly	Tyr	
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cac	gtc	ggc	gca	gta	gca	acc	gcc	ttc	ctt	ggc	ctc	ttc	ctt	atc	gac	480
His	Val	Gly	Ala	Val	Ala	Thr	Ala	Phe	Leu	Gly	Leu	Phe	Leu	Ile	Asp	
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Gly Phe Gly Trp His Ser Met Phe Ile Ala Gly Ala Val Pro Gly Leu	
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Ile Leu Leu Pro Leu Leu Tyr Phe Phe Leu Pro Glu Ser Pro Gln Tyr	
180 185 190	
ctc aaa atc tcc ggc aag ttg gat gag gcg cag gca gtt gca gca tct	624
Leu Lys Ile Ser Gly Lys Leu Asp Glu Ala Gln Ala Val Ala Ala Ser	
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Tyr Gly Leu Ser Leu Asp Asp Asp Leu Asp Arg Glu His Glu Glu Glu	
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Leu Gly Glu Ser Ser Ser Leu Ser Ser Leu Phe Lys Pro Ser Phe Arg	
225 230 235 240	
cgc aac acc ctg gcg att tgg ggc acc tca ttc atg gga ctc ctc ctg	768
Arg Asn Thr Leu Ala Ile Trp Gly Thr Ser Phe Met Gly Leu Leu Leu	
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gtc tac ggc ctg aac aca tgg ctg cca caa atc atg cgc caa gca gac	816
Val Tyr Gly Leu Asn Thr Trp Leu Pro Gln Ile Met Arg Gln Ala Asp	
260 265 270	
tac gac atg ggt aac tcg ctt gga ttc ctc atg gtg ctc aac atc ggc	864
Tyr Asp Met Gly Asn Ser Leu Gly Phe Leu Met Val Leu Asn Ile Gly	
275 280 285	
gca gtg atc ggc ctt tat att gca ggg cga att gcc gat aag aac tcc	912
Ala Val Ile Gly Leu Tyr Ile Ala Gly Arg Ile Ala Asp Lys Asn Ser	
290 295 300	
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Pro Arg Lys Thr Ala Leu Val Trp Phe Val Phe Ser Ala Phe Ser Leu	
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gcg ttg ctt gct gtc cgg atg cca ctg atc ggt ctg tat ggc atc gtg	1008
Ala Leu Leu Ala Val Arg Met Pro Leu Ile Gly Leu Tyr Gly Ile Val	
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Phe Val Gly Glu Asn His Pro Ala Lys Met Arg Ala Thr Ala Met Gly	
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370 375 380	
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<213> Corynebacterium glutamicum

<400> 416

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Thr Gln Ile Ser Thr Ile Gly Leu Val Gly Met Thr Ile Gly Ala Leu
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Thr Ile Gly Phe Leu Thr Asp Arg Leu Gly Arg Arg Arg Val Met Leu
  65           70           75           80

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Pro Gly Thr Lys Ala Gly Ser Ala Ser Thr Thr Leu Met Thr Gly Tyr
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His Val Gly Ala Val Ala Thr Ala Phe Leu Gly Leu Phe Leu Ile Asp
      145          150          155          160

Gly Phe Gly Trp His Ser Met Phe Ile Ala Gly Ala Val Pro Gly Leu
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Ile Leu Leu Pro Leu Leu Tyr Phe Phe Leu Pro Glu Ser Pro Gln Tyr
      180          185          190

Leu Lys Ile Ser Gly Lys Leu Asp Glu Ala Gln Ala Val Ala Ala Ser
      195          200          205

Tyr Gly Leu Ser Leu Asp Asp Asp Leu Asp Arg Glu His Glu Glu Glu
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Leu Gly Glu Ser Ser Ser Leu Ser Ser Leu Phe Lys Pro Ser Phe Arg
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Arg Asn Thr Leu Ala Ile Trp Gly Thr Ser Phe Met Gly Leu Leu Leu
      245          250          255

Val Tyr Gly Leu Asn Thr Trp Leu Pro Gln Ile Met Arg Gln Ala Asp
      260          265          270

Tyr Asp Met Gly Asn Ser Leu Gly Phe Leu Met Val Leu Asn Ile Gly
      275          280          285

Ala Val Ile Gly Leu Tyr Ile Ala Gly Arg Ile Ala Asp Lys Asn Ser
      290          295          300

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Pro Arg Lys Thr Ala Leu Val Trp Phe Val Phe Ser Ala Phe Ser Leu
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Ala Leu Leu Ala Val Arg Met Pro Leu Ile Gly Leu Tyr Gly Ile Val
 325 330 335

Leu Leu Thr Gly Ile Phe Val Phe Ser Ser Gln Val Leu Ile Tyr Ala
 340 345 350

Phe Val Gly Glu Asn His Pro Ala Lys Met Arg Ala Thr Ala Met Gly
 355 360 365

Phe Ser Ala Gly Ile Gly Arg Leu Gly Ala Ile Ser Gly Pro Leu Leu
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Gly Gly Leu Leu Val Ser Ala Asn Leu Ala Tyr Pro Trp Gly Phe
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 <223> RXN00590

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 Met Ala Asp Asn Lys
 1 5

aat gcc gat gac agc cag cta gtc tca gcc agc act gga acc cct ggg 163
 Asn Ala Asp Asp Ser Gln Leu Val Ser Ala Ser Thr Gly Thr Pro Gly
 10 15 20

cct ggc gac att gca aaa gcc aat gcg cca tcc ctc aag caa gct gca 211
 Pro Gly Asp Ile Ala Lys Ala Asn Ala Pro Ser Leu Lys Gln Ala Ala
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gta acc gcc tct ggc cga agc gct ctg atg ggt gcc atc ttc ctc atg 259
 Val Thr Ala Ser Gly Arg Ser Ala Leu Met Gly Ala Ile Phe Leu Met
 40 45 50

gca act tct gcc atc ggc cca ggg ttc ctc acc caa acc gct gtc ttc 307
 Ala Thr Ser Ala Ile Gly Pro Gly Phe Leu Thr Gln Thr Ala Val Phe
 55 60 65

acc aac cag ctc ggc gca gct ttc gca ttt gcg atc ctg gtg tcg atc 355
 Thr Asn Gln Leu Gly Ala Ala Phe Ala Phe Ala Ile Leu Val Ser Ile
 70 75 80 85

ctc att gac atc gcg gtg cag ctg aat gtg tgg cgc atc atc ggc gtc 403
 Leu Ile Asp Ile Ala Val Gln Leu Asn Val Trp Arg Ile Ile Gly Val
 90 95 100

tct gaa atg cgc gcc caa gaa ctc ggc aac acg gtt atc cca ggt ttt	451
Ser Glu Met Arg Ala Gln Glu Leu Gly Asn Thr Val Ile Pro Gly Phe	
105 110 115	
ggg tgg gtg ctg gcc gta ctg gtc tgt att ggc ggc gta gta ttc aac	499
Gly Trp Val Leu Ala Val Leu Val Cys Ile Gly Gly Val Val Phe Asn	
120 125 130	
atc ggc aac atc gcc ggt ggt ggc ctt ggg ctt aac gcg ctg ctt ggc	547
Ile Gly Asn Ile Ala Gly Gly Gly Leu Gly Leu Asn Ala Leu Leu Gly	
135 140 145	
tgg gac gtc aaa gtt ggt ggc gtg atc acc gcg gcc atc gcg att gcg	595
Trp Asp Val Lys Val Gly Gly Val Ile Thr Ala Ala Ile Ala Ile Ala	
150 155 160 165	
atc ttc ttg ttc aag cga ctt ggt gct gct ctg gac aaa ttc ctc gtg	643
Ile Phe Leu Phe Lys Arg Leu Gly Ala Ala Leu Asp Lys Phe Leu Val	
170 175 180	
gtc ctc ggc gtc gtg atg atc ctg ctc acc gtc tac gtg gct ttc gtc	691
Val Leu Gly Val Val Met Ile Leu Leu Thr Val Tyr Val Ala Phe Val	
185 190 195	
tcc caa cct cca gtt ggc tcg gcg ctg aag aat gca gta ctt cct gac	739
Ser Gln Pro Pro Val Gly Ser Ala Leu Lys Asn Ala Val Leu Pro Asp	
200 205 210	
acc atc gac tgg ctt gtc atc acc aca ctt gtg ggt gga acc gtc ggt	787
Thr Ile Asp Trp Leu Val Ile Thr Thr Leu Val Gly Gly Thr Val Gly	
215 220 225	
gga tac atc act tac gct ggc gca cac cgc atg ctg gac tcc gga cga	835
Gly Tyr Ile Thr Tyr Ala Gly Ala His Arg Met Leu Asp Ser Gly Arg	
230 235 240 245	
acc ggc ccc aac aac gtc aaa gct gtt tcc aat tcc tct atc acc ggc	883
Thr Gly Pro Asn Asn Val Lys Ala Val Ser Asn Ser Ser Ile Thr Gly	
250 255 260	
atc ctg atc act ggc ctc atg cgc gtg gtg ctc ttc ctc gcg gtt ctc	931
Ile Leu Ile Thr Gly Leu Met Arg Val Val Leu Phe Leu Ala Val Leu	
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Gly Val Val Ala Gly Gly Val Thr Leu Ser Thr Thr Gly Asn Pro Ala	
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gcg gaa gca ttc cag cac gct gca ggc gat atc gga cta cgc atc ttc	1027
Ala Glu Ala Phe Gln His Ala Ala Gly Asp Ile Gly Leu Arg Ile Phe	
295 300 305	
ggc gcc gtg ctg tgg gca gcg tcc att tcc tca gtc atc ggc gcc agc	1075
Gly Ala Val Leu Trp Ala Ala Ser Ile Ser Ser Val Ile Gly Ala Ser	
310 315 320 325	
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Tyr Thr Ser Ala Thr Phe Leu Val Glu Asn Lys Pro Glu Lys Lys Arg	
330 335 340	
ctg caa aac tgg gtg acc atc atc ttc atc ctg att tct tgc tcc gtg	1171

Leu Gln Asn Trp Val Thr Ile Ile Phe Ile Leu Ile Ser Cys Ser Val
 345 350 355
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 Phe Ile Met Leu Gly Thr Ala Pro Ala Ile Leu Leu Val Phe Ala Gly
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 gca ttc aac ggt ttg gtc ctc ccc gta ggc ttt acc ctg atg atc tac 1267
 Ala Phe Asn Gly Leu Val Leu Pro Val Gly Phe Thr Leu Met Ile Tyr
 375 380 385
 gta gcg atc ttc cgc caa aaa 1288
 Val Ala Ile Phe Arg Gln Lys
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<210> 418
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 418
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 35 40 45
 Ala Ile Phe Leu Met Ala Thr Ser Ala Ile Gly Pro Gly Phe Leu Thr
 50 55 60
 Gln Thr Ala Val Phe Thr Asn Gln Leu Gly Ala Ala Phe Ala Phe Ala
 65 70 75 80
 Ile Leu Val Ser Ile Leu Ile Asp Ile Ala Val Gln Leu Asn Val Trp
 85 90 95
 Arg Ile Ile Gly Val Ser Glu Met Arg Ala Gln Glu Leu Gly Asn Thr
 100 105 110
 Val Ile Pro Gly Phe Gly Trp Val Leu Ala Val Leu Val Cys Ile Gly
 115 120 125
 Gly Val Val Phe Asn Ile Gly Asn Ile Ala Gly Gly Gly Leu Gly Leu
 130 135 140
 Asn Ala Leu Leu Gly Trp Asp Val Lys Val Gly Gly Val Ile Thr Ala
 145 150 155 160
 Ala Ile Ala Ile Ala Ile Phe Leu Phe Lys Arg Leu Gly Ala Ala Leu
 165 170 175
 Asp Lys Phe Leu Val Val Leu Gly Val Val Met Ile Leu Leu Thr Val
 180 185 190
 Tyr Val Ala Phe Val Ser Gln Pro Pro Val Gly Ser Ala Leu Lys Asn
 195 200 205

Ala Val Leu Pro Asp Thr Ile Asp Trp Leu Val Ile Thr Thr Leu Val
 210 215 220

Gly Gly Thr Val Gly Gly Tyr Ile Thr Tyr Ala Gly Ala His Arg Met
 225 230 235 240

Leu Asp Ser Gly Arg Thr Gly Pro Asn Asn Val Lys Ala Val Ser Asn
 245 250 255

Ser Ser Ile Thr Gly Ile Leu Ile Thr Gly Leu Met Arg Val Val Leu
 260 265 270

Phe Leu Ala Val Leu Gly Val Val Ala Gly Gly Val Thr Leu Ser Thr
 275 280 285

Thr Gly Asn Pro Ala Ala Glu Ala Phe Gln His Ala Ala Gly Asp Ile
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Gly Leu Arg Ile Phe Gly Ala Val Leu Trp Ala Ala Ser Ile Ser Ser
 305 310 315 320

Val Ile Gly Ala Ser Tyr Thr Ser Ala Thr Phe Leu Val Glu Asn Lys
 325 330 335

Pro Glu Lys Lys Arg Leu Gln Asn Trp Val Thr Ile Ile Phe Ile Leu
 340 345 350

Ile Ser Cys Ser Val Phe Ile Met Leu Gly Thr Ala Pro Ala Ile Leu
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Leu Val Phe Ala Gly Ala Phe Asn Gly Leu Val Leu Pro Val Gly Phe
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Thr Leu Met Ile Tyr Val Ala Ile Phe Arg Gln Lys
 385 390 395

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA00590

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 Met Arg Val Val Leu
 1 5

ttc ctc gcg gtt ctc ggt gtt gtc gca ggt ggc gtc acc cta tcc acc 163
 Phe Leu Ala Val Leu Gly Val Val Ala Gly Gly Val Thr Leu Ser Thr
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acg ggc aac cca gcc gcg gaa gca ttc cag cac gct gca ggc gat atc 211
 Thr Gly Asn Pro Ala Ala Glu Ala Phe Gln His Ala Ala Gly Asp Ile
 25 30 35

gga cta cgc atc ttc ggc gcc gtg ctg tgg gca gcg tcc att tcc tca 259
 Gly Leu Arg Ile Phe Gly Ala Val Leu Trp Ala Ala Ser Ile Ser Ser
 40 45 50

gtc atc ggc gcc agc tac acc tct gca acc ttc ctg gtg gaa aac aag 307
 Val Ile Gly Ala Ser Tyr Thr Ser Ala Thr Phe Leu Val Glu Asn Lys
 55 60 65

cca gag aag aag cgt ctg caa aac tgg gtg acc atc atc ttc atc ctg 355
 Pro Glu Lys Lys Arg Leu Gln Asn Trp Val Thr Ile Ile Phe Ile Leu
 70 75 80 85

att tct tgc tcc gtg ttc atc atg ctc ggc acg gca cca gca atc ctc 403
 Ile Ser Cys Ser Val Phe Ile Met Leu Gly Thr Ala Pro Ala Ile Leu
 90 95 100

ttg gtc ttc gcc gga gca ttc aac ggt ttg gtc ctc ccc gta ggc ttt 451
 Leu Val Phe Ala Gly Ala Phe Asn Gly Leu Val Leu Pro Val Gly Phe
 105 110 115

acc ctg atg atc tac gta gcg atc ttc cgc caa aaa 487
 Thr Leu Met Ile Tyr Val Ala Ile Phe Arg Gln Lys
 120 125

<210> 420

<211> 129

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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 35 40 45

Ala Ser Ile Ser Ser Val Ile Gly Ala Ser Tyr Thr Ser Ala Thr Phe
 50 55 60

Leu Val Glu Asn Lys Pro Glu Lys Lys Arg Leu Gln Asn Trp Val Thr
 65 70 75 80

Ile Ile Phe Ile Leu Ile Ser Cys Ser Val Phe Ile Met Leu Gly Thr
 85 90 95

Ala Pro Ala Ile Leu Leu Val Phe Ala Gly Ala Phe Asn Gly Leu Val
 100 105 110

Leu Pro Val Gly Phe Thr Leu Met Ile Tyr Val Ala Ile Phe Arg Gln
 115 120 125

Lys

<210> 421

<211> 490
 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA01538

<400> 421

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                                         Met Ala Asp Asn Lys
                                         1           5

aat gcc gat gac agc cag cta gtc tca gcc agc act gga acc cct ggg 163
Asn Ala Asp Asp Ser Gln Leu Val Ser Ala Ser Thr Gly Thr Pro Gly
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cct ggc gac att gca aaa gcc aat gcg cca tcc ctc aag caa gct gca 211
Pro Gly Asp Ile Ala Lys Ala Asn Ala Pro Ser Leu Lys Gln Ala Ala
                25                30                35

gta acc gcc tct ggc cga agc gct ctg atg ggt gcc atc ttc ctc atg 259
Val Thr Ala Ser Gly Arg Ser Ala Leu Met Gly Ala Ile Phe Leu Met
                40                45                50

gca act tct gcc atc ggc cca ggg ttc ctc acc caa acc gct gtc ttc 307
Ala Thr Ser Ala Ile Gly Pro Gly Phe Leu Thr Gln Thr Ala Val Phe
                55                60                65

acc aac cag ctc ggc gca gct ttc gca ttt gcg atc ctg gtg tcg atc 355
Thr Asn Gln Leu Gly Ala Ala Phe Ala Phe Ala Ile Leu Val Ser Ile
                70                75                80                85

ctc att gac atc gcg gtg cag ctg aat gtg tgg cgc atc atc ggc gtc 403
Leu Ile Asp Ile Ala Val Gln Leu Asn Val Trp Arg Ile Ile Gly Val
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tct gaa atg cgc gcc caa gaa ctc ggc aac acg gtt atc cca ggt ttt 451
Ser Glu Met Arg Ala Gln Glu Leu Gly Asn Thr Val Ile Pro Gly Phe
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Gly Trp Val Leu Ala Val Leu Val Cys Ile Gly Gly Val
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<210> 422
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 422

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Leu Lys Gln Ala Ala Val Thr Ala Ser Gly Arg Ser Ala Leu Met Gly
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 Ala Ile Phe Leu Met Ala Thr Ser Ala Ile Gly Pro Gly Phe Leu Thr
 50 55 60
 Gln Thr Ala Val Phe Thr Asn Gln Leu Gly Ala Ala Phe Ala Phe Ala
 65 70 75 80
 Ile Leu Val Ser Ile Leu Ile Asp Ile Ala Val Gln Leu Asn Val Trp
 85 90 95
 Arg Ile Ile Gly Val Ser Glu Met Arg Ala Gln Glu Leu Gly Asn Thr
 100 105 110
 Val Ile Pro Gly Phe Gly Trp Val Leu Ala Val Leu Val Cys Ile Gly
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 Gly Val
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<210> 423
 <211> 1401
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1378)
 <223> RXA01727

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 Met Ser Lys Lys Ser
 1 5
 gtc ctg att act tct ttg atg ctg ttt tcc atg ttc ttc gga gct gga 163
 Val Leu Ile Thr Ser Leu Met Leu Phe Ser Met Phe Phe Gly Ala Gly
 10 15 20
 aac ctc atc ttc ccg ccg atg ctt gga ttg tcg gca gga acc aac tat 211
 Asn Leu Ile Phe Pro Pro Met Leu Gly Leu Ser Ala Gly Thr Asn Tyr
 25 30 35
 cta cca gct atc tta gga ttt cta gca acg agt gtt ctg ctc ccg gtg 259
 Leu Pro Ala Ile Leu Gly Phe Leu Ala Thr Ser Val Leu Leu Pro Val
 40 45 50
 ctg gcg att atc gcg gtg gtg ttg tcg gga gaa aat gtc aag gac atg 307
 Leu Ala Ile Ile Ala Val Val Leu Ser Gly Glu Asn Val Lys Asp Met
 55 60 65
 gct tct cgt ggc ggt aag atc ttt ggc ctg gtg ttt cct att gct gcc 355
 Ala Ser Arg Gly Gly Lys Ile Phe Gly Leu Val Phe Pro Ile Ala Ala
 70 75 80 85
 tat ttg tct atc ggc gcg ttt tac gcg ctg ccg agg act ggg gcg gtg 403
 Tyr Leu Ser Ile Gly Ala Phe Tyr Ala Leu Pro Arg Thr Gly Ala Val

90										95										100									
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Ser	Tyr	Ser	Thr	Ala	Val	Gly	Val	Asp	Asn	Ala	Leu	Tyr	Ser	Gly	Leu														
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ttt	aac	ttt	gtg	ttt	ttt	gcg	gtg	gca	ctg	gcg	ttg	tcg	tgg	aat	ccg														
Phe	Asn	Phe	Val	Phe	Phe	Ala	Val	Ala	Leu	Ala	Leu	Ser	Trp	Asn	Pro														
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aat	ggc	att	gca	gac	aag	ttg	ggt	aag	tgg	ctc	acg	cca	gcg	ttg	ctc														
Asn	Gly	Ile	Ala	Asp	Lys	Leu	Gly	Lys	Trp	Leu	Thr	Pro	Ala	Leu	Leu														
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acg	ttg	att	gtg	gtg	ctg	gtg	gtg	ttg	tcg	gta	gcc	aag	ttg	gat	ggc														
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Thr	Pro	Gly	Glu	Pro	Ser	Ser	Ala	Tyr	Ala	Gln	Gln	Pro	Ala	Gly	Ala														
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ggt	ttg	ctt	gag	ggc	tac	atg	acg	atg	gat	gcg	att	gct	gcg	ttg	gcg														
Gly	Leu	Leu	Glu	Gly	Tyr	Met	Thr	Met	Asp	Ala	Ile	Ala	Ala	Leu	Ala														
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ttt	ggc	atc	gtg	gtg	att	tct	gcg	ttc	aag	tac	caa	aag	ggt	aac	aag														
Phe	Gly	Ile	Val	Val	Ile	Ser	Ala	Phe	Lys	Tyr	Gln	Lys	Val	Asn	Lys														
		200					205							210															
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Val	Arg	Thr	Ala	Thr	Val	Val	Ser	Ala	Phe	Ile	Ala	Gly	Ile	Leu	Leu														
	215					220								225															
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Ala	Leu	Val	Tyr	Leu	Gly	Leu	Gly	Ser	Ile	Gly	Gln	Val	Val	Asn	Gly														
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gag	ttc	gct	gat	ggc	acc	gca	att	ttg	aac	tac	gct	gca	ctg	tcc	acg														
Glu	Phe	Ala	Asp	Gly	Thr	Ala	Ile	Leu	Asn	Tyr	Ala	Ala	Leu	Ser	Thr														
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Cys	Met	Thr	Thr	Ala	Val	Gly	Leu	Ile	Ser	Ala	Thr	Ser	Glu	Phe	Phe														
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Asn	Ser	Leu	Leu	Pro	Gly	Val	Lys	Tyr	His	Val	Trp	Ala	Thr	Val	Phe														
		295				300								305															
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Ala	Leu	Ile	Ser	Phe	Gly	Val	Ala	Thr	Met	Gly	Leu	Asp	Thr	Val	Leu														
	310				315					320				325															
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Ala	Val	Ala	Ala	Pro	Val	Ile	Ser	Phe	Ile	Tyr	Pro	Ser	Ala	Ile	Thr														
				330					335					340															

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 Leu Val Phe Leu Ser Leu Ile Glu Pro Leu Leu Phe Arg Leu Lys Trp
 345 350 355
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 Thr Tyr Leu Phe Gly Ile Trp Thr Ala Val Val Trp Ala Leu Phe Met
 360 365 370
 tct atc cct gcg ctg aat cca ttc atc gaa tgg gcg ccg ctg cac agc 1267
 Ser Ile Pro Ala Leu Asn Pro Phe Ile Glu Trp Ala Pro Leu His Ser
 375 380 385
 atg tct ttg ggt tgg gtt gtc cca gtt ctc gtg gcc tct gcc atc ggt 1315
 Met Ser Leu Gly Trp Val Val Pro Val Leu Val Ala Ser Ala Ile Gly
 390 395 400 405
 ttg gct att gat tgg aac aag aaa ggt gcc cag tct gtt gca aag aag 1363
 Leu Ala Ile Asp Trp Asn Lys Lys Gly Ala Gln Ser Val Ala Lys Lys
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<210> 424

<211> 426

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 424

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 Ala Gly Thr Asn Tyr Leu Pro Ala Ile Leu Gly Phe Leu Ala Thr Ser
 35 40 45
 Val Leu Leu Pro Val Leu Ala Ile Ile Ala Val Val Leu Ser Gly Glu
 50 55 60
 Asn Val Lys Asp Met Ala Ser Arg Gly Gly Lys Ile Phe Gly Leu Val
 65 70 75 80
 Phe Pro Ile Ala Ala Tyr Leu Ser Ile Gly Ala Phe Tyr Ala Leu Pro
 85 90 95
 Arg Thr Gly Ala Val Ser Tyr Ser Thr Ala Val Gly Val Asp Asn Ala
 100 105 110
 Leu Tyr Ser Gly Leu Phe Asn Phe Val Phe Phe Ala Val Ala Leu Ala
 115 120 125
 Leu Ser Trp Asn Pro Asn Gly Ile Ala Asp Lys Leu Gly Lys Trp Leu
 130 135 140
 Thr Pro Ala Leu Leu Thr Leu Ile Val Val Leu Val Val Leu Ser Val
 145 150 155 160

Ala Lys Leu Asp Gly Thr Pro Gly Glu Pro Ser Ser Ala Tyr Ala Gln
 165 170 175
 Gln Pro Ala Gly Ala Gly Leu Leu Glu Gly Tyr Met Thr Met Asp Ala
 180 185 190
 Ile Ala Ala Leu Ala Phe Gly Ile Val Val Ile Ser Ala Phe Lys Tyr
 195 200 205
 Gln Lys Val Asn Lys Val Arg Thr Ala Thr Val Val Ser Ala Phe Ile
 210 215 220
 Ala Gly Ile Leu Leu Ala Leu Val Tyr Leu Gly Leu Gly Ser Ile Gly
 225 230 235 240
 Gln Val Val Asn Gly Glu Phe Ala Asp Gly Thr Ala Ile Leu Asn Tyr
 245 250 255
 Ala Ala Leu Ser Thr Met Gly Gln Ala Gly Arg Ile Met Phe Val Ala
 260 265 270
 Ile Leu Ile Leu Ala Cys Met Thr Thr Ala Val Gly Leu Ile Ser Ala
 275 280 285
 Thr Ser Glu Phe Phe Asn Ser Leu Leu Pro Gly Val Lys Tyr His Val
 290 295 300
 Trp Ala Thr Val Phe Ala Leu Ile Ser Phe Gly Val Ala Thr Met Gly
 305 310 315 320
 Leu Asp Thr Val Leu Ala Val Ala Ala Pro Val Ile Ser Phe Ile Tyr
 325 330 335
 Pro Ser Ala Ile Thr Leu Val Phe Leu Ser Leu Ile Glu Pro Leu Leu
 340 345 350
 Phe Arg Leu Lys Trp Thr Tyr Leu Phe Gly Ile Trp Thr Ala Val Val
 355 360 365
 Trp Ala Leu Phe Met Ser Ile Pro Ala Leu Asn Pro Phe Ile Glu Trp
 370 375 380
 Ala Pro Leu His Ser Met Ser Leu Gly Trp Val Val Pro Val Leu Val
 385 390 395 400
 Ala Ser Ala Ile Gly Leu Ala Ile Asp Trp Asn Lys Lys Gly Ala Gln
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<210> 425

<211> 1461

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1438)

<223> RXA00623

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Glu Ser Ser Ser Val Glu Val Lys Asn Glu His Ile Lys Val Gln Lys
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Pro Pro Lys Lys Asp Arg Thr His Trp Leu Tyr Ile Ala Val Ile Ile
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gca ttg att ggc ggt att acc cta ggc ctg att tca ccg gag ttg ggc 259
Ala Leu Ile Gly Gly Ile Thr Leu Gly Leu Ile Ser Pro Glu Leu Gly
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Lys Glu Phe Lys Ile Leu Gly Thr Met Phe Val Ser Leu Ile Lys Met
                        55                        60                        65

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Ile Ile Ala Pro Val Ile Phe Cys Thr Ile Val Ile Gly Ile Gly Ser
                        70                        75                        80                        85

gtc aag gca gcg gca aca gtc gga cgc gct ggt ggc atc gcc ctt gcg 403
Val Lys Ala Ala Ala Thr Val Gly Arg Ala Gly Gly Ile Ala Leu Ala
                        90                        95                        100

tac ttc atc acg atg tcc aca ttc gca ctc gca gtt ggc ctg cta gtc 451
Tyr Phe Ile Thr Met Ser Thr Phe Ala Leu Ala Val Gly Leu Leu Val
                        105                        110                        115

ggt aac ttc atc cag cca ggt agc gga ctg aac atc tca gtt gat gaa 499
Gly Asn Phe Ile Gln Pro Gly Ser Gly Leu Asn Ile Ser Val Asp Glu
                        120                        125                        130

gaa tct tca ttc gca tcc aca gag agc agc cct gaa gga ctc ttg gga 547
Glu Ser Ser Phe Ala Ser Thr Glu Ser Ser Pro Glu Gly Leu Leu Gly
                        135                        140                        145

ttc atc cac tcg atc atc cct gaa acg ttc ttc tct gca ttt act gat 595
Phe Ile His Ser Ile Ile Pro Glu Thr Phe Phe Ser Ala Phe Thr Asp
                        150                        155                        160                        165

ggt tcg gtg ctg cag gta ctg ttc atc gcc atc ctc gtg ggc ttt gca 643
Gly Ser Val Leu Gln Val Leu Phe Ile Ala Ile Leu Val Gly Phe Ala
                        170                        175                        180

gct cag tcg atg ggt gaa aag gga cag ccc atc ctt gat ttc gta tcc 691
Ala Gln Ser Met Gly Glu Lys Gly Gln Pro Ile Leu Asp Phe Val Ser
                        185                        190                        195

cat ctg cag aag ctc atc ttc aag att ttg aac tgg att ctg tgg ctc 739
His Leu Gln Lys Leu Ile Phe Lys Ile Leu Asn Trp Ile Leu Trp Leu
                        200                        205                        210

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gcc cca gtc ggt gca ttc ggt gca atg gcc ggc gtc gtt ggc gaa aca	787
Ala Pro Val Gly Ala Phe Gly Ala Met Ala Gly Val Val Gly Glu Thr	
215 220 225	
ggc ttt gat gcc gtt gtt cag ctc ggt att ttg atc ctc gcc ttt tac	835
Gly Phe Asp Ala Val Val Gln Leu Gly Ile Leu Ile Leu Ala Phe Tyr	
230 235 240 245	
gtc acc tgc gtg atc ttc atc ttt ggc gtg ctg ggc gcc gta ctg aag	883
Val Thr Cys Val Ile Phe Ile Phe Gly Val Leu Gly Ala Val Leu Lys	
250 255 260	
gtg ttc acc ggc gtg aat atc ttc aag ctg gtc aag tac ctt gcc aag	931
Val Phe Thr Gly Val Asn Ile Phe Lys Leu Val Lys Tyr Leu Ala Lys	
265 270 275	
gaa ttc ctg ctg atc ttt gct acc tca tcc tct gaa tct gcc ttg cca	979
Glu Phe Leu Leu Ile Phe Ala Thr Ser Ser Ser Glu Ser Ala Leu Pro	
280 285 290	
aac ctc atg cgc aag atg gaa cac atc ggt gtg gct aaa cca acc gtc	1027
Asn Leu Met Arg Lys Met Glu His Ile Gly Val Ala Lys Pro Thr Val	
295 300 305	
gga atc gtg gtc cca acc ggc tat tcc ttc aac ttg gac ggc acc gca	1075
Gly Ile Val Val Pro Thr Gly Tyr Ser Phe Asn Leu Asp Gly Thr Ala	
310 315 320 325	
att tac ctc acc atg gca tct atc ttc att gcc gac gcg atg aat atg	1123
Ile Tyr Leu Thr Met Ala Ser Ile Phe Ile Ala Asp Ala Met Asn Met	
330 335 340	
ccg atg agc ctc ggc gag cag gtc ggt ctg ctt gtc ttc atg atc atc	1171
Pro Met Ser Leu Gly Glu Gln Val Gly Leu Leu Val Phe Met Ile Ile	
345 350 355	
gca tcc aag ggc gct gct ggt gtc tcg ggt gcc ggt att gca acg ttg	1219
Ala Ser Lys Gly Ala Ala Gly Val Ser Gly Ala Gly Ile Ala Thr Leu	
360 365 370	
gct gcc gga ttg tct tca cac cgc cca gaa ctt ctg cac ggc gtt gac	1267
Ala Ala Gly Leu Ser Ser His Arg Pro Glu Leu Leu His Gly Val Asp	
375 380 385	
gtg att gtg ggc atc gat aaa ttc atg tct gaa gcc cgc gca cta acc	1315
Val Ile Val Gly Ile Asp Lys Phe Met Ser Glu Ala Arg Ala Leu Thr	
390 395 400 405	
aac ttc gcc gga aac tcc gtg gca aca ctg ctg gtc ggc aag tgg act	1363
Asn Phe Ala Gly Asn Ser Val Ala Thr Leu Leu Val Gly Lys Trp Thr	
410 415 420	
ggc acc gtg gac atg aac caa gtc cat gac gtt ttg aat gga aaa tct	1411
Gly Thr Val Asp Met Asn Gln Val His Asp Val Leu Asn Gly Lys Ser	
425 430 435	
cca ttt gtg gag tta gaa gaa gac cac tagttttcaa caggacgaca	1458
Pro Phe Val Glu Leu Glu Glu Asp His	
440 445	
acg	1461

<210> 426
 <211> 446
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 426

Met	Asp	Ser	Asn	Thr	Glu	Ser	Ser	Ser	Val	Glu	Val	Lys	Asn	Glu	His
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Ile	Lys	Val	Gln	Lys	Pro	Pro	Lys	Lys	Asp	Arg	Thr	His	Trp	Leu	Tyr
			20					25					30		
Ile	Ala	Val	Ile	Ile	Ala	Leu	Ile	Gly	Gly	Ile	Thr	Leu	Gly	Leu	Ile
		35					40					45			
Ser	Pro	Glu	Leu	Gly	Lys	Glu	Phe	Lys	Ile	Leu	Gly	Thr	Met	Phe	Val
	50					55					60				
Ser	Leu	Ile	Lys	Met	Ile	Ile	Ala	Pro	Val	Ile	Phe	Cys	Thr	Ile	Val
	65				70					75					80
Ile	Gly	Ile	Gly	Ser	Val	Lys	Ala	Ala	Ala	Thr	Val	Gly	Arg	Ala	Gly
				85					90					95	
Gly	Ile	Ala	Leu	Ala	Tyr	Phe	Ile	Thr	Met	Ser	Thr	Phe	Ala	Leu	Ala
			100					105					110		
Val	Gly	Leu	Leu	Val	Gly	Asn	Phe	Ile	Gln	Pro	Gly	Ser	Gly	Leu	Asn
		115					120					125			
Ile	Ser	Val	Asp	Glu	Glu	Ser	Ser	Phe	Ala	Ser	Thr	Glu	Ser	Ser	Pro
	130					135						140			
Glu	Gly	Leu	Leu	Gly	Phe	Ile	His	Ser	Ile	Ile	Pro	Glu	Thr	Phe	Phe
	145				150					155					160
Ser	Ala	Phe	Thr	Asp	Gly	Ser	Val	Leu	Gln	Val	Leu	Phe	Ile	Ala	Ile
				165					170					175	
Leu	Val	Gly	Phe	Ala	Ala	Gln	Ser	Met	Gly	Glu	Lys	Gly	Gln	Pro	Ile
			180					185					190		
Leu	Asp	Phe	Val	Ser	His	Leu	Gln	Lys	Leu	Ile	Phe	Lys	Ile	Leu	Asn
	195						200					205			
Trp	Ile	Leu	Trp	Leu	Ala	Pro	Val	Gly	Ala	Phe	Gly	Ala	Met	Ala	Gly
	210					215					220				
Val	Val	Gly	Glu	Thr	Gly	Phe	Asp	Ala	Val	Val	Gln	Leu	Gly	Ile	Leu
	225				230					235					240
Ile	Leu	Ala	Phe	Tyr	Val	Thr	Cys	Val	Ile	Phe	Ile	Phe	Gly	Val	Leu
			245						250					255	
Gly	Ala	Val	Leu	Lys	Val	Phe	Thr	Gly	Val	Asn	Ile	Phe	Lys	Leu	Val
		260						265					270		
Lys	Tyr	Leu	Ala	Lys	Glu	Phe	Leu	Leu	Ile	Phe	Ala	Thr	Ser	Ser	Ser
		275					280					285			

Glu Ser Ala Leu Pro Asn Leu Met Arg Lys Met Glu His Ile Gly Val
 290 295 300
 Ala Lys Pro Thr Val Gly Ile Val Val Pro Thr Gly Tyr Ser Phe Asn
 305 310 315 320
 Leu Asp Gly Thr Ala Ile Tyr Leu Thr Met Ala Ser Ile Phe Ile Ala
 325 330 335
 Asp Ala Met Asn Met Pro Met Ser Leu Gly Glu Gln Val Gly Leu Leu
 340 345 350
 Val Phe Met Ile Ile Ala Ser Lys Gly Ala Ala Gly Val Ser Gly Ala
 355 360 365
 Gly Ile Ala Thr Leu Ala Ala Gly Leu Ser Ser His Arg Pro Glu Leu
 370 375 380
 Leu His Gly Val Asp Val Ile Val Gly Ile Asp Lys Phe Met Ser Glu
 385 390 395 400
 Ala Arg Ala Leu Thr Asn Phe Ala Gly Asn Ser Val Ala Thr Leu Leu
 405 410 415
 Val Gly Lys Trp Thr Gly Thr Val Asp Met Asn Gln Val His Asp Val
 420 425 430
 Leu Asn Gly Lys Ser Pro Phe Val Glu Leu Glu Glu Asp His
 435 440 445

<210> 427

<211> 620

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (55)..(597)

<223> RXA01584

<400> 427

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 Val
 1

gtg ttt ttg ggc gca ctt ctc ggc gcc gta atc atg ggc ggg ttt tat 105
 Val Phe Leu Gly Ala Leu Leu Gly Ala Val Ile Met Gly Gly Phe Tyr
 5 10 15

cca gca ttc att caa gcc gga tcc aca gtg ttc ggc ggc ggc cac gtg 153
 Pro Ala Phe Ile Gln Ala Gly Ser Thr Val Phe Gly Gly Gly His Val
 20 25 30

gtt ttg cca ctg ctg gaa aag ctc gtt gtt gcg ccc ggt ttt att aaa 201
 Val Leu Pro Leu Leu Glu Lys Leu Val Val Ala Pro Gly Phe Ile Lys
 35 40 45

gaa acc gac ttc cta tcc ggc tac tcc gca gcg cag gca gtg cct ggc 249
 Glu Thr Asp Phe Leu Ser Gly Tyr Ser Ala Ala Gln Ala Val Pro Gly

50	55	60	65	
ccc atg ttc agc ttc gcc agc tac ctc ggc gca atc tac ggt ggc atc				297
Pro Met Phe Ser Phe Ala Ser Tyr Leu Gly Ala Ile Tyr Gly Gly Ile	70	75	80	
ggt ggt gca gtg ctg gcc agc ctg gcg atc ttc ttc ccc gcc gca ctc				345
Gly Gly Ala Val Leu Ala Ser Leu Ala Ile Phe Phe Pro Ala Ala Leu	85	90	95	
ttg agc atc agc gga atg tac ttt tgg gga cgc tgg cga aaa gca ccg				393
Leu Ser Ile Ser Gly Met Tyr Phe Trp Gly Arg Trp Arg Lys Ala Pro	100	105	110	
cgc atc caa gca gca gtc acc ggc atc aac gcc ggt gtg gtg ggg ctt				441
Arg Ile Gln Ala Ala Val Thr Gly Ile Asn Ala Gly Val Val Gly Leu	115	120	125	
ttg ggc gca gcg ctc tac gat ccc gta ttc acc cac ggc atc acc agc				489
Leu Gly Ala Ala Leu Tyr Asp Pro Val Phe Thr His Gly Ile Thr Ser	130	135	140	145
gtt tcc gca tta gct atc gca acg gtg tgt tgg ctg ggg cta gcc cac				537
Val Ser Ala Leu Ala Ile Ala Thr Val Cys Trp Leu Gly Leu Ala His	150	155	160	
tgg aaa att ccg ccg tgg gcc atc gcc gcg ggt gcg gcc ctt gca ggc				585
Trp Lys Ile Pro Pro Trp Ala Ile Ala Ala Gly Ala Ala Leu Ala Gly	165-	170	175	
tgg gtc ttg ctt tagaaaacgc tcagacccaa acc				620
Trp Val Leu Leu	180			
<210> 428				
<211> 181				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 428				
Val Val Phe Leu Gly Ala Leu Leu Gly Ala Val Ile Met Gly Gly Phe	1	5	10	15
Tyr Pro Ala Phe Ile Gln Ala Gly Ser Thr Val Phe Gly Gly Gly His	20	25	30	
Val Val Leu Pro Leu Leu Glu Lys Leu Val Val Ala Pro Gly Phe Ile	35	40	45	
Lys Glu Thr Asp Phe Leu Ser Gly Tyr Ser Ala Ala Gln Ala Val Pro	50	55	60	
Gly Pro Met Phe Ser Phe Ala Ser Tyr Leu Gly Ala Ile Tyr Gly Gly	65	70	75	80
Ile Gly Gly Ala Val Leu Ala Ser Leu Ala Ile Phe Phe Pro Ala Ala	85	90	95	
Leu Leu Ser Ile Ser Gly Met Tyr Phe Trp Gly Arg Trp Arg Lys Ala	100	105	110	

Pro Arg Ile Gln Ala Ala Val Thr Gly Ile Asn Ala Gly Val Val Gly
 115 120 125

Leu Leu Gly Ala Ala Leu Tyr Asp Pro Val Phe Thr His Gly Ile Thr
 130 135 140

Ser Val Ser Ala Leu Ala Ile Ala Thr Val Cys Trp Leu Gly Leu Ala
 145 150 155 160

His Trp Lys Ile Pro Pro Trp Ala Ile Ala Ala Gly Ala Ala Leu Ala
 165 170 175

Gly Trp Val Leu Leu
 180

<210> 429
 <211> 813
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(790)
 <223> RXA00852

<400> 429
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agaaatagtt ccaacccact tttcctcaga attgcagttc atg ccc gag atc att 115
 Met Pro Glu Ile Ile 5

ttt gac aac act gaa gta cgc tac gat gac tcg ctc att tta gag ccc 163
 Phe Asp Asn Thr Glu Val Arg Tyr Asp Asp Ser Leu Ile Leu Glu Pro 20

cta tcg tta aaa ctg aca gaa caa cgc att ggc atc atc ggg gct aac 211
 Leu Ser Leu Lys Leu Thr Glu Gln Arg Ile Gly Ile Ile Gly Ala Asn 35

ggc ggt gga aaa tcc acg ctc atc aga atg atc aat ggt ctc ggc gaa 259
 Gly Gly Gly Lys Ser Thr Leu Ile Arg Met Ile Asn Gly Leu Gly Glu 50

cca acc aca ggg cgt gtt cta gtt gat ggc ctt gac gtc tcg cat tcc 307
 Pro Thr Thr Gly Arg Val Leu Val Asp Gly Leu Asp Val Ser His Ser 65

gga cgg gaa gtt cgc aag aag gtt gga ttt gtc ttc tct gac gct gaa 355
 Gly Arg Glu Val Arg Lys Lys Val Gly Phe Val Phe Ser Asp Ala Glu 85

aac cag atc gtg atg cca act gtg cgt gag gat att gcc ttc tcg ctt 403
 Asn Gln Ile Val Met Pro Thr Val Arg Glu Asp Ile Ala Phe Ser Leu 100

cgc cgg cac aaa atg cca cgc gct gaa aag gcg caa cgt gtc gac gag 451
 Arg Arg His Lys Met Pro Arg Ala Glu Lys Ala Gln Arg Val Asp Glu 115

atg atg gcg cga ttc aac ttg agc gag cat gca gat caa tca ccg cac 499
 Met Met Ala Arg Phe Asn Leu Ser Glu His Ala Asp Gln Ser Pro His
 120 125 130
 acc cta tcc ggt ggt caa aag cag ttg tta gcg ctg gct gca gta ctg 547
 Thr Leu Ser Gly Gly Gln Lys Gln Leu Leu Ala Leu Ala Ala Val Leu
 135 140 145
 att ttg gag cca gaa gtg atc atc gct gat gag ccc act acc ctg ctg 595
 Ile Leu Glu Pro Glu Val Ile Ile Ala Asp Glu Pro Thr Thr Leu Leu
 150 155 160 165
 gat ctg cgc aat agg ctg atg atc aaa gac gtg ttc aat aaa ctc gag 643
 Asp Leu Arg Asn Arg Leu Met Ile Lys Asp Val Phe Asn Lys Leu Glu
 170 175 180
 cag caa tta atc gtt gtc agc cat gat tta gat ttc ctc agc gat ttt 691
 Gln Gln Leu Ile Val Val Ser His Asp Leu Asp Phe Leu Ser Asp Phe
 185 190 195
 gag cgg gtc att tgc atc aat gat cat aaa atc gct gct gat ggc cct 739
 Glu Arg Val Ile Cys Ile Asn Asp His Lys Ile Ala Ala Asp Gly Pro
 200 205 210
 ccg caa aag tcc att gac ctg tac gta tcg ctt atg gcg gaa cct gcg 787
 Pro Gln Lys Ser Ile Asp Leu Tyr Val Ser Leu Met Ala Glu Pro Ala
 215 220 225
 aaa tgaacagtat tccttttaggt ttt 813
 Lys
 230

<210> 430

<211> 230

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 430

Met Pro Glu Ile Ile Phe Asp Asn Thr Glu Val Arg Tyr Asp Asp Ser
 1 5 10 15
 Leu Ile Leu Glu Pro Leu Ser Leu Lys Leu Thr Glu Gln Arg Ile Gly
 20 25 30
 Ile Ile Gly Ala Asn Gly Gly Gly Lys Ser Thr Leu Ile Arg Met Ile
 35 40 45
 Asn Gly Leu Gly Glu Pro Thr Thr Gly Arg Val Leu Val Asp Gly Leu
 50 55 60
 Asp Val Ser His Ser Gly Arg Glu Val Arg Lys Lys Val Gly Phe Val
 65 70 75 80
 Phe Ser Asp Ala Glu Asn Gln Ile Val Met Pro Thr Val Arg Glu Asp
 85 90 95
 Ile Ala Phe Ser Leu Arg Arg His Lys Met Pro Arg Ala Glu Lys Ala
 100 105 110

Gln Arg Val Asp Glu Met Met Ala Arg Phe Asn Leu Ser Glu His Ala
 115 120 125

Asp Gln Ser Pro His Thr Leu Ser Gly Gly Gln Lys Gln Leu Leu Ala
 130 135 140

Leu Ala Ala Val Leu Ile Leu Glu Pro Glu Val Ile Ile Ala Asp Glu
 145 150 155 160

Pro Thr Thr Leu Leu Asp Leu Arg Asn Arg Leu Met Ile Lys Asp Val
 165 170 175

Phe Asn Lys Leu Glu Gln Gln Leu Ile Val Val Ser His Asp Leu Asp
 180 185 190

Phe Leu Ser Asp Phe Glu Arg Val Ile Cys Ile Asn Asp His Lys Ile
 195 200 205

Ala Ala Asp Gly Pro Pro Gln Lys Ser Ile Asp Leu Tyr Val Ser Leu
 210 215 220

Met Ala Glu Pro Ala Lys
 225 230

<210> 431
 <211> 1269
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1246)
 <223> RXA00690

<400> 431
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gtgggcgatt cgctgttcag aggtccaggg ttaaagcttc gtg aaa tgg att gag 115
 Val Lys Trp Ile Glu
 1 5

cga tat gtg ctg tcc cgg cgg atg gtt cat ccc tgg gcg tgg tgg gtg 163
 Arg Tyr Val Leu Ser Arg Arg Met Val His Pro Trp Ala Trp Trp Val
 10 15 20

tgg gcg ttg ggt att gct ggt tgt gcc agc atg acc aac aat cct tat 211
 Trp Ala Leu Gly Ile Ala Gly Cys Ala Ser Met Thr Asn Asn Pro Tyr
 25 30 35

att ttg gcg ctc act ttt gcc acg ttg tgt ttt gtg gtg ttt aac cgt 259
 Ile Leu Ala Leu Thr Phe Ala Thr Leu Cys Phe Val Val Phe Asn Arg
 40 45 50

cgt ggg tca tcg ccg tgg tcg cgt gct ttc ccg atc tat ttg atg atc 307
 Arg Gly Ser Ser Pro Trp Ser Arg Ala Phe Pro Ile Tyr Leu Met Ile
 55 60 65

gcg ggt tgg ctc gtg gtg tac cgg ttg gtc atg cac att gtg gtg gga 355
 Ala Gly Trp Leu Val Val Tyr Arg Leu Val Met His Ile Val Val Gly
 70 75 80 85

gca aaa att ggc acc att gaa ctg ttt cgg atc ccg ccg gtg cag ttg	403
Ala Lys Ile Gly Thr Ile Glu Leu Phe Arg Ile Pro Pro Val Gln Leu	
90 95 100	
ccg gaa tgg gct gcg ggt atc cac gtg ttt ggc acg gtg tat ctc gag	451
Pro Glu Trp Ala Ala Gly Ile His Val Phe Gly Thr Val Tyr Leu Glu	
105 110 115	
ggt ctg atc atc gcg acg acg caa ggc tta acg ctt gga acg atg atc	499
Gly Leu Ile Ile Ala Thr Thr Gln Gly Leu Thr Leu Gly Thr Met Ile	
120 125 130	
gtg gcg gtg ggt gct gcg aac tct ttg gcg gat ccc aag aag ctg ctc	547
Val Ala Val Gly Ala Ala Asn Ser Leu Ala Asp Pro Lys Lys Leu Leu	
135 140 145	
aaa tcg ttg cct ggc gca ttg ggc gaa ctg gga act gcg gtg gtc atc	595
Lys Ser Leu Pro Gly Ala Leu Gly Glu Leu Gly Thr Ala Val Val Ile	
150 155 160 165	
ggt att tcc att gca cct cag atg gct gag tcg gcg ttc cgc att aat	643
Gly Ile Ser Ile Ala Pro Gln Met Ala Glu Ser Ala Phe Arg Ile Asn	
170 175 180	
cgt gca cga acc ttg cgt ggt gat gat gcc aaa ggt gtt cgt ggt ttc	691
Arg Ala Arg Thr Leu Arg Gly Asp Asp Ala Lys Gly Val Arg Gly Phe	
185 190 195	
gcg ccg att ttg atg ccg gtt ttc cag gac act ttg gat agg tct ttg	739
Ala Arg Ile Leu Met Pro Val Phe Gln Asp Thr Leu Asp Arg Ser Leu	
200 205 210	
gcc ctg gct aat tcc atg gat gcc cgt ggt tat ggc agg cag gct cat	787
Ala Leu Ala Asn Ser Met Asp Ala Arg Gly Tyr Gly Arg Gln Ala His	
215 220 225	
gta tcc aaa ttc caa cag cgt gtg acc tct att ttt ggt gca ttc gga	835
Val Ser Lys Phe Gln Gln Arg Val Thr Ser Ile Phe Gly Ala Phe Gly	
230 235 240 245	
ata ctc ggc gtg acc gtt ggt ctg ttt gtg gtc tta gat gca tca tca	883
Ile Leu Gly Val Thr Val Gly Leu Phe Val Val Leu Asp Ala Ser Ser	
250 255 260	
ccg atg ttc gtt gcc gtt ccg gtg ttt att acc ggc gtg ggc ttc ttg	931
Pro Met Phe Val Ala Val Pro Val Phe Ile Thr Gly Val Gly Phe Leu	
265 270 275	
atc att tcg ttg gtc gtt gct tca cat aga aaa aca tcc acc act ttt	979
Ile Ile Ser Leu Val Val Ala Ser His Arg Lys Thr Ser Thr Thr Phe	
280 285 290	
gat cag ttg cct tgg ggt gct gcg gaa tgg ctt gtg tgc atc aca ggt	1027
Asp Gln Leu Pro Trp Gly Ala Ala Glu Trp Leu Val Cys Ile Thr Gly	
295 300 305	
gtg att ccg ctg ctc atg gct gcg ctg aca cga tac ctt gat cca ggt	1075
Val Ile Pro Leu Leu Met Ala Ala Leu Thr Arg Tyr Leu Asp Pro Gly	
310 315 320 325	

tcc atg atc acc acc tgg gtt cct ttg cat atg cca gac acc gtt ccg 1123
 Ser Met Ile Thr Thr Trp Val Pro Leu His Met Pro Asp Thr Val Pro
 330 335 340

ttg ctc gtt gtg gca gga ctt gtt gtg gcg acg atg cca gga ttc ttg 1171
 Leu Leu Val Val Ala Gly Leu Val Val Ala Thr Met Pro Gly Phe Leu
 345 350 355

acg ccc cgc ttg ccg aag aac aaa gtg agg gtc aag cgt cga aaa gca 1219
 Thr Pro Arg Leu Pro Lys Asn Lys Val Arg Val Lys Arg Arg Lys Ala
 360 365 370

ata aat agc cca gaa agg gcc gaa gtt taatgagtgcc tccttttagc 1266
 Ile Asn Ser Pro Glu Arg Ala Glu Val
 375 380

gcg 1269

<210> 432

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Val Lys Trp Ile Glu Arg Tyr Val Leu Ser Arg Arg Met Val His Pro
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Trp Ala Trp Trp Val Trp Ala Leu Gly Ile Ala Gly Cys Ala Ser Met
 20 25 30

Thr Asn Asn Pro Tyr Ile Leu Ala Leu Thr Phe Ala Thr Leu Cys Phe
 35 40 45

Val Val Phe Asn Arg Arg Gly Ser Ser Pro Trp Ser Arg Ala Phe Pro
 50 55 60

Ile Tyr Leu Met Ile Ala Gly Trp Leu Val Val Tyr Arg Leu Val Met
 65 70 75 80

His Ile Val Val Gly Ala Lys Ile Gly Thr Ile Glu Leu Phe Arg Ile
 85 90 95

Pro Pro Val Gln Leu Pro Glu Trp Ala Ala Gly Ile His Val Phe Gly
 100 105 110

Thr Val Tyr Leu Glu Gly Leu Ile Ile Ala Thr Thr Gln Gly Leu Thr
 115 120 125

Leu Gly Thr Met Ile Val Ala Val Gly Ala Ala Asn Ser Leu Ala Asp
 130 135 140

Pro Lys Lys Leu Leu Lys Ser Leu Pro Gly Ala Leu Gly Glu Leu Gly
 145 150 155 160

Thr Ala Val Val Ile Gly Ile Ser Ile Ala Pro Gln Met Ala Glu Ser
 165 170 175

Ala Phe Arg Ile Asn Arg Ala Arg Thr Leu Arg Gly Asp Asp Ala Lys
 180 185 190

Gly Val Arg Gly Phe Ala Arg Ile Leu Met Pro Val Phe Gln Asp Thr
 195 200 205
 Leu Asp Arg Ser Leu Ala Leu Ala Asn Ser Met Asp Ala Arg Gly Tyr
 210 215 220
 Gly Arg Gln Ala His Val Ser Lys Phe Gln Gln Arg Val Thr Ser Ile
 225 230 235 240
 Phe Gly Ala Phe Gly Ile Leu Gly Val Thr Val Gly Leu Phe Val Val
 245 250 255
 Leu Asp Ala Ser Ser Pro Met Phe Val Ala Val Pro Val Phe Ile Thr
 260 265 270
 Gly Val Gly Phe Leu Ile Ile Ser Leu Val Val Ala Ser His Arg Lys
 275 280 285
 Thr Ser Thr Thr Phe Asp Gln Leu Pro Trp Gly Ala Ala Glu Trp Leu
 290 295 300
 Val Cys Ile Thr Gly Val Ile Pro Leu Leu Met Ala Ala Leu Thr Arg
 305 310 315 320
 Tyr Leu Asp Pro Gly Ser Met Ile Thr Thr Trp Val Pro Leu His Met
 325 330 335
 Pro Asp Thr Val Pro Leu Leu Val Val Ala Gly Leu Val Val Ala Thr
 340 345 350
 Met Pro Gly Phe Leu Thr Pro Arg Leu Pro Lys Asn Lys Val Arg Val
 355 360 365
 Lys Arg Arg Lys Ala Ile Asn Ser Pro Glu Arg Ala Glu Val
 370 375 380

<210> 433
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(853)
 <223> RXA00827

<400> 433
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 tcgcagcgct gggcgatcac cacattgagg tgagcgcgaa gtg aac ctg ctg atc 115
 Val Asn Leu Leu Ile
 1 5
 aaa att aat ccc gtc acc cgc atc atc gcg ttg atg gta ctg acc acg 163
 Lys Ile Asn Pro Val Thr Arg Ile Ile Ala Leu Met Val Leu Thr Thr
 10 15 20
 ccg ttg ctg ctg agt ttg gat gtg atg tcg gca gcg atc gcg ctg gtg 211
 Pro Leu Leu Leu Ser Leu Asp Val Met Ser Ala Ala Ile Ala Leu Val
 25 30 35

gca acc att att ctg gca cca ttt gcc ggc gtg acc tgg aag atg ctg 259
 Ala Thr Ile Ile Leu Ala Pro Phe Ala Gly Val Thr Trp Lys Met Leu
 40 45 50

ctg aaa cgt ggc tgg atg ctg ttc ctc atg gca ccg gtg gct gca tta 307
 Leu Lys Arg Gly Trp Met Leu Phe Leu Met Ala Pro Val Ala Ala Leu
 55 60 65

tcc atg gcg ctt tat ggc agg ccg gat gga aaa gag tac ttt agc ttc 355
 Ser Met Ala Leu Tyr Gly Arg Pro Asp Gly Lys Glu Tyr Phe Ser Phe
 70 75 80 85

ctg ctc att cac gtc act gat aat tca ctg gct ttg gct gct gcc att 403
 Leu Leu Ile His Val Thr Asp Asn Ser Leu Ala Leu Ala Ala Ile
 90 95 100

ggg ctg cgt gtt ctg gcg att ggt ctg ccc gtt gtg gtg ctg att gct 451
 Gly Leu Arg Val Leu Ala Ile Gly Leu Pro Val Val Val Leu Ile Ala
 105 110 115

cgc att gat ccc acc gac ctg ggc gat ggt ttg gcg cag ctg ctc aaa 499
 Arg Ile Asp Pro Thr Asp Leu Gly Asp Gly Leu Ala Gln Leu Leu Lys
 120 125 130

ctg cct gaa agg ttt gtc atc ggt gct gtg gca gga agc cga ctg atg 547
 Leu Pro Glu Arg Phe Val Ile Gly Ala Val Ala Gly Ser Arg Leu Met
 135 140 145

acg ctt ttt cgg gaa gat tgg tac tcc atg tcc agg gca agg cgt gcc 595
 Thr Leu Phe Arg Glu Asp Trp Tyr Ser Met Ser Arg Ala Arg Arg Ala
 150 155 160 165

cgc gga att gct gat cag ggc aag atc aag cac ttt ttc acc atg act 643
 Arg Gly Ile Ala Asp Gln Gly Lys Ile Lys His Phe Phe Thr Met Thr
 170 175 180

ttt ggt ttg ttg gtg ctc tcg ctt cgc cgt gga tcc aag ctt gca acg 691
 Phe Gly Leu Leu Val Leu Ser Leu Arg Arg Gly Ser Lys Leu Ala Thr
 185 190 195

gcg atg gaa gca cgc ggt ttt ggt cgc acg act ggc cgc acc tgg gca 739
 Ala Met Glu Ala Arg Gly Phe Gly Arg Thr Thr Gly Arg Thr Trp Ala
 200 205 210

agg gaa tcc acc gtc ggc gcg cgc gat ctg gtg ctc atc ttg gtg tgt 787
 Arg Glu Ser Thr Val Gly Ala Arg Asp Leu Val Leu Ile Leu Val Cys
 215 220 225

gct gcc att tcc gcg atc gct cta acc gtg tcc att cag act ggt ttc 835
 Ala Ala Ile Ser Ala Ile Ala Leu Thr Val Ser Ile Gln Thr Gly Phe
 230 235 240 245

ttt aag ttc ttg ggc aca tgatcacagt tttaattgat gga 876
 Phe Lys Phe Leu Gly Thr
 250

<210> 434

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 434

Val Asn Leu Leu Ile Lys Ile Asn Pro Val Thr Arg Ile Ile Ala Leu
 1 5 10 15
 Met Val Leu Thr Thr Pro Leu Leu Leu Ser Leu Asp Val Met Ser Ala
 20 25 30
 Ala Ile Ala Leu Val Ala Thr Ile Ile Leu Ala Pro Phe Ala Gly Val
 35 40 45
 Thr Trp Lys Met Leu Leu Lys Arg Gly Trp Met Leu Phe Leu Met Ala
 50 55 60
 Pro Val Ala Ala Leu Ser Met Ala Leu Tyr Gly Arg Pro Asp Gly Lys
 65 70 75 80
 Glu Tyr Phe Ser Phe Leu Leu Ile His Val Thr Asp Asn Ser Leu Ala
 85 90 95
 Leu Ala Ala Ala Ile Gly Leu Arg Val Leu Ala Ile Gly Leu Pro Val
 100 105 110
 Val Val Leu Ile Ala Arg Ile Asp Pro Thr Asp Leu Gly Asp Gly Leu
 115 120 125
 Ala Gln Leu Leu Lys Leu Pro Glu Arg Phe Val Ile Gly Ala Val Ala
 130 135 140
 Gly Ser Arg Leu Met Thr Leu Phe Arg Glu Asp Trp Tyr Ser Met Ser
 145 150 155 160
 Arg Ala Arg Arg Ala Arg Gly Ile Ala Asp Gln Gly Lys Ile Lys His
 165 170 175
 Phe Phe Thr Met Thr Phe Gly Leu Leu Val Leu Ser Leu Arg Arg Gly
 180 185 190
 Ser Lys Leu Ala Thr Ala Met Glu Ala Arg Gly Phe Gly Arg Thr Thr
 195 200 205
 Gly Arg Thr Trp Ala Arg Glu Ser Thr Val Gly Ala Arg Asp Leu Val
 210 215 220
 Leu Ile Leu Val Cys Ala Ala Ile Ser Ala Ile Ala Leu Thr Val Ser
 225 230 235 240
 Ile Gln Thr Gly Phe Phe Lys Phe Leu Gly Thr
 245 250

<210> 435

<211> 732

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(709)

<223> RXA00851

<400> 435

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ccattgacct gtacgtatcg cttatggcgg aacctgcgaa atg aac agt att cct 115
                                         Met Asn Ser Ile Pro
                                         1           5
tta ggt ttt tac gtc gat aag caa tct gtt gtt cat tct ttt cct gct 163
Leu Gly Phe Tyr Val Asp Lys Gln Ser Val Val His Ser Phe Pro Ala
              10              15              20
ttg tgg aaa ttc cca ctt ctg ctg ttt ttc atc atc ggc ggc tcc atc 211
Leu Trp Lys Phe Pro Leu Leu Leu Phe Phe Ile Ile Gly Gly Ser Ile
              25              30              35
gcg gct tct acc ccg gtt cat ggg ttg att ttg gtg ggg att gca gtg 259
Ala Ala Ser Thr Pro Val His Gly Leu Ile Leu Val Gly Ile Ala Val
              40              45              50
gtg ttt tac gtg ctg gcg aag att ccg ctg aag gtc gcg tgg gag cag 307
Val Phe Tyr Val Leu Ala Lys Ile Pro Leu Lys Val Ala Trp Glu Gln
              55              60              65
ttg tgg cca gtg ctg ccg att ttg atc atg ctc ggt gcg ttt cag tgg 355
Leu Trp Pro Val Leu Pro Ile Leu Ile Met Leu Gly Ala Phe Gln Trp
              70              75              80              85
tgg cag cgc ggc ttt gat ttc gcg gca acc aca gtg ctc acg ctg ttt 403
Trp Gln Arg Gly Phe Asp Phe Ala Ala Thr Thr Val Leu Thr Leu Phe
              90              95              100
tcc gcg gtg atg gcc gcc atg ttg ttg acg ttg acc acg cgg ttg gaa 451
Ser Ala Val Met Ala Ala Met Leu Leu Thr Leu Thr Thr Arg Leu Glu
              105              110              115
gcg ctc atg aat gca gtt gag cgg atg ttg cag cot ttt gca cgt ttt 499
Ala Leu Met Asn Ala Val Glu Arg Met Leu Gln Pro Phe Ala Arg Phe
              120              125              130
ggc ctg cca gta gag acg atc acc ttg gct att tct ctc acg att cgg 547
Gly Leu Pro Val Glu Thr Ile Thr Leu Ala Ile Ser Leu Thr Ile Arg
              135              140              145
ctc att ccg ctg caa tta gcc acg gtg aag gaa gtc ctc gat gcc cgt 595
Leu Ile Pro Leu Gln Leu Ala Thr Val Lys Glu Val Leu Asp Ala Arg
              150              155              160              165
aaa gct cgt ggt gcc ggt ttt tct atc gcc gcg ttt ggc acg cct gtg 643
Lys Ala Arg Gly Ala Gly Phe Ser Ile Ala Ala Phe Gly Thr Pro Val
              170              175              180
atc atc aga tca ata aag agg gcc cgc aat atc ggc gat gct ctt ctc 691
Ile Ile Arg Ser Ile Lys Arg Ala Arg Asn Ile Gly Asp Ala Leu Leu
              185              190              195
gca cgt ggt gcc ggc gat taatttcttt caacacatag caa 732
Ala Arg Gly Ala Gly Asp
              200

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<210> 436
 <211> 203
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 436

Met Asn Ser Ile Pro Leu Gly Phe Tyr Val Asp Lys Gln Ser Val Val
 1 5 10 15

His Ser Phe Pro Ala Leu Trp Lys Phe Pro Leu Leu Leu Phe Phe Ile
 20 25 30

Ile Gly Gly Ser Ile Ala Ala Ser Thr Pro Val His Gly Leu Ile Leu
 35 40 45

Val Gly Ile Ala Val Val Phe Tyr Val Leu Ala Lys Ile Pro Leu Lys
 50 55 60

Val Ala Trp Glu Gln Leu Trp Pro Val Leu Pro Ile Leu Ile Met Leu
 65 70 75 80

Gly Ala Phe Gln Trp Trp Gln Arg Gly Phe Asp Phe Ala Ala Thr Thr
 85 90 95

Val Leu Thr Leu Phe Ser Ala Val Met Ala Ala Met Leu Leu Thr Leu
 100 105 110

Thr Thr Arg Leu Glu Ala Leu Met Asn Ala Val Glu Arg Met Leu Gln
 115 120 125

Pro Phe Ala Arg Phe Gly Leu Pro Val Glu Thr Ile Thr Leu Ala Ile
 130 135 140

Ser Leu Thr Ile Arg Leu Ile Pro Leu Gln Leu Ala Thr Val Lys Glu
 145 150 155 160

Val Leu Asp Ala Arg Lys Ala Arg Gly Ala Gly Phe Ser Ile Ala Ala
 165 170 175

Phe Gly Thr Pro Val Ile Ile Arg Ser Ile Lys Arg Ala Arg Asn Ile
 180 185 190

Gly Asp Ala Leu Leu Ala Arg Gly Ala Gly Asp
 195 200

<210> 437
 <211> 725
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (3)..(695)

<223> RXS03220

<400> 437

ccatg ggc tta agg gaa att ttg tcc agc aag tgg ctt gtg cgc atc ctc 50
 Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
 1 5 10 15

ctg gta ggt atc gga ttg ggt gtc gca cag cag ctg acc ggc atc aac	98
Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn	
20 25 30	
tcc atc atg tac tac ggc cag gtt gtt ctc att gag gct ggt ttc tcc	146
Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser	
35 40 45	
gag aat gca gct ctg atc gcc aac gtg gcg cca gga gtg atc gca gtt	194
Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val	
50 55 60	
gtc ggt gca ttc atc gca ctg tgg atg atg gat ggt atc aac cgc cgt	242
Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg	
65 70 75 80	
acc acc ctc att acc ggt tat tct ctc acc acc att agc cac gta ttg	290
Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu	
85 90 95	
atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct ctt cgc ccc	338
Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro	
100 105 110	
tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc atg cag acc	386
Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser Met Gln Thr	
115 120 125	
ttc ctc aac gta gct acc tgg gtt atg ctc tct gag ctc ttc ccg ctg	434
Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu	
130 135 140	
gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc ctc tgg atc	482
Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile	
145 150 155 160	
gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg gaa gca gta	530
Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val	
165 170 175	
gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt gtg gtt gcc	578
Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala	
180 185 190	
ttg atc ttc atc tac acc cag gtt cct gaa act cgt gga cgt acc ttg	626
Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu	
195 200 205	
gag gag att gat gag gat gtt act tcc ggt gtc att ttc aac aag gac	674
Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp	
210 215 220	
atc cga aaa gga aag gtg cac taaaaaccca gacactgcat agataacacg	725
Ile Arg Lys Gly Lys His	
225 230	

<210> 438

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
 1 5 10 15

Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn
 20 25 30

Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser
 35 40 45

Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val
 50 55 60

Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg
 65 70 75 80

Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu
 85 90 95

Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro
 100 105 110

Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser Met Gln Thr
 115 120 125

Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu
 130 135 140

Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile
 145 150 155 160

Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val
 165 170 175

Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala
 180 185 190

Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu
 195 200 205

Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp
 210 215 220

Ile Arg Lys Gly Lys Val His
 225 230

<210> 439

<211> 408

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(385)

<223> FRXA02762

<400> 439

ttcccgatcg gcgatcctct tcgccctac gttatcttga ctctggttgt ggtcttcgtg 60

<220>
 <221> CDS
 <222> (101)..(766)
 <223> RXN00092

<400> 441

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cgaaaccaga aacaccagc ggctcctcgt cgaaaagcga atctttgaac tagaagccca 60

ggcacgttgg ctcgaccgaa ttgaagcatt ggagcagtaa atg aca aac acg cct 115
                                         Met Thr Asn Thr Pro
                                         1           5

ttc ccc ctt gaa ctt caa aac atc tcc tgc gcc ttc gga gaa ggc cca 163
Phe Pro Leu Glu Leu Gln Asn Ile Ser Cys Ala Phe Gly Glu Gly Pro
                        10                15                20

cgc cac gtc tcc gcg ctc aac aac gtc tgc ctg gca gtc aat ccc ggc 211
Arg His Val Ser Ala Leu Asn Asn Val Ser Leu Ala Val Asn Pro Gly
                        25                30                35

gaa ctc gtt gcc atc atg ggc ccg tcc ggc tca gga aaa tcc acc ttg 259
Glu Leu Val Ala Ile Met Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu
                        40                45                50

ctc aac gtc gcc ggc ctc ctg cag cgc gca acc tct ggc cat gtg ctt 307
Leu Asn Val Ala Gly Leu Leu Gln Arg Ala Thr Ser Gly His Val Leu
                        55                60                65

atc gac ggt gcc agc gcc tca gac ctc aac gcc aaa cgc gca gct gaa 355
Ile Asp Gly Ala Ser Ala Ser Asp Leu Asn Ala Lys Arg Ala Ala Glu
                        70                75                80                85

acc agg cgt cgc cac atc gga gtt att ttc caa aac tac aac ctg gtc 403
Thr Arg Arg Arg His Ile Gly Val Ile Phe Gln Asn Tyr Asn Leu Val
                        90                95                100

ccc acc ctc acc gtc gga gaa aac gtc ggt ctg ccc cta gaa ctc gac 451
Pro Thr Leu Thr Val Gly Glu Asn Val Gly Leu Pro Leu Glu Leu Asp
                        105                110                115

ggc aaa acc gac cgc cag gca gta gca atc gca ctc gcg gaa gtc ggc 499
Gly Lys Thr Asp Arg Gln Ala Val Ala Ile Ala Leu Ala Glu Val Gly
                        120                125                130

ctc gaa ggc ttc gac gac cgc ttc ccc gaa gag atc tcc ggc ggc caa 547
Leu Glu Gly Phe Asp Asp Arg Phe Pro Glu Glu Ile Ser Gly Gly Gln
                        135                140                145

gcc cag cgc gtc gcc atc gcg aga gcc ctc atc ggc ccc cga aaa atc 595
Ala Gln Arg Val Ala Ile Ala Arg Ala Leu Ile Gly Pro Arg Lys Ile
                        150                155                160                165

ttg ctt gcc gac gaa ccc acc ggc gcc ctc gac acc tcc acc ggc gac 643
Leu Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp Thr Ser Thr Gly Asp
                        170                175                180

gca gtc ctc cgc gtc ctc cgc caa aga atc gat tcc ggt gcc gca ggc 691
Ala Val Leu Arg Val Leu Arg Gln Arg Ile Asp Ser Gly Ala Ala Gly
                        185                190                195

ctc ctt gtc acc cac gaa ccc cgc ttc gcc gcg tgg gca gac cga aca 739

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Leu Leu Val Thr His Glu Pro Arg Phe Ala Ala Trp Ala Asp Arg Thr
 200 205 210

atc atg ctt agg gat ggt gaa atc cag.tgaccacact tctagcagca 786
 Ile Met Leu Arg Asp Gly Glu Ile Gln
 215 220

acc 789

<210> 442

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 442

Met Thr Asn Thr Pro Phe Pro Leu Glu Leu Gln Asn Ile Ser Cys Ala
 1 5 10 15

Phe Gly Glu Gly Pro Arg His Val Ser Ala Leu Asn Asn Val Ser Leu
 20 25 30

Ala Val Asn Pro Gly Glu Leu Val Ala Ile Met Gly Pro Ser Gly Ser
 35 40 45

Gly Lys Ser Thr Leu Leu Asn Val Ala Gly Leu Leu Gln Arg Ala Thr
 50 55 60

Ser Gly His Val Leu Ile Asp Gly Ala Ser Ala Ser Asp Leu Asn Ala
 65 70 75 80

Lys Arg Ala Ala Glu Thr Arg Arg Arg His Ile Gly Val Ile Phe Gln
 85 90 95

Asn Tyr Asn Leu Val Pro Thr Leu Thr Val Gly Glu Asn Val Gly Leu
 100 105 110

Pro Leu Glu Leu Asp Gly Lys Thr Asp Arg Gln Ala Val Ala Ile Ala
 115 120 125

Leu Ala Glu Val Gly Leu Glu Gly Phe Asp Asp Arg Phe Pro Glu Glu
 130 135 140

Ile Ser Gly Gly Gln Ala Gln Arg Val Ala Ile Ala Arg Ala Leu Ile
 145 150 155 160

Gly Pro Arg Lys Ile Leu Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp
 165 170 175

Thr Ser Thr Gly Asp Ala Val Leu Arg Val Leu Arg Gln Arg Ile Asp
 180 185 190

Ser Gly Ala Ala Gly Leu Leu Val Thr His Glu Pro Arg Phe Ala Ala
 195 200 205

Trp Ala Asp Arg Thr Ile Met Leu Arg Asp Gly Glu Ile Gln
 210 215 220

<210> 443

<211> 227

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(204)

<223> FRXA00092

<400> 443

atc gcg aga gcc ctc atc ggc ccc cga aaa atc ttg ctt gcc gac gaa 48
 Ile Ala Arg Ala Leu Ile Gly Pro Arg Lys Ile Leu Leu Ala Asp Glu
 1 5 10 15

ccc acc ggc gcc ctc gac acc tcc acc ggc gac gca gtc ctc cgc gtc 96
 Pro Thr Gly Ala Leu Asp Thr Ser Thr Gly Asp Ala Val Leu Arg Val
 20 25 30

ctc cgc caa aga atc gat tcc ggt gcc gca ggc ctc ctt gtc acc cac 144
 Leu Arg Gln Arg Ile Asp Ser Gly Ala Ala Gly Leu Leu Val Thr His
 35 40 45

gaa ccc cgc ttc gcc gcg tgg gca gac cga aca atc atg ctt agg gat 192
 Glu Pro Arg Phe Ala Ala Trp Ala Asp Arg Thr Ile Met Leu Arg Asp
 50 55 60

ggt gaa atc cag tgaccacact tctagcagca acc 227
 Gly Glu Ile Gln
 65

<210> 444

<211> 68

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

Ile Ala Arg Ala Leu Ile Gly Pro Arg Lys Ile Leu Leu Ala Asp Glu
 1 5 10 15

Pro Thr Gly Ala Leu Asp Thr Ser Thr Gly Asp Ala Val Leu Arg Val
 20 25 30

Leu Arg Gln Arg Ile Asp Ser Gly Ala Ala Gly Leu Leu Val Thr His
 35 40 45

Glu Pro Arg Phe Ala Ala Trp Ala Asp Arg Thr Ile Met Leu Arg Asp
 50 55 60

Gly Glu Ile Gln
 65

<210> 445

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXN03060

Leu Asp Ser Asn Ser Ser Arg Glu Val Leu Asp Ile Leu Arg Thr Ala
 215 220 225
 gtt gat cag gat gat cag acc gtt gtg atc gtt acc cac gat gcc aag 835
 Val Asp Gln Asp Asp Gln Thr Val Val Ile Val Thr His Asp Ala Lys
 230 235 240 245
 gcg gcg tcc tat gca gat cgt gtc att ttc ttg gcg gac ggt cgt atc 883
 Ala Ala Ser Tyr Ala Asp Arg Val Ile Phe Leu Ala Asp Gly Arg Ile
 250 255 260
 gtg aac cag ttg ttt gat ccc acc atc gag gaa atc ttg gcc acg atg 931
 Val Asn Gln Leu Phe Asp Pro Thr Ile Glu Glu Ile Leu Ala Thr Met
 265 270 275
 aac gga att gag gat att gcc taatgaattc cggttcacaca atg 975
 Asn Gly Ile Glu Asp Ile Ala
 280

<210> 446

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 446

Met Ser Asn Pro Ala Ala Ser Thr Pro Ala Asn Asn Ser Asp Asp Val
 1 5 10 15
 Ala Lys Glu Asn Trp Asp Ser Ser Phe Thr Pro Lys Thr Asp Ile Asp
 20 25 30
 Ser Ser Gln Pro Val Asn Asn Ser Thr Gly Glu Ala Ala Ala Arg Ala
 35 40 45
 Val Asn Leu Tyr Lys Ala Tyr Gly Gln Gly Asp Thr Thr Val Thr Ala
 50 55 60
 Leu Asp His Val Asn Val Glu Phe Glu Lys Asn Lys Phe Thr Ala Ile
 65 70 75 80
 Met Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Met His Cys Met Ala
 85 90 95
 Gly Leu Asp Ala Ala Thr Gly Gly Ser Ala Phe Ile Gly Asp Thr Asp
 100 105 110
 Leu Ser Arg Leu Lys Asp Lys Glu Met Thr Ser Leu Arg Arg Asp Arg
 115 120 125
 Leu Gly Phe Ile Phe Gln Ser Phe Asn Leu Val Pro Thr Leu Thr Ala
 130 135 140
 Ser Glu Asn Ile Thr Leu Pro Thr Asp Ile Ala Gly Arg Lys Ile Asp
 145 150 155 160
 Gln Ser Trp Phe Asp Glu Ile Thr Ser Arg Leu Gly Leu Thr Glu Arg
 165 170 175
 Leu Lys His Arg Pro Ala Glu Leu Ser Gly Gly Gln Gln Gln Arg Val
 180 185 190

Ala Cys Ala Arg Ala Leu Val Ser Arg Pro Glu Ile Ile Phe Gly Asp
 195 200 205

Glu Pro Thr Gly Asn Leu Asp Ser Asn Ser Ser Arg Glu Val Leu Asp
 210 215 220

Ile Leu Arg Thr Ala Val Asp Gln Asp Asp Gln Thr Val Val Ile Val
 225 230 235 240

Thr His Asp Ala Lys Ala Ala Ser Tyr Ala Asp Arg Val Ile Phe Leu
 245 250 255

Ala Asp Gly Arg Ile Val Asn Gln Leu Phe Asp Pro Thr Ile Glu Glu
 260 265 270

Ile Leu Ala Thr Met Asn Gly Ile Glu Asp Ile Ala
 275 280

<210> 447
 <211> 538
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(538)
 <223> FRXA02618

<400> 447
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ggcacgttgg ctcgaccgaa ttgaagcatt ggagcagtaa atg aca aac acg cct 115
 Met Thr Asn Thr Pro
 1 5

ttc ccc ctt gaa ctt caa aac atc tcc tgc gcc ttc gga gaa ggc cca 163
 Phe Pro Leu Glu Leu Gln Asn Ile Ser Cys Ala Phe Gly Glu Gly Pro
 10 15 20

cgc cac gtc tcc gcg ctc aac aac gtc tcg ctg gca gtc aat ccc ggc 211
 Arg His Val Ser Ala Leu Asn Asn Val Ser Leu Ala Val Asn Pro Gly
 25 30 35

gaa ctc gtt gcc atc atg ggc ccg tcc ggc tca gga aaa tcc acc ttg 259
 Glu Leu Val Ala Ile Met Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu
 40 45 50

ctc aac gtc gcc ggc ctc ctg cag cgc gca acc tct ggc cat gtg ctt 307
 Leu Asn Val Ala Gly Leu Leu Gln Arg Ala Thr Ser Gly His Val Leu
 55 60 65

atc gac ggt gcc agc gcc tca gac ctc aac gcc aaa cgc gca gct gaa 355
 Ile Asp Gly Ala Ser Ala Ser Asp Leu Asn Ala Lys Arg Ala Ala Glu
 70 75 80 85

acc agg cgt cgc cac atc gga gtt att ttc caa aac tac aac ctg gtc 403
 Thr Arg Arg Arg His Ile Gly Val Ile Phe Gln Asn Tyr Asn Leu Val
 90 95 100

ccc acc ctc acc gtc gga gaa aac atc ggt ctg ccc cta gaa ctc gac 451
 Pro Thr Leu Thr Val Gly Glu Asn Ile Gly Leu Pro Leu Glu Leu Asp
 105 110 115

ggc aaa acc gac cgc cag gca gta gca atc gca ctc gcg gaa gtc ggc 499
 Gly Lys Thr Asp Arg Gln Ala Val Ala Ile Ala Leu Ala Glu Val Gly
 120 125 130

ctc aag ggc tct acg acc gct ttt ccc gag aga tct ctg 538
 Leu Lys Gly Ser Thr Thr Ala Phe Pro Glu Arg Ser Leu
 135 140 145

<210> 448

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 448

Met Thr Asn Thr Pro Phe Pro Leu Glu Leu Gln Asn Ile Ser Cys Ala
 1 5 10 15

Phe Gly Glu Gly Pro Arg His Val Ser Ala Leu Asn Asn Val Ser Leu
 20 25 30

Ala Val Asn Pro Gly Glu Leu Val Ala Ile Met Gly Pro Ser Gly Ser
 35 40 45

Gly Lys Ser Thr Leu Leu Asn Val Ala Gly Leu Leu Gln Arg Ala Thr
 50 55 60

Ser Gly His Val Leu Ile Asp Gly Ala Ser Ala Ser Asp Leu Asn Ala
 65 70 75 80

Lys Arg Ala Ala Glu Thr Arg Arg Arg His Ile Gly Val Ile Phe Gln
 85 90 95

Asn Tyr Asn Leu Val Pro Thr Leu Thr Val Gly Glu Asn Ile Gly Leu
 100 105 110

Pro Leu Glu Leu Asp Gly Lys Thr Asp Arg Gln Ala Val Ala Ile Ala
 115 120 125

Leu Ala Glu Val Gly Leu Lys Gly Ser Thr Thr Ala Phe Pro Glu Arg
 130 135 140

Ser Leu
 145

<210> 449

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> FRXA02900

<400> 449

tatgtccttt ggctccggtta cctctggcagg agtacctggg ctgttttttct aaaatggcct																60
gacgtttttca agattgaatt taaggaaagc atcgtagttc atg agt aac cct gcc																115
Met Ser Asn Pro Ala																5
gcg agc aca cct gcc aac aat tcg gac gat gtt gcg aag gag aat tgg																163
Ala Ser Thr Pro Ala Asn Asn Ser Asp Asp Val Ala Lys Glu Asn Trp																20
gac tct tct ttt acg ccg aag act gac att gac tct tcc cag cct gtc																211
Asp Ser Ser Phe Thr Pro Lys Thr Asp Ile Asp Ser Ser Gln Pro Val																25
aat aac tcg act ggt gaa gcc gct gcg cgc gca gtg aac ctg tac aag																259
Asn Asn Ser Thr Gly Glu Ala Ala Ala Arg Ala Val Asn Leu Tyr Lys																40
gcg tat ggc cag ggt gat acc act gtc acc gcg ttg gat cac gtc aac																307
Ala Tyr Gly Gln Gly Asp Thr Thr Val Thr Ala Leu Asp His Val Asn																55
gtg gag ttt gag aag aac aag ttc act gcc atc atg ggt cct tct ggc																355
Val Glu Phe Glu Lys Asn Lys Phe Thr Ala Ile Met Gly Pro Ser Gly																70
tcg ggt aag tcc acg ttg atg cac tgc atg gct ggt ctg gat gct gcg																403
Ser Gly Lys Ser Thr Leu Met His Cys Met Ala Gly Leu Asp Ala Ala																90
act ggt ggt tcg gca ttc att ggt gat acg gat ctg tcg cgg ttg aag																451
Thr Gly Gly Ser Ala Phe Ile Gly Asp Thr Asp Leu Ser Arg Leu Lys																105
gac aaa gag atg acc tct ttg cgt cgt gat cgt ttg gga ttc att ttc																499
Asp Lys Glu Met Thr Ser Leu Arg Arg Asp Arg Leu Gly Phe Ile Phe																120
cag tcg ttc aac ttg gtt cct act ctg acg gcg tcg gag aac att acg																547
Gln Ser Phe Asn Leu Val Pro Thr Leu Thr Ala Ser Glu Asn Ile Thr																135
ctg cct acc gat atc gcg ggc cgc aag att gat cag tcg tgg ttc gat																595
Leu Pro Thr Asp Ile Ala Gly Arg Lys Ile Asp Gln Ser Trp Phe Asp																150
gag att acc tct cgt ctg ggt ctg act gag cgc ctt aag cac cgt cct																643
Glu Ile Thr Ser Arg Leu Gly Leu Thr Glu Arg Leu Lys His Arg Pro																170
gca gag ctc tct ggt ggt cag cag cag cgt gtg gcg tgt gct cgt gcg																691
Ala Glu Leu Ser Gly Gly Gln Gln Gln Arg Val Ala Cys Ala Arg Ala																185
ttg gtg tct cgt ccg gag atc att ttc ggc gac gag cca acc ggt aac																739
Leu Val Ser Arg Pro Glu Ile Ile Phe Gly Asp Glu Pro Thr Gly Asn																200
ttg gat tcg aac tct tct agg gaa gtg ctg gat atc ctg cgc acc gca																787
Leu Asp Ser Asn Ser Ser Arg Glu Val Leu Asp Ile Leu Arg Thr Ala																215

gtt gat cag gat gat cag acc gtt gtg atc gtt acc cac gat gcc aag 835
 Val Asp Gln Asp Asp Gln Thr Val Val Ile Val Thr His Asp Ala Lys
 230 235 240 245

gcg gcg tcc tat gca gat cgt gtc att ttc ttg gcg gac ggt cgt atc 883
 Ala Ala Ser Tyr Ala Asp Arg Val Ile Phe Leu Ala Asp Gly Arg Ile
 250 255 260

gtg aac cag ttg ttt gat ccc acc atc gag gaa atc ttg gcc acg atg 931
 Val Asn Gln Leu Phe Asp Pro Thr Ile Glu Glu Ile Leu Ala Thr Met
 265 270 275

aac gga att gag gat att gcc taatgaattc cggttcacaca atg 975
 Asn Gly Ile Glu Asp Ile Ala
 280

<210> 450

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Ser Asn Pro Ala Ala Ser Thr Pro Ala Asn Asn Ser Asp Asp Val
 1 5 10 15

Ala Lys Glu Asn Trp Asp Ser Ser Phe Thr Pro Lys Thr Asp Ile Asp
 20 25 30

Ser Ser Gln Pro Val Asn Asn Ser Thr Gly Glu Ala Ala Ala Arg Ala
 35 40 45

Val Asn Leu Tyr Lys Ala Tyr Gly Gln Gly Asp Thr Thr Val Thr Ala
 50 55 60

Leu Asp His Val Asn Val Glu Phe Glu Lys Asn Lys Phe Thr Ala Ile
 65 70 75 80

Met Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Met His Cys Met Ala
 85 90 95

Gly Leu Asp Ala Ala Thr Gly Gly Ser Ala Phe Ile Gly Asp Thr Asp
 100 105 110

Leu Ser Arg Leu Lys Asp Lys Glu Met Thr Ser Leu Arg Arg Asp Arg
 115 120 125

Leu Gly Phe Ile Phe Gln Ser Phe Asn Leu Val Pro Thr Leu Thr Ala
 130 135 140

Ser Glu Asn Ile Thr Leu Pro Thr Asp Ile Ala Gly Arg Lys Ile Asp
 145 150 155 160

Gln Ser Trp Phe Asp Glu Ile Thr Ser Arg Leu Gly Leu Thr Glu Arg
 165 170 175

Leu Lys His Arg Pro Ala Glu Leu Ser Gly Gly Gln Gln Gln Arg Val
 180 185 190

Ala Cys Ala Arg Ala Leu Val Ser Arg Pro Glu Ile Ile Phe Gly Asp

	195					200					205					
Glu	Pro	Thr	Gly	Asn	Leu	Asp	Ser	Asn	Ser	Ser	Arg	Glu	Val	Leu	Asp	
	210					215					220					
Ile	Leu	Arg	Thr	Ala	Val	Asp	Gln	Asp	Asp	Gln	Thr	Val	Val	Ile	Val	
225					230					235					240	
Thr	His	Asp	Ala	Lys	Ala	Ala	Ser	Tyr	Ala	Asp	Arg	Val	Ile	Phe	Leu	
				245					250					255		
Ala	Asp	Gly	Arg	Ile	Val	Asn	Gln	Leu	Phe	Asp	Pro	Thr	Ile	Glu	Glu	
			260					265					270			
Ile	Leu	Ala	Thr	Met	Asn	Gly	Ile	Glu	Asp	Ile	Ala					
		275					280									

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<210> 451
<211> 1452
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(1452)  
<223> BXS03212
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<400> 451																
gcc tca ctt aac tgg tca gtc atc gtt cca gcc cta gtc att gtc cta	48															
Ala Ser Leu Asn Trp Ser Val Ile Val Pro Ala Leu Val Ile Val Leu																
1 5 10 15																
gcg aca gtg gtg tgg ggt atc gga ttc aaa gat agc ttt acc aac ttt	96															
Ala Thr Val Val Trp Gly Ile Gly Phe Lys Asp Ser Phe Thr Asn Phe																
20 25 30																
gct agt tct gcg ttg tca gca gta gtt gac aat ctc ggc tgg gcc ttc	144															
Ala Ser Ser Ala Leu Ser Ala Val Val Asp Asn Leu Gly Trp Ala Phe																
35 40 45																
att ttg ttt ggc aca gtc ttt gta ttt ttt atc gtt gtt atc gcc gct	192															
Ile Leu Phe Gly Thr Val Phe Val Phe Phe Ile Val Val Ile Ala Ala																
50 55 60																
agt aaa ttc ggc acg att cgc tta ggc cgc att gat gaa gca cca gag	240															
Ser Lys Phe Gly Thr Ile Arg Leu Gly Arg Ile Asp Glu Ala Pro Glu																
65 70 75 80																
ttt cgc acg gtg tca tgg att tcc atg atg ttt gct gca ggt atg ggt	288															
Phe Arg Thr Val Ser Trp Ile Ser Met Met Phe Ala Ala Gly Met Gly																
85 90 95																
att ggt ttg atg ttc tac gga acc aca gaa cct tta acc ttc tac cgc	336															
Ile Gly Leu Met Phe Tyr Gly Thr Thr Glu Pro Leu Thr Phe Tyr Arg																
100 105 110																
aat ggt gta cct gga cat gat gaa cac aat gtt ggc gtt gct atg tcc	384															
Asn Gly Val Pro Gly His Asp Glu His Asn Val Gly Val Ala Met Ser																
115 120 125																

acg aca atg ttc cac tgg acc ttg cat cca tgg gct atc tac gca att	432
Thr Thr Met Phe His Trp Thr Leu His Pro Trp Ala Ile Tyr Ala Ile	
130 135 140	
gtg ggc cta gcc att gcc tat tcg acc ttc cga gtg ggc cgt aaa cag	480
Val Gly Leu Ala Ile Ala Tyr Ser Thr Phe Arg Val Gly Arg Lys Gln	
145 150 155 160	
ctt cta agc tct gca ttc gtg cca ctc att ggt gaa aaa ggt gca gaa	528
Leu Leu Ser Ser Ala Phe Val Pro Leu Ile Gly Glu Lys Gly Ala Glu	
165 170 175	
gga tgg ttg ggc aag ctc atc gac atc ctg gcg att atc gcc acc gta	576
Gly Trp Leu Gly Lys Leu Ile Asp Ile Leu Ala Ile Ile Ala Thr Val	
180 185 190	
ttc ggc acg gca tgt tcc ctt ggc ctt ggt gcc ctg cag att ggt gca	624
Phe Gly Thr Ala Cys Ser Leu Gly Leu Gly Ala Leu Gln Ile Gly Ala	
195 200 205	
ggc ctg tcc gca gca aac atc att gaa gat cca agc gat tgg acc atc	672
Gly Leu Ser Ala Ala Asn Ile Ile Glu Asp Pro Ser Asp Trp Thr Ile	
210 215 220	
gtt ggc att gtt tct gtt ttg acc ctg gca ttt atc ttc tcc gct att	720
Val Gly Ile Val Ser Val Leu Thr Leu Ala Phe Ile Phe Ser Ala Ile	
225 230 235 240	
tct ggt gtg ggc aag gga atc cag tac ctc tcc aac gcc aac atg gtt	768
Ser Gly Val Gly Lys Gly Ile Gln Tyr Leu Ser Asn Ala Asn Met Val	
245 250 255	
ctg gca gct ctg ctc gcg att ttc gtg ttc gtt gtc gga cca acc gtg	816
Leu Ala Ala Leu Leu Ala Ile Phe Val Phe Val Val Gly Pro Thr Val	
260 265 270	
tcg att ttg aac ctg ctg cca ggt tct att ggc aac tac ctg tcc aac	864
Ser Ile Leu Asn Leu Leu Pro Gly Ser Ile Gly Asn Tyr Leu Ser Asn	
275 280 285	
ttc ttt caa atg gca ggc cgc act gcc atg agt gcc gac ggc aca gca	912
Phe Phe Gln Met Ala Gly Arg Thr Ala Met Ser Ala Asp Gly Thr Ala	
290 295 300	
ggt gag tgg cta ggt agc tgg acc atc ttc tac tgg gca tgg tgg atc	960
Gly Glu Trp Leu Gly Ser Trp Thr Ile Phe Tyr Trp Ala Trp Trp Ile	
305 310 315 320	
tct tgg tca cca ttc gta gga atg ttc ttg gca cgt att tcc cgt ggc	1008
Ser Trp Ser Pro Phe Val Gly Met Phe Leu Ala Arg Ile Ser Arg Gly	
325 330 335	
cgc tcc atc cgt gag ttc atc ctg ggc gtg ttg ctc gtc cca gca ggt	1056
Arg Ser Ile Arg Glu Phe Ile Leu Gly Val Leu Leu Val Pro Ala Gly	
340 345 350	
gtg tcc acc gta tgg ttc tcc att ttt ggt ggc act gcg att gtc ttc	1104
Val Ser Thr Val Trp Phe Ser Ile Phe Gly Gly Thr Ala Ile Val Phe	
355 360 365	
gaa caa aat ggg gaa tcc att tgg ggt gat ggt gca gca gaa gag cag	1152

Glu Gln Asn Gly Glu Ser Ile Trp Gly Asp Gly Ala Ala Glu Glu Gln
 370 375 380
 ctt ttt gga ttg ctt cat gca ctt cca ggt ggg caa atc atg ggc atc 1200
 Leu Phe Gly Leu Leu His Ala Leu Pro Gly Gly Gln Ile Met Gly Ile
 385 390 395 400
 atc gcc atg att ttg ctg ggt act ttc ttc att acc tct gct gac tct 1248
 Ile Ala Met Ile Leu Leu Gly Thr Phe Phe Ile Thr Ser Ala Asp Ser
 405 410 415
 gct tcc acc gtc atg ggc acc atg agt cag cac ggc cag ctg gaa gcc 1296
 Ala Ser Thr Val Met Gly Thr Met Ser Gln His Gly Gln Leu Glu Ala
 420 425 430
 aac aag tgg gtg aca gct gcc tgg ggt gtt gct acc gca gct att gga 1344
 Asn Lys Trp Val Thr Ala Ala Trp Gly Val Ala Thr Ala Ala Ile Gly
 435 440 445
 cta acg cta ttg ctt tct ggt ggt gac aat gcc ttg agc aac ttg caa 1392
 Leu Thr Leu Leu Leu Ser Gly Gly Asp Asn Ala Leu Ser Asn Leu Gln
 450 455 460
 aac gtc acc atc gtg gct gca aca cca ttc ttg ttt gtg gtt att gga 1440
 Asn Val Thr Ile Val Ala Ala Thr Pro Phe Leu Phe Val Val Ile Gly
 465 470 475 480
 ttg atg ttt gcg 1452
 Leu Met Phe Ala

<210> 452

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 452

Ala Ser Leu Asn Trp Ser Val Ile Val Pro Ala Leu Val Ile Val Leu
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 Ala Thr Val Val Trp Gly Ile Gly Phe Lys Asp Ser Phe Thr Asn Phe
 20 25 30
 Ala Ser Ser Ala Leu Ser Ala Val Val Asp Asn Leu Gly Trp Ala Phe
 35 40 45
 Ile Leu Phe Gly Thr Val Phe Val Phe Phe Ile Val Val Ile Ala Ala
 50 55 60
 Ser Lys Phe Gly Thr Ile Arg Leu Gly Arg Ile Asp Glu Ala Pro Glu
 65 70 75 80
 Phe Arg Thr Val Ser Trp Ile Ser Met Met Phe Ala Ala Gly Met Gly
 85 90 95
 Ile Gly Leu Met Phe Tyr Gly Thr Thr Glu Pro Leu Thr Phe Tyr Arg
 100 105 110
 Asn Gly Val Pro Gly His Asp Glu His Asn Val Gly Val Ala Met Ser
 115 120 125

Thr Thr Met Phe His Trp Thr Leu His Pro Trp Ala Ile Tyr Ala Ile
 130 135 140
 Val Gly Leu Ala Ile Ala Tyr Ser Thr Phe Arg Val Gly Arg Lys Gln
 145 150 155 160
 Leu Leu Ser Ser Ala Phe Val Pro Leu Ile Gly Glu Lys Gly Ala Glu
 165 170 175
 Gly Trp Leu Gly Lys Leu Ile Asp Ile Leu Ala Ile Ile Ala Thr Val
 180 185 190
 Phe Gly Thr Ala Cys Ser Leu Gly Leu Gly Ala Leu Gln Ile Gly Ala
 195 200 205
 Gly Leu Ser Ala Ala Asn Ile Ile Glu Asp Pro Ser Asp Trp Thr Ile
 210 215 220
 Val Gly Ile Val Ser Val Leu Thr Leu Ala Phe Ile Phe Ser Ala Ile
 225 230 235 240
 Ser Gly Val Gly Lys Gly Ile Gln Tyr Leu Ser Asn Ala Asn Met Val
 245 250 255
 Leu Ala Ala Leu Leu Ala Ile Phe Val Phe Val Val Gly Pro Thr Val
 260 265 270
 Ser Ile Leu Asn Leu Leu Pro Gly Ser Ile Gly Asn Tyr Leu Ser Asn
 275 280 285
 Phe Phe Gln Met Ala Gly Arg Thr Ala Met Ser Ala Asp Gly Thr Ala
 290 295 300
 Gly Glu Trp Leu Gly Ser Trp Thr Ile Phe Tyr Trp Ala Trp Trp Ile
 305 310 315 320
 Ser Trp Ser Pro Phe Val Gly Met Phe Leu Ala Arg Ile Ser Arg Gly
 325 330 335
 Arg Ser Ile Arg Glu Phe Ile Leu Gly Val Leu Leu Val Pro Ala Gly
 340 345 350
 Val Ser Thr Val Trp Phe Ser Ile Phe Gly Gly Thr Ala Ile Val Phe
 355 360 365
 Glu Gln Asn Gly Glu Ser Ile Trp Gly Asp Gly Ala Ala Glu Glu Gln
 370 375 380
 Leu Phe Gly Leu Leu His Ala Leu Pro Gly Gly Gln Ile Met Gly Ile
 385 390 395 400
 Ile Ala Met Ile Leu Leu Gly Thr Phe Phe Ile Thr Ser Ala Asp Ser
 405 410 415
 Ala Ser Thr Val Met Gly Thr Met Ser Gln His Gly Gln Leu Glu Ala
 420 425 430
 Asn Lys Trp Val Thr Ala Ala Trp Gly Val Ala Thr Ala Ala Ile Gly
 435 440 445

Leu Thr Leu Leu Leu Ser Gly Gly Asp Asn Ala Leu Ser Asn Leu Gln
 450 455 460

Asn Val Thr Ile Val Ala Ala Thr Pro Phe Leu Phe Val Val Ile Gly
 465 470 475 480

Leu Met Phe Ala

<210> 453
 <211> 945
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(945)
 <223> FRXA01591

<400> 453

gcc tca ctt aac tgg tca gtc atc gtt cca gcc cta gtc att gtc cta	48
Ala Ser Leu Asn Trp Ser Val Ile Val Pro Ala Leu Val Ile Val Leu	
1 5 10 15	
gcg aca gtg gtg tgg ggt atc gga ttc aaa gat agc ttt acc acc ttt	96
Ala Thr Val Val Trp Gly Ile Gly Phe Lys Asp Ser Phe Thr Thr Phe	
20 25 30	
gct agt tct gcg ttg tca gca gta gtt gac aat ctc ggc tgg gcc ttc	144
Ala Ser Ser Ala Leu Ser Ala Val Val Asp Asn Leu Gly Trp Ala Phe	
35 40 45	
att ttg ttt ggc aca gtc ttt gta ttt ttt atc gtt gtt atc gcc gct	192
Ile Leu Phe Gly Thr Val Phe Val Phe Phe Ile Val Val Ile Ala Ala	
50 55 60	
agt aaa ttc ggc acg att cgc tta ggc cgc att gat gaa gca cca gag	240
Ser Lys Phe Gly Thr Ile Arg Leu Gly Arg Ile Asp Glu Ala Pro Glu	
65 70 75 80	
ttt cgc acg gtg tca tgg att tcc atg atg ttt gct gca ggt atg ggt	288
Phe Arg Thr Val Ser Trp Ile Ser Met Met Phe Ala Ala Gly Met Gly	
85 90 95	
att ggt ttg atg ttc tac gga acc aca gaa cct tta acc ttc tac cgc	336
Ile Gly Leu Met Phe Tyr Gly Thr Thr Glu Pro Leu Thr Phe Tyr Arg	
100 105 110	
aat ggt gta cct gga cat gat gaa cac aat gtt ggc gtt gct atg tcc	384
Asn Gly Val Pro Gly His Asp Glu His Asn Val Gly Val Ala Met Ser	
115 120 125	
acg aca atg ttc cac tgg acc ttg cat cca tgg gct atc tac gca att	432
Thr Thr Met Phe His Trp Thr Leu His Pro Trp Ala Ile Tyr Ala Ile	
130 135 140	
gtg ggc cta gcc att gcc tat tcg acc ttc cga gtg ggc cgt aaa cag	480
Val Gly Leu Ala Ile Ala Tyr Ser Thr Phe Arg Val Gly Arg Lys Gln	
145 150 155 160	

ctt cta agc tct gca ttc gtg cca ctc att ggt gaa aaa ggt gca gaa 528
 Leu Leu Ser Ser Ala Phe Val Pro Leu Ile Gly Glu Lys Gly Ala Glu
 165 170 175

gga tgg ttg ggc aag ctc atc gac atc ctg gcg att atc gcc acc gta 576
 Gly Trp Leu Gly Lys Leu Ile Asp Ile Leu Ala Ile Ile Ala Thr Val
 180 185 190

ttc ggc acg gca tgt tcc ctt ggc ctt ggt gcc ctg cag att ggt gca 624
 Phe Gly Thr Ala Cys Ser Leu Gly Leu Gly Ala Leu Gln Ile Gly Ala
 195 200 205

ggc ctg tcc gca gca aac atc att gaa gat cca agc gat tgg acc atc 672
 Gly Leu Ser Ala Ala Asn Ile Ile Glu Asp Pro Ser Asp Trp Thr Ile
 210 215 220

gtt ggc att gtt tct gtt ttg acc ctg gca ttt atc ttc tcc gct att 720
 Val Gly Ile Val Ser Val Leu Thr Leu Ala Phe Ile Phe Ser Ala Ile
 225 230 235 240

tct ggt gtg ggc aag gga atc cag tac ctc tcc aac gcc aac atg gtt 768
 Ser Gly Val Gly Lys Gly Ile Gln Tyr Leu Ser Asn Ala Asn Met Val
 245 250 255

ctg gca gct ctg ctc gcg att ttc gtg ttc gtt gtc gga cca acc gtg 816
 Leu Ala Ala Leu Leu Ala Ile Phe Val Phe Val Val Gly Pro Thr Val
 260 265 270

tcg att ttg aac ctg ctg cca ggt tct att gtg aac tac ctg tcc aac 864
 Ser Ile Leu Asn Leu Leu Pro Gly Ser Ile Val Asn Tyr Leu Ser Asn
 275 280 285

ttc ttt caa atg gta ggc cgc act gcc atg agt gcc gac ggc aca cca 912
 Phe Phe Gln Met Val Gly Arg Thr Ala Met Ser Ala Asp Gly Thr Pro
 290 295 300

ggt gag tgg ctt ggt ggc tgc acc atc ttc tac 945
 Gly Glu Trp Leu Gly Gly Cys Thr Ile Phe Tyr
 305 310 315

<210> 454
 <211> 315
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 454
 Ala Ser Leu Asn Trp Ser Val Ile Val Pro Ala Leu Val Ile Val Leu
 1 5 10 15
 Ala Thr Val Val Trp Gly Ile Gly Phe Lys Asp Ser Phe Thr Thr Phe
 20 25 30
 Ala Ser Ser Ala Leu Ser Ala Val Val Asp Asn Leu Gly Trp Ala Phe
 35 40 45
 Ile Leu Phe Gly Thr Val Phe Val Phe Phe Ile Val Val Ile Ala Ala
 50 55 60
 Ser Lys Phe Gly Thr Ile Arg Leu Gly Arg Ile Asp Glu Ala Pro Glu
 65 70 75 80

Phe Arg Thr Val Ser Trp Ile Ser Met Met Phe Ala Ala Gly Met Gly
 85 90 95
 Ile Gly Leu Met Phe Tyr Gly Thr Thr Glu Pro Leu Thr Phe Tyr Arg
 100 105 110
 Asn Gly Val Pro Gly His Asp Glu His Asn Val Gly Val Ala Met Ser
 115 120 125
 Thr Thr Met Phe His Trp Thr Leu His Pro Trp Ala Ile Tyr Ala Ile
 130 135 140
 Val Gly Leu Ala Ile Ala Tyr Ser Thr Phe Arg Val Gly Arg Lys Gln
 145 150 155 160
 Leu Leu Ser Ser Ala Phe Val Pro Leu Ile Gly Glu Lys Gly Ala Glu
 165 170 175
 Gly Trp Leu Gly Lys Leu Ile Asp Ile Leu Ala Ile Ile Ala Thr Val
 180 185 190
 Phe Gly Thr Ala Cys Ser Leu Gly Leu Gly Ala Leu Gln Ile Gly Ala
 195 200 205
 Gly Leu Ser Ala Ala Asn Ile Ile Glu Asp Pro Ser Asp Trp Thr Ile
 210 215 220
 Val Gly Ile Val Ser Val Leu Thr Leu Ala Phe Ile Phe Ser Ala Ile
 225 230 235 240
 Ser Gly Val Gly Lys Gly Ile Gln Tyr Leu Ser Asn Ala Asn Met Val
 245 250 255
 Leu Ala Ala Leu Leu Ala Ile Phe Val Phe Val Val Gly Pro Thr Val
 260 265 270
 Ser Ile Leu Asn Leu Leu Pro Gly Ser Ile Val Asn Tyr Leu Ser Asn
 275 280 285
 Phe Phe Gln Met Val Gly Arg Thr Ala Met Ser Ala Asp Gly Thr Pro
 290 295 300
 Gly Glu Trp Leu Gly Gly Cys Thr Ile Phe Tyr
 305 310 315

<210> 455

<211> 292

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(292)

<223> RXN00201

<400> 455

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 ttacgccatc gcgcggctcg ggcacaccga tacctgggca gtg gca gat tgc gga 115

	Val	Ala	Asp	Cys	Gly		
	1				5		
tta ccc atc cca gaa cac gta gag atc atc gat ttg gca ctc gtg ttt						163	
Leu Pro Ile Pro Glu His Val Glu Ile Ile Asp Leu Ala Leu Val Phe							
	10			15	20		
ggg atc ccc acc ttt gaa caa gta ctg aat gct ctc aag ccg gaa gta						211	
Gly Ile Pro Thr Phe Glu Gln Val Leu Asn Ala Leu Lys Pro Glu Val							
	25		30		35		
gtt gtg gaa ggc gcg gtg att gcc gaa ggg gca ccc caa cgt atc cgc						259	
Val Val Glu Gly Ala Val Ile Ala Glu Gly Ala Pro Gln Arg Ile Arg							
	40		45		50		
gaa atg gtg gat acg gat gtg gaa gta tgt gcg						292	
Glu Met Val Asp Thr Asp Val Glu Val Cys Ala							
	55		60				

<210> 456
 <211> 64
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 456
Val Ala Asp Cys Gly Leu Pro Ile Pro Glu His Val Glu Ile Ile Asp
1 5 10 15
Leu Ala Leu Val Phe Gly Ile Pro Thr Phe Glu Gln Val Leu Asn Ala
20 25 30
Leu Lys Pro Glu Val Val Val Glu Gly Ala Val Ile Ala Glu Gly Ala
35 40 45
Pro Gln Arg Ile Arg Glu Met Val Asp Thr Asp Val Glu Val Cys Ala
50 55 60

<210> 457
 <211> 286
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(286)
 <223> FRXA00201

<400> 457	
acgtcgcgga cttcaagtag tcggcgatga aaaagtccgt ttactaaacc ccgatctgtg	60
ttacgccatc gcgcggctcg ggcacaccga tacctgggca	
gtg gca gat tgc gga	115
Val Ala Asp Cys Gly	
1 5	
tta ccc atc cca gaa cac gta gag atc atc gat ttg gca ctc gtg ttt	163
Leu Pro Ile Pro Glu His Val Glu Ile Ile Asp Leu Ala Leu Val Phe	

	10	15	20	
ggg atc ccc acc ttt gaa caa gta ctg aat gct ctc aag ccg gaa gta				211
Gly Ile Pro Thr Phe Glu Gln Val Leu Asn Ala Leu Lys Pro Glu Val				
	25	30	35	
gtt gtg gaa ggc gcg gtg att gcc gaa ggg gca ccc caa cgt atc cgc				259
Val Val Glu Gly Ala Val Ile Ala Glu Gly Ala Pro Gln Arg Ile Arg				
	40	45	50	
gaa atg gtg gat acg gat gtg gaa gtt				286
Glu Met Val Asp Thr Asp Val Glu Val				
	55	60		

<210> 458

<211> 62

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

Val Ala Asp Cys Gly Leu Pro Ile Pro Glu His Val Glu Ile Ile Asp				
1	5	10	15	
Leu Ala Leu Val Phe Gly Ile Pro Thr Phe Glu Gln Val Leu Asn Ala				
	20	25	30	
Leu Lys Pro Glu Val Val Val Glu Gly Ala Val Ile Ala Glu Gly Ala				
	35	40	45	
Pro Gln Arg Ile Arg Glu Met Val Asp Thr Asp Val Glu Val				
	50	55	60	

<210> 459

<211> 849

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(826)

<223> RXA01221

<400> 459

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aactttccgc gctcaaaaat aaggccagga aggccacctc atg agc ctt aaa atc	115
	Met Ser Leu Lys Ile
	1 5
acc aac ctc aaa gtc gct ttc ggg tcg ttc atc gcc gtg aat gag att	163
Thr Asn Leu Lys Val Ala Phe Gly Ser Phe Ile Ala Val Asn Glu Ile	
	10 15 20
agt ttt cag gtg ctg ccc ggt cac gtc cac ttc ctc atc ggt gcc aac	211
Ser Phe Gln Val Leu Pro Gly His Val His Phe Leu Ile Gly Ala Asn	
	25 30 35
ggt gca ggt aaa acc acc tgc att gac gcg atc agc gga ttg gcg ccg	259
Gly Ala Gly Lys Thr Thr Cys Ile Asp Ala Ile Ser Gly Leu Ala Pro	

40	45	50	
ggg cag gga tca gtg cag ttg gat ggc act gag att ctg gga acc cct Gly Gln Gly Ser Val Gln Leu Asp Gly Thr Glu Ile Leu Gly Thr Pro 55 60 65			307
gtg cac cgc att gct cgg atg ggt gtg ggg cga acg ttt cag acc gcc Val His Arg Ile Ala Arg Met Gly Val Gly Arg Thr Phe Gln Thr Ala 70 75 80 85			355
agc gtg ttt gaa gaa ttg tct gtg ttg cag aat ctg gat att gcg tgc Ser Val Phe Glu Glu Leu Ser Val Leu Gln Asn Leu Asp Ile Ala Cys 90 95 100			403
ggg att cat cgt ccg ttg cgg gcg ctt ctc ggg gtg cgt cat cgg att Gly Ile His Arg Pro Leu Arg Ala Leu Leu Gly Val Arg His Arg Ile 105 110 115			451
gat ccc cga att gaa cac gcc ctg gag gtc acg ggt ctt gct gat ctg Asp Pro Arg Ile Glu His Ala Leu Glu Val Thr Gly Leu Ala Asp Leu 120 125 130			499
gtg aat gct cag gcg gga acc ttg tgc cat ggg cag aaa cag tgg ctg Val Asn Ala Gln Ala Gly Thr Leu Ser His Gly Gln Lys Gln Trp Leu 135 140 145			547
gaa att gca atg ttg ctg gtg cag gat gcg cag gtg ctc atg ctg gat Glu Ile Ala Met Leu Leu Val Gln Asp Ala Gln Val Leu Met Leu Asp 150 155 160 165			595
gag ccg gtg gcg ggc atg agt gag gag gag cgt gtc gca acg ggt gag Glu Pro Val Ala Gly Met Ser Glu Glu Glu Arg Val Ala Thr Gly Glu 170 175 180			643
ctt ttg cag agg gtt gcg cgg gga cgg gtg gtg ttg gtg gtg gag cac Leu Leu Gln Arg Val Ala Arg Gly Arg Val Val Leu Val Val Glu His 185 190 195			691
gat atg gag ttc atg cgt cgt ttt gcc act cgc gtc act gtg atg aat Asp Met Glu Phe Met Arg Arg Phe Ala Thr Arg Val Thr Val Met Asn 200 205 210			739
cgc ggc acg atc ttg tgt gag ggg tgc gtc gat gag att cag gcg aat Arg Gly Thr Ile Leu Cys Glu Gly Ser Val Asp Glu Ile Gln Ala Asn 215 220 225			787
ccg gat gtg cag tcc att tat tta ggt acg gca ggg aag tgagttagtc Pro Asp Val Gln Ser Ile Tyr Leu Gly Thr Ala Gly Lys 230 235 240			836
atgttggaata tca			849

<210> 460

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

Met	Ser	Leu	Lys	Ile	Thr	Asn	Leu	Lys	Val	Ala	Phe	Gly	Ser	Phe	Ile
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Ala Val Asn Glu Ile Ser Phe Gln Val Leu Pro Gly His Val His Phe
 20 25 30
 Leu Ile Gly Ala Asn Gly Ala Gly Lys Thr Thr Cys Ile Asp Ala Ile
 35 40 45
 Ser Gly Leu Ala Pro Gly Gln Gly Ser Val Gln Leu Asp Gly Thr Glu
 50 55 60
 Ile Leu Gly Thr Pro Val His Arg Ile Ala Arg Met Gly Val Gly Arg
 65 70 75 80
 Thr Phe Gln Thr Ala Ser Val Phe Glu Glu Leu Ser Val Leu Gln Asn
 85 90 95
 Leu Asp Ile Ala Cys Gly Ile His Arg Pro Leu Arg Ala Leu Leu Gly
 100 105 110
 Val Arg His Arg Ile Asp Pro Arg Ile Glu His Ala Leu Glu Val Thr
 115 120 125
 Gly Leu Ala Asp Leu Val Asn Ala Gln Ala Gly Thr Leu Ser His Gly
 130 135 140
 Gln Lys Gln Trp Leu Glu Ile Ala Met Leu Leu Val Gln Asp Ala Gln
 145 150 155 160
 Val Leu Met Leu Asp Glu Pro Val Ala Gly Met Ser Glu Glu Glu Arg
 165 170 175
 Val Ala Thr Gly Glu Leu Leu Gln Arg Val Ala Arg Gly Arg Val Val
 180 185 190
 Leu Val Val Glu His Asp Met Glu Phe Met Arg Arg Phe Ala Thr Arg
 195 200 205
 Val Thr Val Met Asn Arg Gly Thr Ile Leu Cys Glu Gly Ser Val Asp
 210 215 220
 Glu Ile Gln Ala Asn Pro Asp Val Gln Ser Ile Tyr Leu Gly Thr Ala
 225 230 235 240

Gly Lys

<210> 461

<211> 822

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(799)

<223> RXA01222

<400> 461

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cagtccattt atttaggtac ggcaggaag tgagttagtc atg ttg gaa atc act 115

	Met	Leu	Glu	Ile	Thr	
	1				5	
aat ttg tgt gca ggt tat ggc cgc acg cag gta ctt cat tct ctt tca						163
Asn Leu Cys Ala Gly Tyr Gly Arg Thr Gln Val Leu His Ser Leu Ser						
	10			15	20	
atc tcc acg agc agc aac ggc atc ctg tct atc ctc ggc cac aat ggc						211
Ile Ser Thr Ser Ser Asn Gly Ile Leu Ser Ile Leu Gly His Asn Gly						
	25			30	35	
gct ggt aaa tcc acc ttg ctg cga acc gcg gtg ggg ttg att aag ccg						259
Ala Gly Lys Ser Thr Leu Leu Arg Thr Ala Val Gly Leu Ile Lys Pro						
	40			45	50	
act tcc gga gag gtc aaa ctt ttc ggc cag gat gtc acc tct ttg tcc						307
Thr Ser Gly Glu Val Lys Leu Phe Gly Gln Asp Val Thr Ser Leu Ser						
	55			60	65	
acg cat gag cga gta aag cgc gga atg gct tat gtg ccg cag ggc cag						355
Thr His Glu Arg Val Lys Arg Gly Met Ala Tyr Val Pro Gln Gly Gln						
	70			75	80	85
cag tct ttt acg cag ctt agt tgc atg gaa aat ttg cag gtg gta gcg						403
Gln Ser Phe Thr Gln Leu Ser Cys Met Glu Asn Leu Gln Val Val Ala						
	90			95	100	
gat ctg cag gga cgt gtg ggc aag gca cgc atc gcg gag gcg ctt gat						451
Asp Leu Gln Gly Arg Val Gly Lys Ala Arg Ile Ala Glu Ala Leu Asp						
	105			110	115	
cgc ttt ccg gcg ctg acc cag gtg ctg gac cgc caa gcc ggc ctg ttg						499
Arg Phe Pro Ala Leu Thr Gln Val Leu Asp Arg Gln Ala Gly Leu Leu						
	120			125	130	
tcg ggt ggt cag cgt cag cag ctt gcc atc gcc cgc gcg ctg atc acg						547
Ser Gly Gly Gln Arg Gln Gln Leu Ala Ile Ala Arg Ala Leu Ile Thr						
	135			140	145	
gcg cca aag ctt ttg ctt ctc gac gaa ccc acc gag ggt att cag cct						595
Ala Pro Lys Leu Leu Leu Leu Asp Glu Pro Thr Glu Gly Ile Gln Pro						
	150			155	160	165
tcg gtg gtt gct gaa att cag cag acc atc atc gat ttg gct aag gac						643
Ser Val Val Ala Glu Ile Gln Gln Thr Ile Ile Asp Leu Ala Lys Asp						
	170			175	180	
ggc atg agc att gtc ctg gtg gag caa aac att ggt ttt gca ttg gat						691
Gly Met Ser Ile Val Leu Val Glu Gln Asn Ile Gly Phe Ala Leu Asp						
	185			190	195	
gct gca aca agc tac gcc att gtg gcg cgt ggt cag gtc gtg gaa tct						739
Ala Ala Thr Ser Tyr Ala Ile Val Ala Arg Gly Gln Val Val Glu Ser						
	200			205	210	
gga caa ggc gct gaa acc acc gca gag aag cag act aaa gtg cgg gaa						787
Gly Gln Gly Ala Glu Thr Thr Ala Glu Lys Gln Thr Lys Val Arg Glu						
	215			220	225	
tct cta gca atc tagcggctgt ggatagcgtt ttg						822
Ser Leu Ala Ile						

230

<210> 462

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

Met Leu Glu Ile Thr Asn Leu Cys Ala Gly Tyr Gly Arg Thr Gln Val
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Leu His Ser Leu Ser Ile Ser Thr Ser Ser Asn Gly Ile Leu Ser Ile
 20 25 30

Leu Gly His Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Thr Ala Val
 35 40 45

Gly Leu Ile Lys Pro Thr Ser Gly Glu Val Lys Leu Phe Gly Gln Asp
 50 55 60

Val Thr Ser Leu Ser Thr His Glu Arg Val Lys Arg Gly Met Ala Tyr
 65 70 75 80

Val Pro Gln Gly Gln Gln Ser Phe Thr Gln Leu Ser Cys Met Glu Asn
 85 90 95

Leu Gln Val Val Ala Asp Leu Gln Gly Arg Val Gly Lys Ala Arg Ile
 100 105 110

Ala Glu Ala Leu Asp Arg Phe Pro Ala Leu Thr Gln Val Leu Asp Arg
 115 120 125

Gln Ala Gly Leu Leu Ser Gly Gly Gln Arg Gln Gln Leu Ala Ile Ala
 130 135 140

Arg Ala Leu Ile Thr Ala Pro Lys Leu Leu Leu Leu Asp Glu Pro Thr
 145 150 155 160

Glu Gly Ile Gln Pro Ser Val Val Ala Glu Ile Gln Gln Thr Ile Ile
 165 170 175

Asp Leu Ala Lys Asp Gly Met Ser Ile Val Leu Val Glu Gln Asn Ile
 180 185 190

Gly Phe Ala Leu Asp Ala Ala Thr Ser Tyr Ala Ile Val Ala Arg Gly
 195 200 205

Gln Val Val Glu Ser Gly Gln Gly Ala Glu Thr Thr Ala Glu Lys Gln
 210 215 220

Thr Lys Val Arg Glu Ser Leu Ala Ile
 225 230

<210> 463

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> RXA01219

<400> 463

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ggccaagacc accgctgcga ctctctaaga gataaaaatc atg gac att tta ctc 115
                                         Met Asp Ile Leu Leu
                                         1           5

aat cag ctc gta gcc ggg ctt tca gtt gga tgc gtc ctt cta ttg gtc 163
Asn Gln Leu Val Ala Gly Leu Ser Val Gly Ser Val Leu Leu Leu Val
          10          15          20

gca gtg gga ttg tca ctg acc ttt gga cag atg ggc gtt att aat atg 211
Ala Val Gly Leu Ser Leu Thr Phe Gly Gln Met Gly Val Ile Asn Met
          25          30          35

gcg cac gga gag ttc atc atg gtc ggc gca tac acc gca tat gtg gtg 259
Ala His Gly Glu Phe Ile Met Val Gly Ala Tyr Thr Ala Tyr Val Val
          40          45          50

cag ctg gtc gtc ggt tct gcc ggt tta tcc cta ctg atc agc att ccg 307
Gln Leu Val Val Gly Ser Ala Gly Leu Ser Leu Leu Ile Ser Ile Pro
          55          60          65

ctg gcc ttt att atc ggt ggg ctt ttc gga gtt ctc ctc gaa caa ttc 355
Leu Ala Phe Ile Ile Gly Gly Leu Phe Gly Val Leu Leu Glu Gln Phe
          70          75          80          85

ctg ctg aag tat ctt tat cac agg cca cta gac acg ctg ctg gcc aca 403
Leu Leu Lys Tyr Leu Tyr His Arg Pro Leu Asp Thr Leu Leu Ala Thr
          90          95          100

ttc ggt gtc ggt ttg atc ctt cag cag ctg gcc cga aac att ttc gga 451
Phe Gly Val Gly Leu Ile Leu Gln Gln Leu Ala Arg Asn Ile Phe Gly
          105          110          115

gct ccc gca gtg gat gtc agg gca ccg gaa ttt ctc cgc gga aac gtc 499
Ala Pro Ala Val Asp Val Arg Ala Pro Glu Phe Leu Arg Gly Asn Val
          120          125          130

gaa gtt cta ggc gtc ttg gtg ccg acc gcg cga cta ttc atc ctg gcg 547
Glu Val Leu Gly Val Leu Val Pro Thr Ala Arg Leu Phe Ile Leu Ala
          135          140          145

ctg gcc atc gca tca gtg act gca cta gct gtg ttc cta aat cgc act 595
Leu Ala Ile Ala Ser Val Thr Ala Leu Ala Val Phe Leu Asn Arg Thr
          150          155          160          165

gcc tgg ggc cga cgc atc cgc gcc gtg gtt ctg aac cgc gac ctc gcg 643
Ala Trp Gly Arg Ile Arg Ala Val Val Leu Asn Arg Asp Leu Ala
          170          175          180

gaa acc gca ggt att gat acc cga gct act gac cga atg acg ttc ttt 691
Glu Thr Ala Gly Ile Asp Thr Arg Ala Thr Asp Arg Met Thr Phe Phe
          185          190          195

gtg ggc tcc ggt ctt gcc gga atc gcc ggg gta gct atc aca ttg att 739
Val Gly Ser Gly Leu Ala Gly Ile Ala Gly Val Ala Ile Thr Leu Ile

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200	205	210	
ggc gcg acc ggc ccc acc atc ggt cag aac tac atc gtg gat gcc ttc			787
Gly Ala Thr Gly Pro Thr Ile Gly Gln Asn Tyr Ile Val Asp Ala Phe			
215	220	225	
ctt gtt gtt gcc gcc ggt ggc atc ggc cgg gtg aag ggc gct gtg atc			835
Leu Val Val Ala Ala Gly Gly Ile Gly Arg Val Lys Gly Ala Val Ile			
230	235	240	245
atg gct ttc gtg ctg gga att act caa gca ttc gtg gaa tat acg aca			883
Met Ala Phe Val Leu Gly Ile Thr Gln Ala Phe Val Glu Tyr Thr Thr			
250	255	260	
ggc gcg agc atc gcg aag ttc atc gta ctc atc gct gtt gtt gcc ttc			931
Gly Ala Ser Ile Ala Lys Phe Ile Val Leu Ile Ala Val Val Ala Phe			
265	270	275	
ctg cag ttt agg cct caa gga ctc ttc caa acc caa act agg agc ctc			979
Leu Gln Phe Arg Pro Gln Gly Leu Phe Gln Thr Gln Thr Arg Ser Leu			
280	285	290	
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Val			

<210> 464

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 464

Met Asp Ile Leu Leu Asn Gln Leu Val Ala Gly Leu Ser Val Gly Ser	
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Gly Val Ile Asn Met Ala His Gly Glu Phe Ile Met Val Gly Ala Tyr	
35 40 45	
Thr Ala Tyr Val Val Gln Leu Val Val Gly Ser Ala Gly Leu Ser Leu	
50 55 60	
Leu Ile Ser Ile Pro Leu Ala Phe Ile Ile Gly Gly Leu Phe Gly Val	
65 70 75 80	
Leu Leu Glu Gln Phe Leu Leu Lys Tyr Leu Tyr His Arg Pro Leu Asp	
85 90 95	
Thr Leu Leu Ala Thr Phe Gly Val Gly Leu Ile Leu Gln Gln Leu Ala	
100 105 110	
Arg Asn Ile Phe Gly Ala Pro Ala Val Asp Val Arg Ala Pro Glu Phe	
115 120 125	
Leu Arg Gly Asn Val Glu Val Leu Gly Val Leu Val Pro Thr Ala Arg	
130 135 140	
Leu Phe Ile Leu Ala Leu Ala Ile Ala Ser Val Thr Ala Leu Ala Val	

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<210> 465
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(1177)  
<223> RXA01220
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								1								
aag	ctg	aag	aag	ccc	gca	aag	aag	aaa	act	acg	ccg	aaa	ctt	agc	gtc	163
Lys	Leu	Lys	Lys	Pro	Ala	Lys	Lys	Lys	Thr	Thr	Pro	Lys	Leu	Ser	Val	
				10				15					20			
gta	aat	gct	ccc	acg	ctg	cgc	act	gcg	gcg	ttg	ggc	ctg	gcc	gcg	ctc	211
Val	Asn	Ala	Pro	Thr	Leu	Arg	Thr	Ala	Ala	Leu	Gly	Leu	Ala	Ala	Leu	
			25					30					35			
gct	gcg	gta	ttg	ctg	tgc	gcc	ccg	ctc	ttt	tta	tcc	aca	ttc	cag	ctg	259
Ala	Ala	Val	Leu	Leu	Cys	Ala	Pro	Leu	Phe	Leu	Ser	Thr	Phe	Gln	Leu	
		40					45					50				
acg	ttg	atg	tgc	cgc	ttg	gtg	tgt	tat	gcg	atc	gtc	gca	gtc	ggc	atc	307
Thr	Leu	Met	Ser	Arg	Leu	Val	Cys	Tyr	Ala	Ile	Val	Ala	Val	Gly	Ile	

55	60	65	
ggg ctg gcg tgg ggc aga ggc ggc atg ctc acg ctg ggg caa ggc gtg Gly Leu Ala Trp Gly Arg Gly Gly Met Leu Thr Leu Gly Gln Gly Val 70 75 80 85			355
ttc ttt gga atc ggc gcg tac atc atg gcc atg cac atg ctg tac agc Phe Phe Gly Ile Gly Ala Tyr Ile Met Ala Met His Met Leu Tyr Ser 90 95 100			403
gat tcg cag att ttt ggg acc aca gtt ccg caa tgg tgg tcc att ttt Asp Ser Gln Ile Phe Gly Thr Thr Val Pro Gln Trp Trp Ser Ile Phe 105 110 115			451
gcc aac ccg gca gtc gca ctc atc gca gtt gtg gcg ctt ccc ggc atc Ala Asn Pro Ala Val Ala Leu Ile Ala Val Val Ala Leu Pro Gly Ile 120 125 130			499
gtg gct ttt gtg ctc ggc ttc tcc att ttc aaa cga cgc atc aaa ggc Val Ala Phe Val Leu Gly Phe Ser Ile Phe Lys Arg Arg Ile Lys Gly 135 140 145			547
gcc tac ttt gcc atc gtg aac caa gcg ctc gcc gca gct gtt gtg gtg Ala Tyr Phe Ala Ile Val Asn Gln Ala Leu Ala Ala Ala Val Val Val 150 155 160 165			595
ttg ctg gtc gga caa caa gat tcc ctt gga ggt tcc aat ggt ctt tcc Leu Leu Val Gly Gln Gln Asp Ser Leu Gly Gly Ser Asn Gly Leu Ser 170 175 180			643
gga ttt cga tcg ttc atg ggt ttt gcc gtc tac gac ccc atc aac cgc Gly Phe Arg Ser Phe Met Gly Phe Ala Val Tyr Asp Pro Ile Asn Arg 185 190 195			691
atc atg ttt tac ttc acc gca gtg gga gtt ctc ttg gct ttg gtg gct Ile Met Phe Tyr Phe Thr Ala Val Gly Val Leu Leu Ala Leu Val Ala 200 205 210			739
atc tca tat tgg ctc atg cgc agc cgc tat gga gaa ctg ctc gtg gcc Ile Ser Tyr Trp Leu Met Arg Ser Arg Tyr Gly Glu Leu Leu Val Ala 215 220 225			787
acc aga gat gca gaa gaa cgc gtc cga ttc ctc gga tat gat ccc gca Thr Arg Asp Ala Glu Glu Arg Val Arg Phe Leu Gly Tyr Asp Pro Ala 230 235 240 245			835
ttg atc aaa acc gcc gca tat gtc att gct gcg atg att gcc gga atc Leu Ile Lys Thr Ala Ala Tyr Val Ile Ala Ala Met Ile Ala Gly Ile 250 255 260			883
gcc gga gcg ctg ttc gtg ccg atc gtg ggc atc att tca ccc gca gaa Ala Gly Ala Leu Phe Val Pro Ile Val Gly Ile Ile Ser Pro Ala Glu 265 270 275			931
atc ggc gtg gtg cca tca atc gtg ttc gtg atc gcc gtc gcc gct ggt Ile Gly Val Val Pro Ser Ile Val Phe Val Ile Ala Val Ala Ala Gly 280 285 290			979
ggc agg gca tcc cta ttc ggt ccc gta gtt ggc gcg ctg gtg ctg ggc Gly Arg Ala Ser Leu Phe Gly Pro Val Val Gly Ala Leu Val Leu Gly 295 300 305			1027

tgg gtg gaa tcc aca ctt gct caa act ttc ccc agc atg tgg tcc tat 1075
 Trp Val Glu Ser Thr Leu Ala Gln Thr Phe Pro Ser Met Trp Ser Tyr
 310 315 320 325

 ttc cag ggt gcg atc ctg gtt ctc gtg atc gtg ttg ctg ccg ggc gga 1123
 Phe Gln Gly Ala Ile Leu Val Leu Val Ile Val Leu Leu Pro Gly Gly
 330 335 340

 att gct tca att aaa ctt tcc gcg ctc aaa aat aag gcc agg aag gcc 1171
 Ile Ala Ser Ile Lys Leu Ser Ala Leu Lys Asn Lys Ala Arg Lys Ala
 345 350 355

 acc tca tgagccttaa aatcaccaac ctc 1200
 Thr Ser

<210> 466

<211> 359

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 466

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 Pro Lys Leu Ser Val Val Asn Ala Pro Thr Leu Arg Thr Ala Ala Leu
 20 25 30

 Gly Leu Ala Ala Leu Ala Ala Val Leu Leu Cys Ala Pro Leu Phe Leu
 35 40 45

 Ser Thr Phe Gln Leu Thr Leu Met Ser Arg Leu Val Cys Tyr Ala Ile
 50 55 60

 Val Ala Val Gly Ile Gly Leu Ala Trp Gly Arg Gly Gly Met Leu Thr
 65 70 75 80

 Leu Gly Gln Gly Val Phe Phe Gly Ile Gly Ala Tyr Ile Met Ala Met
 85 90 95

 His Met Leu Tyr Ser Asp Ser Gln Ile Phe Gly Thr Thr Val Pro Gln
 100 105 110

 Trp Trp Ser Ile Phe Ala Asn Pro Ala Val Ala Leu Ile Ala Val Val
 115 120 125

 Ala Leu Pro Gly Ile Val Ala Phe Val Leu Gly Phe Ser Ile Phe Lys
 130 135 140

 Arg Arg Ile Lys Gly Ala Tyr Phe Ala Ile Val Asn Gln Ala Leu Ala
 145 150 155 160

 Ala Ala Val Val Val Leu Leu Val Gly Gln Gln Asp Ser Leu Gly Gly
 165 170 175

 Ser Asn Gly Leu Ser Gly Phe Arg Ser Phe Met Gly Phe Ala Val Tyr
 180 185 190

 Asp Pro Ile Asn Arg Ile Met Phe Tyr Phe Thr Ala Val Gly Val Leu

195	200	205
Leu Ala Leu Val Ala Ile Ser Tyr Trp Leu Met Arg Ser Arg Tyr Gly 210 215 220		
Glu Leu Leu Val Ala Thr Arg Asp Ala Glu Glu Arg Val Arg Phe Leu 225 230 235 240		
Gly Tyr Asp Pro Ala Leu Ile Lys Thr Ala Ala Tyr Val Ile Ala Ala 245 250 255		
Met Ile Ala Gly Ile Ala Gly Ala Leu Phe Val Pro Ile Val Gly Ile 260 265 270		
Ile Ser Pro Ala Glu Ile Gly Val Val Pro Ser Ile Val Phe Val Ile 275 280 285		
Ala Val Ala Ala Gly Gly Arg Ala Ser Leu Phe Gly Pro Val Val Gly 290 295 300		
Ala Leu Val Leu Gly Trp Val Glu Ser Thr Leu Ala Gln Thr Phe Pro 305 310 315 320		
Ser Met Trp Ser Tyr Phe Gln Gly Ala Ile Leu Val Leu Val Ile Val 325 330 335		
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Lys Ala Arg Lys Ala Thr Ser 355		

<210> 467
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(853)
 <223> RXA00091

<400> 467
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 Val Ile Thr Leu Thr
 1 5
 aat gtc cgc aag gaa tac tcc agc gac gtt gcc atc ggc ccc gtc aac 163
 Asn Val Arg Lys Glu Tyr Ser Ser Asp Val Ala Ile Gly Pro Val Asn
 10 15 20
 ctt gag atc cca gcc ggc ggc atc acc gcg ttg gtc ggc cca aac ggt 211
 Leu Glu Ile Pro Ala Gly Gly Ile Thr Ala Leu Val Gly Pro Asn Gly
 25 30 35
 gca ggc aag tca aca ctg ctc acc atg atc ggt cga ctc ctc ggc atc 259
 Ala Gly Lys Ser Thr Leu Leu Thr Met Ile Gly Arg Leu Leu Gly Ile
 40 45 50

gat gaa ggc aac atc acc gta gcc tcc tac gat gtc acc tca acc gca 307
Asp Glu Gly Asn Ile Thr Val Ala Ser Tyr Asp Val Thr Ser Thr Ala
55 60 65

tcc aaa gat ctg gcc aag atc atc tcc atc ctg cgc cag gaa aac cac 355
Ser Lys Asp Leu Ala Lys Ile Ile Ser Ile Leu Arg Gln Glu Asn His
70 75 80 85

ttt gtt acc aag ctg acc gtg cgc cag ctc gta ggt ttc gga cgc ttc 403
Phe Val Thr Lys Leu Thr Val Arg Gln Leu Val Gly Phe Gly Arg Phe
90 95 100

cca tat agc aag ggc cgg ctg acg gaa gaa gac gag gga atc atc tcc 451
Pro Tyr Ser Lys Gly Arg Leu Thr Glu Glu Asp Glu Gly Ile Ile Ser
105 110 115

cgc tac atc gac ttc ttc aat ctc acc gaa ctc gaa gac cgc tac ctc 499
Arg Tyr Ile Asp Phe Phe Asn Leu Thr Glu Leu Glu Asp Arg Tyr Leu
120 125 130

gac cag ctt tcc ggc ggc cag cgc cag cgc gcc tat gtc gcc atg gtg 547
Asp Gln Leu Ser Gly Gly Gln Arg Gln Arg Ala Tyr Val Ala Met Val
135 140 145

ctg tgc caa gag acg gac tac gtg ctt ctc gac gaa ccc ctc aac aat 595
Leu Cys Gln Glu Thr Asp Tyr Val Leu Leu Asp Glu Pro Leu Asn Asn
150 155 160 165

ctt gat atc gca cac tcg gtg gaa atg atg aaa cac ctc gag aat gct 643
Leu Asp Ile Ala His Ser Val Glu Met Met Lys His Leu Glu Asn Ala
170 175 180

gca gcc caa ttt ggc cgc acc atc atc gtg gtt ctt cac gac atc aac 691
Ala Ala Gln Phe Gly Arg Thr Ile Ile Val Val Leu His Asp Ile Asn
185 190 195

ttc gcc gcg cgc tac gcc gat tac atc gtg gcc gta aag cac gga atg 739
Phe Ala Ala Arg Tyr Ala Asp Tyr Ile Val Ala Val Lys His Gly Met
200 205 210

atc gaa aaa gag gga aca cct gaa cag atc atg aaa aac gag atc ctt 787
Ile Glu Lys Glu Gly Thr Pro Glu Gln Ile Met Lys Asn Glu Ile Leu
215 220 225

tca gaa atc ttc aat aca gag atc gaa gtt att gaa gga cca cac ggc 835
Ser Glu Ile Phe Asn Thr Glu Ile Glu Val Ile Glu Gly Pro His Gly
230 235 240 245

aag att gct tgc tac cac taaatgaaga gaaataagcc gac 876
Lys Ile Ala Cys Tyr His
250

<210> 468

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

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Val Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Thr Met Ile Gly	35	40	45
Arg Leu Leu Gly Ile Asp Glu Gly Asn Ile Thr Val Ala Ser Tyr Asp	50	55	60
Val Thr Ser Thr Ala Ser Lys Asp Leu Ala Lys Ile Ile Ser Ile Leu	65	70	75
Arg Gln Glu Asn His Phe Val Thr Lys Leu Thr Val Arg Gln Leu Val	85	90	95
Gly Phe Gly Arg Phe Pro Tyr Ser Lys Gly Arg Leu Thr Glu Glu Asp	100	105	110
Glu Gly Ile Ile Ser Arg Tyr Ile Asp Phe Phe Asn Leu Thr Glu Leu	115	120	125
Glu Asp Arg Tyr Leu Asp Gln Leu Ser Gly Gly Gln Arg Gln Arg Ala	130	135	140
Tyr Val Ala Met Val Leu Cys Gln Glu Thr Asp Tyr Val Leu Leu Asp	145	150	155
Glu Pro Leu Asn Asn Leu Asp Ile Ala His Ser Val Glu Met Met Lys	165	170	175
His Leu Glu Asn Ala Ala Ala Gln Phe Gly Arg Thr Ile Ile Val Val	180	185	190
Leu His Asp Ile Asn Phe Ala Ala Arg Tyr Ala Asp Tyr Ile Val Ala	195	200	205
Val Lys His Gly Met Ile Glu Lys Glu Gly Thr Pro Glu Gln Ile Met	210	215	220
Lys Asn Glu Ile Leu Ser Glu Ile Phe Asn Thr Glu Ile Glu Val Ile	225	230	235
Glu Gly Pro His Gly Lys Ile Ala Cys Tyr His	245	250	

<210> 469

<211> 692

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (79)..(669)

<223> RXA00228

<400> 469

ccgcatggca tccgccgaaa gaattcccct ccggagggaat ggcacgcctc atgggagaac 60

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gcacgcggcaaa aaactgacatg cgc gac ctc cgc tcc atg atc ggc gtc agc 111
      Met Arg Asp Leu Arg Ser Met Ile Gly Val Ser
      1             5             10

tcc tcc gca tta ggc aac cga atc ccc tcc gaa gaa aaa gtc tct gac 159
Ser Ser Ala Leu Gly Asn Arg Ile Pro Ser Glu Glu Lys Val Ser Asp
      15             20             25

cta gtc atc tcc gca ggc tac gca atc ctc ggc cgc tgg cgc gaa gac 207
Leu Val Ile Ser Ala Gly Tyr Ala Ile Leu Gly Arg Trp Arg Glu Asp
      30             35             40

tac gac gaa atg gac ttc gga caa gcc acc gaa atc ctc gaa caa gtc 255
Tyr Asp Glu Met Asp Phe Gly Gln Ala Thr Glu Ile Leu Glu Gln Val
      45             50             55

gga gcc atg cac cta gcc gac cgc acc tgg gga acc ctc tcc gaa ggc 303
Gly Ala Met His Leu Ala Asp Arg Thr Trp Gly Thr Leu Ser Glu Gly
      60             65             70             75

gaa cgc aaa cga gtc ctg gtc gca cgc gca ctc atg acc aac ccg gaa 351
Glu Arg Lys Arg Val Leu Val Ala Arg Ala Leu Met Thr Asn Pro Glu
      80             85             90

ctc ctc atc ctt gac gaa cca acc gca gga atg gac ctc ggc gga cgc 399
Leu Leu Ile Leu Asp Glu Pro Thr Ala Gly Met Asp Leu Gly Gly Arg
      95             100             105

gaa gac ctc gtc ggc tac ctc gga gaa ctc gcc atg gac cca gac gca 447
Glu Asp Leu Val Gly Tyr Leu Gly Glu Leu Ala Met Asp Pro Asp Ala
      110             115             120

cct gcc atc gtc atg atc acc cac cac gtc gaa gaa atc ccc gcc gga 495
Pro Ala Ile Val Met Ile Thr His His Val Glu Glu Ile Pro Ala Gly
      125             130             135

ttc acc cac gca atg ctc ctc gac gaa ggt gaa atc gta gcc caa ggc 543
Phe Thr His Ala Met Leu Leu Asp Glu Gly Glu Ile Val Ala Gln Gly
      140             145             150             155

ctg atc aac acc gtc atg aca aac gag aac cta tcc aaa gca ttc cac 591
Leu Ile Asn Thr Val Met Thr Asn Glu Asn Leu Ser Lys Ala Phe His
      160             165             170

cag cca atc caa gta gac cgc atc ggg gaa cgc tac ttt gcc cgc cgt 639
Gln Pro Ile Gln Val Asp Arg Ile Gly Glu Arg Tyr Phe Ala Arg Arg
      175             180             185

gtg aga acc gcc agg agt cat agg gct cag taggtttttt ggagttgtgg 689
Val Arg Thr Ala Arg Ser His Arg Ala Gln
      190             195

gcc 692

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<210> 470

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 470

Met Arg Asp Leu Arg Ser Met Ile Gly Val Ser Ser Ser Ala Leu Gly
 1 5 10 15
 Asn Arg Ile Pro Ser Glu Glu Lys Val Ser Asp Leu Val Ile Ser Ala
 20 25 30
 Gly Tyr Ala Ile Leu Gly Arg Trp Arg Glu Asp Tyr Asp Glu Met Asp
 35 40 45
 Phe Gly Gln Ala Thr Glu Ile Leu Glu Gln Val Gly Ala Met His Leu
 50 55 60
 Ala Asp Arg Thr Trp Gly Thr Leu Ser Glu Gly Glu Arg Lys Arg Val
 65 70 75 80
 Leu Val Ala Arg Ala Leu Met Thr Asn Pro Glu Leu Leu Ile Leu Asp
 85 90 95
 Glu Pro Thr Ala Gly Met Asp Leu Gly Gly Arg Glu Asp Leu Val Gly
 100 105 110
 Tyr Leu Gly Glu Leu Ala Met Asp Pro Asp Ala Pro Ala Ile Val Met
 115 120 125
 Ile Thr His His Val Glu Glu Ile Pro Ala Gly Phe Thr His Ala Met
 130 135 140
 Leu Leu Asp Glu Gly Glu Ile Val Ala Gln Gly Leu Ile Asn Thr Val
 145 150 155 160
 Met Thr Asn Glu Asn Leu Ser Lys Ala Phe His Gln Pro Ile Gln Val
 165 170 175
 Asp Arg Ile Gly Glu Arg Tyr Phe Ala Arg Arg Val Arg Thr Ala Arg
 180 185 190
 Ser His Arg Ala Gln
 195

<210> 471
 <211> 813
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(790)
 <223> RXA00346

<400> 471
 atctatgaga cccctcaaaa caccgagaat ttcctcgatg cattcaccaa ggcagttgat 60
 gatctcaccg ctgccactaa ccagggttag aattatttaa atg ctg ttg act ttc 115
 Met Leu Leu Thr Phe
 1 5
 aat gat gct gcg gtg gat ccc ctc tgg agg ggc ctg aat tta gag ctc 163
 Asn Asp Ala Ala Val Asp Pro Leu Trp Arg Gly Leu Asn Leu Glu Leu
 10 15 20

cga cag ggg gaa ttt ctt gcg gtt tta ggc ccc aac ggc gtg gga aaa 211
 Arg Gln Gly Glu Phe Leu Ala Val Leu Gly Pro Asn Gly Val Gly Lys
 25 30 35

tcc acg ctc atc ggt acg att ttg ggc acc cga aaa ctc acc cac ggt 259
 Ser Thr Leu Ile Gly Thr Ile Leu Gly Thr Arg Lys Leu Thr His Gly
 40 45 50

tcg gtt aaa act gat gcc cgg gtg ggt tat att ccg caa caa cga att 307
 Ser Val Lys Thr Asp Ala Arg Val Gly Tyr Ile Pro Gln Gln Arg Ile
 55 60 65

ttc gat gtc ccg ttg cgt gcc cgc gat atg gtt tcg ctg tcc gcg gcg 355
 Phe Asp Val Pro Leu Arg Ala Arg Asp Met Val Ser Leu Ser Ala Ala
 70 75 80 85

cat ggc gtg gtt tcc aaa agg gga ccc gcg aag ggt gac gtc gat aag 403
 His Gly Val Val Ser Lys Arg Gly Pro Ala Lys Gly Asp Val Asp Lys
 90 95 100

ctt ctt gcc cgc gtg ggc gct tcc gga atc gcc gat cga cgc gtc ggc 451
 Leu Leu Ala Arg Val Gly Ala Ser Gly Ile Ala Asp Arg Arg Val Gly
 105 110 115

gag ctc tcc ggc ggg cag cag cag ctc gtc cgc caa gcc cag gcc ctt 499
 Glu Leu Ser Gly Gly Gln Gln Gln Leu Val Arg Gln Ala Gln Ala Leu
 120 125 130

gcc acg cgc ccg caa tta ttg ctt gcc gac gaa ccc ctc ctc agc ctt 547
 Ala Thr Arg Pro Gln Leu Leu Ala Asp Glu Pro Leu Leu Ser Leu
 135 140 145

gac ccc ggc gtc gcg cag cgc acg gtg tcc cta ttt ggt gaa ttg aag 595
 Asp Pro Gly Val Ala Gln Arg Thr Val Ser Leu Phe Gly Glu Leu Lys
 150 155 160 165

gcc gaa ggc gtc ggc gtt gtt gtg gtc acc cac gat gtc aat cca cta 643
 Ala Glu Gly Val Gly Val Val Val Val Thr His Asp Val Asn Pro Leu
 170 175 180

atg ggc ctg gta gat cgc att ttg tac ctc gcc ccc aac ggc cac acc 691
 Met Gly Leu Val Asp Arg Ile Leu Tyr Leu Ala Pro Asn Gly His Thr
 185 190 195

atc ggc acg gtt ggc gat gtc atg cag tcc gaa aaa ctc agc gaa ctc 739
 Ile Gly Thr Val Gly Asp Val Met Gln Ser Glu Lys Leu Ser Glu Leu
 200 205 210

tac aac gca ccc gtc acg gtg gct cgc atc aac gac aga atc gtg gtg 787
 Tyr Asn Ala Pro Val Thr Val Ala Arg Ile Asn Asp Arg Ile Val Val
 215 220 225

gtt taagtggatc tatccacctg gct 813
 Val
 230

<210> 472

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Leu Leu Thr Phe Asn Asp Ala Ala Val Asp Pro Leu Trp Arg Gly
 1 5 10 15

Leu Asn Leu Glu Leu Arg Gln Gly Glu Phe Leu Ala Val Leu Gly Pro
 20 25 30

Asn Gly Val Gly Lys Ser Thr Leu Ile Gly Thr Ile Leu Gly Thr Arg
 35 40 45

Lys Leu Thr His Gly Ser Val Lys Thr Asp Ala Arg Val Gly Tyr Ile
 50 55 60

Pro Gln Gln Arg Ile Phe Asp Val Pro Leu Arg Ala Arg Asp Met Val
 65 70 75 80

Ser Leu Ser Ala Ala His Gly Val Val Ser Lys Arg Gly Pro Ala Lys
 85 90 95

Gly Asp Val Asp Lys Leu Leu Ala Arg Val Gly Ala Ser Gly Ile Ala
 100 105 110

Asp Arg Arg Val Gly Glu Leu Ser Gly Gly Gln Gln Gln Leu Val Arg
 115 120 125

Gln Ala Gln Ala Leu Ala Thr Arg Pro Gln Leu Leu Leu Ala Asp Glu
 130 135 140

Pro Leu Leu Ser Leu Asp Pro Gly Val Ala Gln Arg Thr Val Ser Leu
 145 150 155 160

Phe Gly Glu Leu Lys Ala Glu Gly Val Gly Val Val Val Val Thr His
 165 170 175

Asp Val Asn Pro Leu Met Gly Leu Val Asp Arg Ile Leu Tyr Leu Ala
 180 185 190

Pro Asn Gly His Thr Ile Gly Thr Val Gly Asp Val Met Gln Ser Glu
 195 200 205

Lys Leu Ser Glu Leu Tyr Asn Ala Pro Val Thr Val Ala Arg Ile Asn
 210 215 220

Asp Arg Ile Val Val Val
 225 230

<210> 473

<211> 433

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(433)

<223> RXA00524

<400> 473

tcctcggcac ccgctacccc gtcggagttg tcaccggcgc attcggcgcc ccattcctta 60

tctatttact cattcggttcc aaccgcgcgg gagtaaccct gtg acc acc aac cat 115
 Val Thr Thr Asn His
 1 5

caa cta tcc gcc gaa gaa att tcc ctg gcg tac ggc gag cgc acc atc 163
 Gln Leu Ser Ala Glu Ile Ser Leu Ala Tyr Gly Glu Arg Thr Ile
 10 15 20

atc gat tcg ctc agc gtc gac atc gtc ccc ggc aaa atc acc tcc atc 211
 Ile Asp Ser Leu Ser Val Asp Ile Val Pro Gly Lys Ile Thr Ser Ile
 25 30 35

gtc ggc ccc aac gga tgc ggc aaa tca acg ctg ctg cgc gcc ttt gcg 259
 Val Gly Pro Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Ala Phe Ala
 40 45 50

cgc ctc ctt aaa cct agc gcc ggg caa gcg ctt atc gac gcc cac ccc 307
 Arg Leu Leu Lys Pro Ser Ala Gly Gln Ala Leu Ile Asp Ala His Pro
 55 60 65

ctt cct tca ctg cca ggc aaa gaa cta gct cgc atg ctc ggc ctg tta 355
 Leu Pro Ser Leu Pro Gly Lys Glu Leu Ala Arg Met Leu Gly Leu Leu
 70 75 80 85

ccg caa tcc ccc acc gga cct gaa ggc atc gtc gtc gcc gac ctc gtg 403
 Pro Gln Ser Pro Thr Gly Pro Glu Gly Ile Val Val Ala Asp Leu Val
 90 95 100

ggc cgc ggc cgc cac ccc cac caa gga ctc 433
 Gly Arg Gly Arg His Pro His Gln Gly Leu
 105 110

<210> 474

<211> 111

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Val Thr Thr Asn His Gln Leu Ser Ala Glu Glu Ile Ser Leu Ala Tyr
 1 5 10 15

Gly Glu Arg Thr Ile Ile Asp Ser Leu Ser Val Asp Ile Val Pro Gly
 20 25 30

Lys Ile Thr Ser Ile Val Gly Pro Asn Gly Cys Gly Lys Ser Thr Leu
 35 40 45

Leu Arg Ala Phe Ala Arg Leu Leu Lys Pro Ser Ala Gly Gln Ala Leu
 50 55 60

Ile Asp Ala His Pro Leu Pro Ser Leu Pro Gly Lys Glu Leu Ala Arg
 65 70 75 80

Met Leu Gly Leu Leu Pro Gln Ser Pro Thr Gly Pro Glu Gly Ile Val
 85 90 95

Val Ala Asp Leu Val Gly Arg Gly Arg His Pro His Gln Gly Leu
 100 105 110

<400> 475																	
gcaacacggt gatactgagc tgcacacgcc cggtggcctg gtgaccagtt tgctgggcgg																	60
ggtgtatttg atgtggcttt tgagccgaaa ggaggcataa atg ctg caa gcg cat																	115
Met Leu Gln Ala His																	5
1																	
gat ctc acg ctg agt tac ggc ggc cga aat att gta gaa ggg ctc agt																	163
Asp Leu Thr Leu Ser Tyr Gly Gly Arg Asn Ile Val Glu Gly Leu Ser																	20
10 15																	
ctg gac ctt ccg gaa aga ggc ctc agc atc atc att ggc ccc aac gga																	211
Leu Asp Leu Pro Glu Arg Gly Leu Ser Ile Ile Ile Gly Pro Asn Gly																	35
25 30																	
tgc ggg aaa tca acc gtt ttg aaa gcg ttg ggc aga ctg ctg aaa cca																	259
Cys Gly Lys Ser Thr Val Leu Lys Ala Leu Gly Arg Leu Leu Lys Pro																	50
40 45																	
caa ttg ggg aag atc acg cta ggt ggc cga gat att tcc agc atg ggc																	307
Gln Leu Gly Lys Ile Thr Leu Gly Gly Arg Asp Ile Ser Ser Met Gly																	65
55 60																	
acc aag cat gtg gcg aaa cac atc ggc gtg ctt ccg caa ccc cca tat																	355
Thr Lys His Val Ala Lys His Ile Gly Val Leu Pro Gln Pro Pro Tyr																	85
70 75 80																	
gcg ccc gat ggg gtg agc gtc acg gag ctg gtc agc cgc ggg cgg tat																	403
Ala Pro Asp Gly Val Ser Val Thr Glu Leu Val Ser Arg Gly Arg Tyr																	100
90 95																	
ccg cac caa cat ctg ctg tcg caa tgg tcg aaa gac gat gaa gcc att																	451
Pro His Gln His Leu Leu Ser Gln Trp Ser Lys Asp Asp Glu Ala Ile																	115
105 110																	
gtg gcg cgc tcg ctg gcg gaa gtc ggc atg cac acc cat gct gag cat																	499
Val Ala Arg Ser Leu Ala Glu Val Gly Met His Thr His Ala Glu His																	130
120 125																	
tta gtg tcg gaa ctt tca ggc ggc cag cgc caa cgg gcg tgg atc gcc																	547
Leu Val Ser Glu Leu Ser Gly Gly Gln Arg Gln Arg Ala Trp Ile Ala																	145
135 140																	
atg gcg ctc gct cag gaa aca gac att ttg ctt ctc gac gag ccc acc																	595
Met Ala Leu Ala Gln Glu Thr Asp Ile Leu Leu Leu Asp Glu Pro Thr																	165
150 155 160																	
acg ttc ctc gac gta gcc cac caa ata tcc gtc ctc gat tta tgc tcc																	643
Thr Phe Leu Asp Val Ala His Gln Ile Ser Val Leu Asp Leu Cys Ser																	180
170 175 180																	

gac ctg cac caa cgt ggt cgc acc ctg gcc att gtt cta cac gat ctg 691
 Asp Leu His Gln Arg Gly Arg Thr Leu Ala Ile Val Leu His Asp Leu
 185 190 195

 aac atg gct gca cgg tat gcc acc cac atc atc gcc atg cgg gac ggc 739
 Asn Met Ala Ala Arg Tyr Ala Thr His Ile Ile Ala Met Arg Asp Gly
 200 205 210

 acc atc atc gac caa gga aaa ccc gaa gaa ata ctc act aaa gcg ctg 787
 Thr Ile Ile Asp Gln Gly Lys Pro Glu Glu Ile Leu Thr Lys Ala Leu
 215 220 225

 ctc aaa gaa gtt ttt gac ctc gac gca ctc atc ctc aaa gac ccc aac 835
 Leu Lys Glu Val Phe Asp Leu Asp Ala Leu Ile Leu Lys Asp Pro Asn
 230 235 240 245

 aac ggc cga cca ctc atc gtg ccc aca gac agg aga aac tca 877
 Asn Gly Arg Pro Leu Ile Val Pro Thr Asp Arg Arg Asn Ser
 250 255

 tgaaagaaac cgacaaccta ctg 900

<210> 476

<211> 259

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 476

Met Leu Gln Ala His Asp Leu Thr Leu Ser Tyr Gly Gly Arg Asn Ile
 1 5 10 15

 Val Glu Gly Leu Ser Leu Asp Leu Pro Glu Arg Gly Leu Ser Ile Ile
 20 25 30

 Ile Gly Pro Asn Gly Cys Gly Lys Ser Thr Val Leu Lys Ala Leu Gly
 35 40 45

 Arg Leu Leu Lys Pro Gln Leu Gly Lys Ile Thr Leu Gly Gly Arg Asp
 50 55 60

 Ile Ser Ser Met Gly Thr Lys His Val Ala Lys His Ile Gly Val Leu
 65 70 75 80

 Pro Gln Pro Pro Tyr Ala Pro Asp Gly Val Ser Val Thr Glu Leu Val
 85 90 95

 Ser Arg Gly Arg Tyr Pro His Gln His Leu Leu Ser Gln Trp Ser Lys
 100 105 110

 Asp Asp Glu Ala Ile Val Ala Arg Ser Leu Ala Glu Val Gly Met His
 115 120 125

 Thr His Ala Glu His Leu Val Ser Glu Leu Ser Gly Gly Gln Arg Gln
 130 135 140

 Arg Ala Trp Ile Ala Met Ala Leu Ala Gln Glu Thr Asp Ile Leu Leu
 145 150 155 160

 Leu Asp Glu Pro Thr Thr Phe Leu Asp Val Ala His Gln Ile Ser Val
 165 170 175

Leu Asp Leu Cys Ser Asp Leu His Gln Arg Gly Arg Thr Leu Ala Ile
 180 185 190
 Val Leu His Asp Leu Asn Met Ala Ala Arg Tyr Ala Thr His Ile Ile
 195 200 205
 Ala Met Arg Asp Gly Thr Ile Ile Asp Gln Gly Lys Pro Glu Glu Ile
 210 215 220
 Leu Thr Lys Ala Leu Leu Lys Glu Val Phe Asp Leu Asp Ala Leu Ile
 225 230 235 240
 Leu Lys Asp Pro Asn Asn Gly Arg Pro Leu Ile Val Pro Thr Asp Arg
 245 250 255
 Arg Asn Ser

<210> 477
 <211> 906
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(883)
 <223> RXA02767

<400> 477
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 ccagtctaag ccctggcctt acgccagtaa ggtgttaccc atg cgc gaa cta gca 115
 Met Arg Glu Leu Ala
 1 5
 ctc aac atg gcc ggc gtc acc gtg cgg cgc ggc gag aaa ttg ctt ctc 163
 Leu Asn Met Ala Gly Val Thr Val Arg Arg Gly Glu Lys Leu Leu Leu
 10 15 20
 gac gat atc tcc ctc tca att ccg caa ggg tcg cac tgg gcc gta ctt 211
 Asp Asp Ile Ser Leu Ser Ile Pro Gln Gly Ser His Trp Ala Val Leu
 25 30 35
 ggt cca aat ggc gcc ggt aaa acc acc atg ctg aag atc gca gcc acc 259
 Gly Pro Asn Gly Ala Gly Lys Thr Thr Met Leu Lys Ile Ala Ala Thr
 40 45 50
 ttg ctg tac cca tcg gaa ggc acc gtg gac atc ctg ggg cat cgc ttt 307
 Leu Leu Tyr Pro Ser Glu Gly Thr Val Asp Ile Leu Gly His Arg Phe
 55 60 65
 ggt cgg gtg gat act cgt gag ctg cgg aaa aca atc ggc ctg gtg gac 355
 Gly Arg Val Asp Thr Arg Glu Leu Arg Lys Thr Ile Gly Leu Val Asp
 70 75 80 85
 ccg aag caa aga ttt acc aac ctg ccg gcc cac gaa att gtg ctg tcg 403
 Pro Lys Gln Arg Phe Thr Asn Leu Pro Ala His Glu Ile Val Leu Ser
 90 95 100

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ggg tta acc gcc tcc aac ggg ttg ttg cca cgg tgg tcg gct tcg gct 451
Gly Leu Thr Ala Ser Asn Gly Leu Leu Pro Arg Trp Ser Ala Ser Ala
      105                      110                      115

tcg gag ttg gag cgg tgc gct ttg atg ttg gag ttg gtg ggc atg aca 499
Ser Glu Leu Glu Arg Cys Ala Leu Met Leu Glu Leu Val Gly Met Thr
      120                      125                      130

gcg cgt gcc gat cgt tac tgg gcc gat atg agc cag ggc gaa aaa gcc 547
Ala Arg Ala Asp Arg Tyr Trp Ala Asp Met Ser Gln Gly Glu Lys Ala
      135                      140                      145

cgc acc ctg att gct cgt gcg ctg att atc tca ccg acc cta ctg ctg 595
Arg Thr Leu Ile Ala Arg Ala Leu Ile Ile Ser Pro Thr Leu Leu Leu
      150                      155                      160                      165

ctt gat gaa ccc acc acc ggc ctt gac ctg ccc gga cgt gaa act ttg 643
Leu Asp Glu Pro Thr Thr Gly Leu Asp Leu Pro Gly Arg Glu Thr Leu
      170                      175                      180

ctc agt gtg att gat ggt ttg cga gcc gct ctt cct ggt ctg acg aca 691
Leu Ser Val Ile Asp Gly Leu Arg Ala Ala Leu Pro Gly Leu Thr Thr
      185                      190                      195

gtg atg atc acc cac cac gtc gaa gag atc gcc gcc tcc acg aca gat 739
Val Met Ile Thr His His Val Glu Glu Ile Ala Ala Ser Thr Thr Asp
      200                      205                      210

atc ctc atg atc aag gac gcc cgc ata ctg gct tcg ggg act gtt tca 787
Ile Leu Met Ile Lys Asp Ala Arg Ile Leu Ala Ser Gly Thr Val Ser
      215                      220                      225

gaa gtg atg act cct gaa aat ttg ggc gcg ctg tat gac atg tcg gtg 835
Glu Val Met Thr Pro Glu Asn Leu Gly Ala Leu Tyr Asp Met Ser Val
      230                      235                      240                      245

tcg ttg gaa act gtg cgc agc cgg tgg ttc gcg ttc gat gct ctg cat 883
Ser Leu Glu Thr Val Arg Ser Arg Trp Phe Ala Phe Asp Ala Leu His
      250                      255                      260

taaaaggggc tagttttaca caa 906

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<210> 478

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 478

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Met Arg Glu Leu Ala Leu Asn Met Ala Gly Val Thr Val Arg Arg Gly
  1              5              10              15

Glu Lys Leu Leu Leu Asp Asp Ile Ser Leu Ser Ile Pro Gln Gly Ser
      20              25              30

His Trp Ala Val Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Met Leu
      35              40              45

Lys Ile Ala Ala Thr Leu Leu Tyr Pro Ser Glu Gly Thr Val Asp Ile
      50              55              60

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Leu Gly His Arg Phe Gly Arg Val Asp Thr Arg Glu Leu Arg Lys Thr
 65 70 75 80
 Ile Gly Leu Val Asp Pro Lys Gln Arg Phe Thr Asn Leu Pro Ala His
 85 90 95
 Glu Ile Val Leu Ser Gly Leu Thr Ala Ser Asn Gly Leu Leu Pro Arg
 100 105 110
 Trp Ser Ala Ser Ala Ser Glu Leu Glu Arg Cys Ala Leu Met Leu Glu
 115 120 125
 Leu Val Gly Met Thr Ala Arg Ala Asp Arg Tyr Trp Ala Asp Met Ser
 130 135 140
 Gln Gly Glu Lys Ala Arg Thr Leu Ile Ala Arg Ala Leu Ile Ile Ser
 145 150 155 160
 Pro Thr Leu Leu Leu Leu Asp Glu Pro Thr Thr Gly Leu Asp Leu Pro
 165 170 175
 Gly Arg Glu Thr Leu Leu Ser Val Ile Asp Gly Leu Arg Ala Ala Leu
 180 185 190
 Pro Gly Leu Thr Thr Val Met Ile Thr His His Val Glu Glu Ile Ala
 195 200 205
 Ala Ser Thr Thr Asp Ile Leu Met Ile Lys Asp Ala Arg Ile Leu Ala
 210 215 220
 Ser Gly Thr Val Ser Glu Val Met Thr Pro Glu Asn Leu Gly Ala Leu
 225 230 235 240
 Tyr Asp Met Ser Val Ser Leu Glu Thr Val Arg Ser Arg Trp Phe Ala
 245 250 255
 Phe Asp Ala Leu His
 260

<210> 479

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXA02792

<400> 479

agaacaaagt gctgcccata ctcatgaact ttgccgaacc cccaaccccg ctggccgctcg 60

atggcctaga aaaaatcatc gactttgtgg aaaccacccc atg atc gag gcc aca 115
 Met Ile Glu Ala Thr
 1 5

cac cta cgc cac agt ttt ggc gac aac atc gtc atc gat gac gtc acc 163
 His Leu Arg His Ser Phe Gly Asp Asn Ile Val Ile Asp Asp Val Thr
 10 15 20

ctc cat cta cct gca cac ggc acc gtc agc ttg gtc ggc ccc aac ggc	211
Leu His Leu Pro Ala His Gly Thr Val Ser Leu Val Gly Pro Asn Gly	
25 30 35	
agt ggc aaa acc acc ctg ctg cgt gca cta tac gga gca ctg caa cca	259
Ser Gly Lys Thr Thr Leu Leu Arg Ala Leu Tyr Gly Ala Leu Gln Pro	
40 45 50	
aat gaa ggg cac atc cac gta gat ggc gtt cca cta ata agc ttg cac	307
Asn Glu Gly His Ile His Val Asp Gly Val Pro Leu Ile Ser Leu His	
55 60 65	
cgc aaa gac atc gca aaa acc atg gcc gta gtc atc caa gaa cat gac	355
Arg Lys Asp Ile Ala Lys Thr Met Ala Val Val Ile Gln Glu His Asp	
70 75 80 85	
tcc gac ctc ccc atg acc gtc gct gac ctg gtc tta cta ggc aga ctc	403
Ser Asp Leu Pro Met Thr Val Ala Asp Leu Val Leu Leu Gly Arg Leu	
90 95 100	
ccc cac caa aag atg ttt gcc ggc aac tct caa gct gat cag tta ctc	451
Pro His Gln Lys Met Phe Ala Gly Asn Ser Gln Ala Asp Gln Leu Leu	
105 110 115	
gtt aag gaa gca ctc acc cga gtc ggc gcc att cac ctg gcc gac cga	499
Val Lys Glu Ala Leu Thr Arg Val Gly Ala Ile His Leu Ala Asp Arg	
120 125 130	
caa ttc ggc gca ctt tca ggc ggt gaa cgc caa cgc gtc ctc atc gca	547
Gln Phe Gly Ala Leu Ser Gly Gly Glu Arg Gln Arg Val Leu Ile Ala	
135 140 145	
cga gca ctc gta caa aac gcc aca cac att ctg ctc gac gaa ccc acc	595
Arg Ala Leu Val Gln Asn Ala Thr His Ile Leu Leu Asp Glu Pro Thr	
150 155 160 165	
aac cac ctc gac atc cgc tac cag cac gaa gtc ctt cac ctc gtc cgc	643
Asn His Leu Asp Ile Arg Tyr Gln His Glu Val Leu His Leu Val Arg	
170 175 180	
gaa ctc agc tca agt tcc atc atc gtc ctc cac gac ctc aac ctc gca	691
Glu Leu Ser Ser Ser Ser Ile Ile Val Leu His Asp Leu Asn Leu Ala	
185 190 195	
ggt gcc tac agc gac cac atc atc ctc ctt gac caa gga cgt gtg gtt	739
Gly Ala Tyr Ser Asp His Ile Ile Leu Leu Asp Gln Gly Arg Val Val	
200 205 210	
act caa gga acg ccc tca gag gta ttg acc cca gag cat ttg gaa cct	787
Thr Gln Gly Thr Pro Ser Glu Val Leu Thr Pro Glu His Leu Glu Pro	
215 220 225	
gtg tat ggc gtt cgt gtt gag cgc ttt gac cta ggc gat gaa gtc cac	835
Val Tyr Gly Val Arg Val Glu Arg Phe Asp Leu Gly Asp Glu Val His	
230 235 240 245	
ctt cgg ttc aag cgt cac taggagtttt gttgaggagg tgg	876
Leu Arg Phe Lys Arg His	
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<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 480

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Ile Asp Asp Val Thr Leu His Leu Pro Ala His Gly Thr Val Ser Leu
 20 25 30

Val Gly Pro Asn Gly Ser Gly Lys Thr Thr Leu Leu Arg Ala Leu Tyr
 35 40 45

Gly Ala Leu Gln Pro Asn Glu Gly His Ile His Val Asp Gly Val Pro
 50 55 60

Leu Ile Ser Leu His Arg Lys Asp Ile Ala Lys Thr Met Ala Val Val
 65 70 75 80

Ile Gln Glu His Asp Ser Asp Leu Pro Met Thr Val Ala Asp Leu Val
 85 90 95

Leu Leu Gly Arg Leu Pro His Gln Lys Met Phe Ala Gly Asn Ser Gln
 100 105 110

Ala Asp Gln Leu Leu Val Lys Glu Ala Leu Thr Arg Val Gly Ala Ile
 115 120 125

His Leu Ala Asp Arg Gln Phe Gly Ala Leu Ser Gly Gly Glu Arg Gln
 130 135 140

Arg Val Leu Ile Ala Arg Ala Leu Val Gln Asn Ala Thr His Ile Leu
 145 150 155 160

Leu Asp Glu Pro Thr Asn His Leu Asp Ile Arg Tyr Gln His Glu Val
 165 170 175

Leu His Leu Val Arg Glu Leu Ser Ser Ser Ser Ile Ile Val Leu His
 180 185 190

Asp Leu Asn Leu Ala Gly Ala Tyr Ser Asp His Ile Ile Leu Leu Asp
 195 200 205

Gln Gly Arg Val Val Thr Gln Gly Thr Pro Ser Glu Val Leu Thr Pro
 210 215 220

Glu His Leu Glu Pro Val Tyr Gly Val Arg Val Glu Arg Phe Asp Leu
 225 230 235 240

Gly Asp Glu Val His Leu Arg Phe Lys Arg His
 245 250

<210> 481

<211> 1161

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1138)

<223> RXN02929

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tgcttcttct gaagctgtgc cggccgctgc ttaagttttc gtg ctg aag aga att 115
                               Val Leu Lys Arg Ile
                               1           5

ttc ctc aac ccc tgg gtg gct acc gcg ttg tcg gta gtc att ttg ggg 163
Phe Leu Asn Pro Trp Val Ala Thr Ala Leu Ser Val Val Ile Leu Gly
                        10                15                20

ttt gtg gtg ctg ttt tca ggt ttt agc ggt gtt att gat tta agc ccc 211
Phe Val Val Leu Phe Ser Gly Phe Ser Gly Val Ile Asp Leu Ser Pro
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aca gca gtg att aga cat ttg agt ggg cag gac acg ctc acc cct cga 259
Thr Ala Val Ile Arg His Leu Ser Gly Gln Asp Thr Leu Thr Pro Arg
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gat cag gcc atc ttc ttt gat atc cgg ctg cct cga att atc gct ggt 307
Asp Gln Ala Ile Phe Phe Asp Ile Arg Leu Pro Arg Ile Ile Ala Gly
                        55                60                65

gtc att gtc gga gca acg ctg gct att tct ggt gct tct tac caa gcg 355
Val Ile Val Gly Ala Thr Leu Ala Ile Ser Gly Ala Ser Tyr Gln Ala
                        70                75                80                85

gta ttt aga aac ccg ctg gct gat cct tat ttg ttg ggt gtg tcc gca 403
Val Phe Arg Asn Pro Leu Ala Asp Pro Tyr Leu Leu Gly Val Ser Ala
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ggg tct ggc ctt ggt gtc acg gca gtg att gtt ggc ggt acc gtg ctg 451
Gly Ser Gly Leu Gly Val Thr Ala Val Ile Val Gly Gly Thr Val Leu
                        105                110                115

gga ttt tct gca ccg agc atc ggc gtg att ggt gca gca ttt gta ggt 499
Gly Phe Ser Ala Pro Ser Ile Gly Val Ile Gly Ala Ala Phe Val Gly
                        120                125                130

ggg gtt gcc gca gta ctt gcc acg ctg atg gtg agt cgg gga gta gga 547
Gly Val Ala Ala Val Leu Ala Thr Leu Met Val Ser Arg Gly Val Gly
                        135                140                145

cag gga tca tca acc acc gtg gtt att ttg gcg ggc gtg gcg gtt gct 595
Gln Gly Ser Ser Thr Thr Val Val Ile Leu Ala Gly Val Ala Val Ala
                        150                155                160                165

gct ttt gcc agt tcc atc cag acc tat att cag caa cga cac atc gat 643
Ala Phe Ala Ser Ser Ile Gln Thr Tyr Ile Gln Gln Arg His Ile Asp
                        170                175                180

acg gtg gcg cgc gta tat gtg tgg atg ttg ggc aac ctc aat gtc acc 691
Thr Val Ala Arg Val Tyr Val Trp Met Leu Gly Asn Leu Asn Val Thr
                        185                190                195

aac tgg atg tcg atc ttc atc gtg gct gtg gtg gcg gga cta tgc gcg 739
Asn Trp Met Ser Ile Phe Ile Val Ala Val Val Ala Gly Leu Cys Ala

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gcc gtg atc atg tcc tgc gcc agg ttg tta gac gtg atg gct gtt ggt Ala Val Ile Met Ser Cys Ala Arg Leu Leu Asp Val Met Ala Val Gly 215 220 225			787
gat gtg gaa gcc cgc aca ttg ggc gtc gat cca ggc ctc gta cgc att Asp Val Glu Ala Arg Thr Leu Gly Val Asp Pro Gly Leu Val Arg Ile 230 235 240 245			835
ggc att gtc atc gtg gca acc ctt ggt aca gct gca gtg gta tcc att Gly Ile Val Ile Val Ala Thr Leu Gly Thr Ala Ala Val Val Ser Ile 250 255 260			883
tcc ggt ctc atc ggg ttt gtg ggc atc att gtt ccg cac gcc ctg cgc Ser Gly Leu Ile Gly Phe Val Gly Ile Ile Val Pro His Ala Leu Arg 265 270 275			931
cta att gtt ggc ccg ggg cat cgg att tta ctg cca ctg tct ttc gta Leu Ile Val Gly Pro Gly His Arg Ile Leu Leu Pro Leu Ser Phe Val 280 285 290			979
tgg ggt gcc att ttc ctc gtg ttg gca gat acc gca ggg cga aca ttg Trp Gly Ala Ile Phe Leu Val Leu Ala Asp Thr Ala Gly Arg Thr Leu 295 300 305			1027
atg gct cct cag gaa ctt ccc gtg ggt gtg gtg aca gct gca ctc ggc Met Ala Pro Gln Glu Leu Pro Val Gly Val Val Thr Ala Ala Leu Gly 310 315 320 325			1075
gca ccg ttc ttc tta ttt att ttg cgc aga acc agc aga caa cga gtt Ala Pro Phe Phe Leu Phe Ile Leu Arg Arg Thr Ser Arg Gln Arg Val 330 335 340			1123
cca aaa agg agt gct taagtggcga tcattgaatg cga Pro Lys Arg Ser Ala 345			1161

<210> 482

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 482

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		20						25					30		

Ile	Asp	Leu	Ser	Pro	Thr	Ala	Val	Ile	Arg	His	Leu	Ser	Gly	Gln	Asp
		35					40					45			

Thr	Leu	Thr	Pro	Arg	Asp	Gln	Ala	Ile	Phe	Phe	Asp	Ile	Arg	Leu	Pro
	50					55					60				

Arg	Ile	Ile	Ala	Gly	Val	Ile	Val	Gly	Ala	Thr	Leu	Ala	Ile	Ser	Gly
	65				70					75					80

Ala	Ser	Tyr	Gln	Ala	Val	Phe	Arg	Asn	Pro	Leu	Ala	Asp	Pro	Tyr	Leu
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85					90					95					
Leu	Gly	Val	Ser	Ala	Gly	Ser	Gly	Leu	Gly	Val	Thr	Ala	Val	Ile	Val
			100					105					110		
Gly	Gly	Thr	Val	Leu	Gly	Phe	Ser	Ala	Pro	Ser	Ile	Gly	Val	Ile	Gly
		115					120					125			
Ala	Ala	Phe	Val	Gly	Gly	Val	Ala	Ala	Val	Leu	Ala	Thr	Leu	Met	Val
		130					135					140			
Ser	Arg	Gly	Val	Gly	Gln	Gly	Ser	Ser	Thr	Thr	Val	Val	Ile	Leu	Ala
		145					150					155			160
Gly	Val	Ala	Val	Ala	Ala	Phe	Ala	Ser	Ser	Ile	Gln	Thr	Tyr	Ile	Gln
			165					170						175	
Gln	Arg	His	Ile	Asp	Thr	Val	Ala	Arg	Val	Tyr	Val	Trp	Met	Leu	Gly
		180						185					190		
Asn	Leu	Asn	Val	Thr	Asn	Trp	Met	Ser	Ile	Phe	Ile	Val	Ala	Val	Val
		195					200					205			
Ala	Gly	Leu	Cys	Ala	Ala	Val	Ile	Met	Ser	Cys	Ala	Arg	Leu	Leu	Asp
		210					215					220			
Val	Met	Ala	Val	Gly	Asp	Val	Glu	Ala	Arg	Thr	Leu	Gly	Val	Asp	Pro
		225					230					235			240
Gly	Leu	Val	Arg	Ile	Gly	Ile	Val	Ile	Val	Ala	Thr	Leu	Gly	Thr	Ala
			245					250						255	
Ala	Val	Val	Ser	Ile	Ser	Gly	Leu	Ile	Gly	Phe	Val	Gly	Ile	Ile	Val
			260					265					270		
Pro	His	Ala	Leu	Arg	Leu	Ile	Val	Gly	Pro	Gly	His	Arg	Ile	Leu	Leu
		275					280					285			
Pro	Leu	Ser	Phe	Val	Trp	Gly	Ala	Ile	Phe	Leu	Val	Leu	Ala	Asp	Thr
		290					295					300			
Ala	Gly	Arg	Thr	Leu	Met	Ala	Pro	Gln	Glu	Leu	Pro	Val	Gly	Val	Val
		305					310					315			320
Thr	Ala	Ala	Leu	Gly	Ala	Pro	Phe	Phe	Leu	Phe	Ile	Leu	Arg	Arg	Thr
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Ser	Arg	Gln	Arg	Val	Pro	Lys	Arg	Ser	Ala						
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<211> 1095

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1072)

<223> FRXA01235

<400> 483

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ctgggtggct accgcgttgt cggtagtcatt tttggggttt  gtg  gtg  ctg  ttt  tca    115
                                         Val Val Leu Phe Ser
                                         1          5

ggt ttt agc ggt gtt att gat tta agc ccc aca gca gtg att aga cat    163
Gly Phe Ser Gly Val Ile Asp Leu Ser Pro Thr Ala Val Ile Arg His
                        10                      15                      20

ttg agt ggg cag gac acg ctc acc cct cga gat cag gcc atc ttc ttt    211
Leu Ser Gly Gln Asp Thr Leu Thr Pro Arg Asp Gln Ala Ile Phe Phe
                        25                      30                      35

gat atc cgg ctg cct cga att atc gct ggt gtc att gtc gga gca acg    259
Asp Ile Arg Leu Pro Arg Ile Ile Ala Gly Val Ile Val Gly Ala Thr
                        40                      45                      50

ctg gct att tct ggt gct gct tac caa gcg gta ttt aga aac ccg ctg    307
Leu Ala Ile Ser Gly Ala Ala Tyr Gln Ala Val Phe Arg Asn Pro Leu
                        55                      60                      65

gct gat cct tat ttg ttg ggt gtg tcc gca ggt tct ggc ctt ggt gtc    355
Ala Asp Pro Tyr Leu Leu Gly Val Ser Ala Gly Ser Gly Leu Gly Val
                        70                      75                      80                      85

acg gca gtg att gtt ggc ggt acc gtg ctg gga ttt tct gca ccg agc    403
Thr Ala Val Ile Val Gly Gly Thr Val Leu Gly Phe Ser Ala Pro Ser
                        90                      95                      100

atc ggc gtg att ggt gca gca ttt gta ggt ggt gtt gcc gca gta ctt    451
Ile Gly Val Ile Gly Ala Ala Phe Val Gly Gly Val Ala Ala Val Leu
                        105                      110                      115

gcc acg ctg atg gtg agt cgg gga gta gga cag gga tca tca acc acc    499
Ala Thr Leu Met Val Ser Arg Gly Val Gly Gln Gly Ser Ser Thr Thr
                        120                      125                      130

gtg gtt att ttg gcg ggc gtg gcg gtt gct gct ttt gcc agt tcc atc    547
Val Val Ile Leu Ala Gly Val Ala Val Ala Ala Phe Ala Ser Ser Ile
                        135                      140                      145

cag acc tat att cag caa cga cac atc gat acg gtg gcg cgc gta tat    595
Gln Thr Tyr Ile Gln Gln Arg His Ile Asp Thr Val Ala Arg Val Tyr
                        150                      155                      160                      165

gtg tgg atg ttg ggc aac ctc aat gtc acc aac tgg atg tcg atc ttc    643
Val Trp Met Leu Gly Asn Leu Asn Val Thr Asn Trp Met Ser Ile Phe
                        170                      175                      180

atc gtg gct gtg gtg gcg gga cta tgc gcg gcc gtg atc atg tcc tgc    691
Ile Val Ala Val Val Ala Gly Leu Cys Ala Ala Val Ile Met Ser Cys
                        185                      190                      195

gcc agg ttg tta gac gtg atg gct gtt ggt gat gtg gaa gcc cgc aca    739
Ala Arg Leu Leu Asp Val Met Ala Val Gly Asp Val Glu Ala Arg Thr
                        200                      205                      210

ttg ggc gtc gat cca ggc ctc gta cgc att ggc att gtc atc gtg gca    787
Leu Gly Val Asp Pro Gly Leu Val Arg Ile Gly Ile Val Ile Val Ala

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215	220	225	
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Thr Leu Gly Thr Ala Ala Val Val Ser Ile Ser Gly Leu Ile Gly Phe			
230	235	240	245
gtg ggc atc att gtt ccg cac gcc ctg cgc cta att gtt ggc ccg ggg			883
Val Gly Ile Ile Val Pro His Ala Leu Arg Leu Ile Val Gly Pro Gly			
250	255		260
cat cgg att tta ctg cca ctg tct ttc gta tgg ggt gcc att ttc ctc			931
His Arg Ile Leu Leu Pro Leu Ser Phe Val Trp Gly Ala Ile Phe Leu			
265	270		275
gtg ttg gca gat acc gca ggg cga aca ttg atg gct cct cag gaa ctt			979
Val Leu Ala Asp Thr Ala Gly Arg Thr Leu Met Ala Pro Gln Glu Leu			
280	285		290
ccc gtg ggt gtg gtg aca gct gca ctc ggc gca ccg ttc ttc tta ttt			1027
Pro Val Gly Val Val Thr Ala Ala Leu Gly Ala Pro Phe Phe Leu Phe			
295	300		305
att ttg cgc aga acc agc aga caa cga gtt cca aaa agg agt gct			1072
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<213> Corynebacterium glutamicum			
<400> 484			
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Gln Ala Ile Phe Phe Asp Ile Arg Leu Pro Arg Ile Ile Ala Gly Val			
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Ile Val Gly Ala Thr Leu Ala Ile Ser Gly Ala Ala Tyr Gln Ala Val			
50	55		60
Phe Arg Asn Pro Leu Ala Asp Pro Tyr Leu Leu Gly Val Ser Ala Gly			
65	70		75
Ser Gly Leu Gly Val Thr Ala Val Ile Val Gly Gly Thr Val Leu Gly			
85	90		95
Phe Ser Ala Pro Ser Ile Gly Val Ile Gly Ala Ala Phe Val Gly Gly			
100	105		110
Val Ala Ala Val Leu Ala Thr Leu Met Val Ser Arg Gly Val Gly Gln			
115	120		125
Gly Ser Ser Thr Thr Val Val Ile Leu Ala Gly Val Ala Val Ala Ala			
130	135		140

Phe Ala Ser Ser Ile Gln Thr Tyr Ile Gln Gln Arg His Ile Asp Thr
 145 150 155 160
 Val Ala Arg Val Tyr Val Trp Met Leu Gly Asn Leu Asn Val Thr Asn
 165 170 175
 Trp Met Ser Ile Phe Ile Val Ala Val Val Ala Gly Leu Cys Ala Ala
 180 185 190
 Val Ile Met Ser Cys Ala Arg Leu Leu Asp Val Met Ala Val Gly Asp
 195 200 205
 Val Glu Ala Arg Thr Leu Gly Val Asp Pro Gly Leu Val Arg Ile Gly
 210 215 220
 Ile Val Ile Val Ala Thr Leu Gly Thr Ala Ala Val Val Ser Ile Ser
 225 230 235 240
 Gly Leu Ile Gly Phe Val Gly Ile Ile Val Pro His Ala Leu Arg Leu
 245 250 255
 Ile Val Gly Pro Gly His Arg Ile Leu Leu Pro Leu Ser Phe Val Trp
 260 265 270
 Gly Ala Ile Phe Leu Val Leu Ala Asp Thr Ala Gly Arg Thr Leu Met
 275 280 285
 Ala Pro Gln Glu Leu Pro Val Gly Val Val Thr Ala Ala Leu Gly Ala
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 Pro Phe Phe Leu Phe Ile Leu Arg Arg Thr Ser Arg Gln Arg Val Pro
 305 310 315 320
 Lys Arg Ser Ala

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 <211> 1197
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1174)
 <223> RXN02794

<400> 485
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 Met Leu Leu Ser Ala
 1 5
 cgc aca cac acg agt ttc caa gaa ctt gga ctc aat gct agt cgg cgc 163
 Arg Thr His Thr Ser Phe Gln Glu Leu Gly Leu Asn Ala Ser Arg Arg
 10 15 20
 aaa gca atc aac tgg aca ctg gca ctc act gtg gtg cta att gcc tcc 211
 Lys Ala Ile Asn Trp Thr Leu Ala Leu Thr Val Val Leu Ile Ala Ser

25										30										35									
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Met	Phe	Val	Gly	Val	Leu	Ile	Gly	Ala	Ser	Gly	Thr	Ser	Val	Phe	Ser														
		40					45					50																	
acg	tgg	acc	gta	att	agc	cac	cat	ctt	ttt	ggc	act	gag	cta	ggg	ggc														
Thr	Trp	Thr	Val	Ile	Ser	His	His	Leu	Phe	Gly	Thr	Glu	Leu	Gly	Gly														
	55					60					65																		
tcc	gac	act	gcc	gac	gcc	atc	att	tgg	tac	atc	cgc	acc	cca	cgc	gtc														
Ser	Asp	Thr	Ala	Asp	Ala	Ile	Ile	Trp	Tyr	Ile	Arg	Thr	Pro	Arg	Val														
	70				75					80					85														
ttg	ctc	gct	gcc	att	gtg	ggc	gca	ggc	ctt	gcc	ctg	gca	ggg	gcc	atc														
Leu	Leu	Ala	Ala	Ile	Val	Gly	Ala	Gly	Leu	Ala	Leu	Ala	Gly	Ala	Ile														
				90				95						100															
atg	caa	gta	ctg	gtc	cga	aac	atg	ctg	gca	gac	ccc	tat	atc	ctc	ggg														
Met	Gln	Val	Leu	Val	Arg	Asn	Met	Leu	Ala	Asp	Pro	Tyr	Ile	Leu	Gly														
			105					110					115																
gtg	aac	tca	ggg	gcc	agt	tgc	ggg	gcg	gcc	gct	gcc	tta	ctg	ttc	gga														
Val	Asn	Ser	Gly	Ala	Ser	Cys	Gly	Ala	Ala	Ala	Ala	Leu	Leu	Phe	Gly														
		120					125					130																	
gtg	ggc	gct	gga	ttt	ggc	gat	tac	gcc	ctc	caa	ggc	agc	gcg	ttt	ctc														
Val	Gly	Ala	Gly	Phe	Gly	Asp	Tyr	Ala	Leu	Gln	Gly	Ser	Ala	Phe	Leu														
	135					140					145																		
ggc	gca	atg	gca	gct	tcc	gga	ttg	atc	ttc	ttc	gtg	gcg	cgc	gca	gcg														
Gly	Ala	Met	Ala	Ala	Ser	Gly	Leu	Ile	Phe	Phe	Val	Ala	Arg	Ala	Ala														
	150				155				160					165															
ggg	cgc	atc	tcc	tcg	acc	cgc	ttg	ttg	atg	tcc	ggc	gta	gcg	atc	gga														
Gly	Arg	Ile	Ser	Ser	Thr	Arg	Leu	Leu	Met	Ser	Gly	Val	Ala	Ile	Gly														
				170					175					180															
tac	atg	ctc	tct	gcg	gca	aca	agc	ttt	ctc	atc	ttc	tcc	tcc	gac	tcc														
Tyr	Met	Leu	Ser	Ala	Ala	Thr	Ser	Phe	Leu	Ile	Phe	Ser	Ser	Asp	Ser														
			185					190						195															
gcc	gaa	ggc	agc	cgc	tcc	gtg	ttg	ttc	tgg	ctg	ctt	gga	tcc	tta	gga														
Ala	Glu	Gly	Ser	Arg	Ser	Val	Leu	Phe	Trp	Leu	Leu	Gly	Ser	Leu	Gly														
		200					205					210																	
ctt	gcc	gca	tgg	aat	ggg	cgc	atg	gcg	atc	atc	ttc	ctc	atc	gtg	ggc														
Leu	Ala	Ala	Trp	Asn	Gly	Pro	Met	Ala	Ile	Ile	Phe	Leu	Ile	Val	Gly														
	215				220						225																		
att	gcc	ctg	gcg	ttg	ctc	atg	gtg	ttg	ggg	cgc	caa	ttg	gat	gcc	tta														
Ile	Ala	Leu	Ala	Leu	Leu	Met	Val	Leu	Gly	Pro	Gln	Leu	Asp	Ala	Leu														
	230				235				240					245															
aac	tcc	ggc	gat	gaa	acc	gca	ctt	acc	ttg	gga	gta	tcc	cct	gat	cgc														
Asn	Ser	Gly	Asp	Glu	Thr	Ala	Leu	Thr	Leu	Gly	Val	Ser	Pro	Asp	Arg														
				250				255						260															
ctc	cgc	att	ctc	ctc	ctg	gtg	atc	acc	tgc	ctg	ctg	gtg	gga	tcc	atg														
Leu	Arg	Ile	Leu	Leu	Leu	Val	Ile	Thr	Cys	Leu	Leu	Val	Gly	Ser	Met														
			265				270						275																

gtt gcc atg gcc ggc agc atc gga ttc atc ggc ctt gtc atc ccc cac 979
 Val Ala Met Ala Gly Ser Ile Gly Phe Ile Gly Leu Val Ile Pro His
 280 285 290

ctg gcc agg cgt ttt gtt agt gga aaa cac cga ctc atg ctg cct gta 1027
 Leu Ala Arg Arg Phe Val Ser Gly Lys His Arg Leu Met Leu Pro Val
 295 300 305

tcc gcg ttg atg ggc gca att ttg ctc atc tgg gct gat atc gcc gcc 1075
 Ser Ala Leu Met Gly Ala Ile Leu Leu Ile Trp Ala Asp Ile Ala Ala
 310 315 320 325

cgc acc ctg ctt gcg ccc caa gag att ccc atc ggc atc atc acc gca 1123
 Arg Thr Leu Leu Ala Pro Gln Glu Ile Pro Ile Gly Ile Ile Thr Ala
 330 335 340

ctc atc gga gca ccc ttc ctc ctg att ctg gtt cgc cgg atg cac acc 1171
 Leu Ile Gly Ala Pro Phe Leu Leu Ile Leu Val Arg Arg Met His Thr
 345 350 355

tac tgatttttaa ggaattatgc gta 1197
 Tyr

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 <211> 358
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 486
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Val Leu Ile Ala Ser Met Phe Val Gly Val Leu Ile Gly Ala Ser Gly
 35 40 45

Thr Ser Val Phe Ser Thr Trp Thr Val Ile Ser His His Leu Phe Gly
 50 55 60

Thr Glu Leu Gly Gly Ser Asp Thr Ala Asp Ala Ile Ile Trp Tyr Ile
 65 70 75 80

Arg Thr Pro Arg Val Leu Leu Ala Ala Ile Val Gly Ala Gly Leu Ala
 85 90 95

Leu Ala Gly Ala Ile Met Gln Val Leu Val Arg Asn Met Leu Ala Asp
 100 105 110

Pro Tyr Ile Leu Gly Val Asn Ser Gly Ala Ser Cys Gly Ala Ala Ala
 115 120 125

Ala Leu Leu Phe Gly Val Gly Ala Gly Phe Gly Asp Tyr Ala Leu Gln
 130 135 140

Gly Ser Ala Phe Leu Gly Ala Met Ala Ala Ser Gly Leu Ile Phe Phe
 145 150 155 160

Val Ala Arg Ala Ala Gly Arg Ile Ser Ser Thr Arg Leu Leu Met Ser
 165 170 175
 Gly Val Ala Ile Gly Tyr Met Leu Ser Ala Ala Thr Ser Phe Leu Ile
 180 185 190
 Phe Ser Ser Asp Ser Ala Glu Gly Ser Arg Ser Val Leu Phe Trp Leu
 195 200 205
 Leu Gly Ser Leu Gly Leu Ala Ala Trp Asn Gly Pro Met Ala Ile Ile
 210 215 220
 Phe Leu Ile Val Gly Ile Ala Leu Ala Leu Leu Met Val Leu Gly Pro
 225 230 235 240
 Gln Leu Asp Ala Leu Asn Ser Gly Asp Glu Thr Ala Leu Thr Leu Gly
 245 250 255
 Val Ser Pro Asp Arg Leu Arg Ile Leu Leu Leu Val Ile Thr Cys Leu
 260 265 270
 Leu Val Gly Ser Met Val Ala Met Ala Gly Ser Ile Gly Phe Ile Gly
 275 280 285
 Leu Val Ile Pro His Leu Ala Arg Arg Phe Val Ser Gly Lys His Arg
 290 295 300
 Leu Met Leu Pro Val Ser Ala Leu Met Gly Ala Ile Leu Leu Ile Trp
 305 310 315 320
 Ala Asp Ile Ala Ala Arg Thr Leu Leu Ala Pro Gln Glu Ile Pro Ile
 325 330 335
 Gly Ile Ile Thr Ala Leu Ile Gly Ala Pro Phe Leu Leu Ile Leu Val
 340 345 350
 Arg Arg Met His Thr Tyr
 355

<210> 487
 <211> 364
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(364)
 <223> FRXA01419

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 gctaatagtc aaatgatcat ttgagtgtta gtgttttctc atg ctt ctt tcc gcc 115
 Met Leu Leu Ser Ala
 1 5

cgc aca cac acg agt ttc caa gaa ctt gga ctc aat gct agt cgg cgc 163
 Arg Thr His Thr Ser Phe Gln Glu Leu Gly Leu Asn Ala Ser Arg Arg
 10 15 20


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aaa gca atc aac tgg aca ctg gca ctc act gtg gtg cta att gcc tcc 211
Lys Ala Ile Asn Trp Thr Leu Ala Leu Thr Val Val Leu Ile Ala Ser
      25                      30                      35

atg ttt gtt ggc gtg ctc atc ggt gca tcc ggg acc tca gtg ttt tcc 259
Met Phe Val Gly Val Leu Ile Gly Ala Ser Gly Thr Ser Val Phe Ser
      40                      45                      50

acg tgg acc gta att agc cac cat ctt ttt ggc act gag cta ggt ggc 307
Thr Trp Thr Val Ile Ser His His Leu Phe Gly Thr Glu Leu Gly Gly
      55                      60                      65

tcc gac act gcc gac gcc atc att tgg tac atc cgc acc cca cgc gtc 355
Ser Asp Thr Ala Asp Ala Ile Ile Trp Tyr Ile Arg Thr Pro Arg Val
      70                      75                      80                      85

ttg ctc gct 364
Leu Leu Ala

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<210> 488
<211> 88
<212> PRT
<213> Corynebacterium glutamicum

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<400> 488
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Asn Ala Ser Arg Arg Lys Ala Ile Asn Trp Thr Leu Ala Leu Thr Val
      20                      25                      30

Val Leu Ile Ala Ser Met Phe Val Gly Val Leu Ile Gly Ala Ser Gly
      35                      40                      45

Thr Ser Val Phe Ser Thr Trp Thr Val Ile Ser His His Leu Phe Gly
      50                      55                      60

Thr Glu Leu Gly Gly Ser Asp Thr Ala Asp Ala Ile Ile Trp Tyr Ile
      65                      70                      75                      80

Arg Thr Pro Arg Val Leu Leu Ala
      85

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<210> 489
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

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<220>
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<223> FRXA02794

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ttggcgatta cgccctccaa gcagcgcgtt tctcggcgca atg gca gct tcc gga 115

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															Met	Ala	Ala	Ser	Gly	
															1				5	
ttg atc ttc ttc gtg gcg cgc gca gcg ggg cgc atc tcc tcg acc cgc	163																			
Leu Ile Phe Phe Val Ala Arg Ala Ala Gly Arg Ile Ser Ser Thr Arg																				
				10				15					20							
ttg ttg atg tcc ggc gta gcg atc gga tac atg ctc tct gcg gca aca	211																			
Leu Leu Met Ser Gly Val Ala Ile Gly Tyr Met Leu Ser Ala Ala Thr																				
			25					30					35							
agc ttt ctc atc ttc tcc tcc gac tcc gcc gaa ggc agc cgc tcc gtg	259																			
Ser Phe Leu Ile Phe Ser Ser Asp Ser Ala Glu Gly Ser Arg Ser Val																				
			40				45					50								
ttg ttc tgg ctg ctt gga tcc tta gga ctt gcc gca tgg aat ggg ccg	307																			
Leu Phe Trp Leu Leu Gly Ser Leu Gly Leu Ala Ala Trp Asn Gly Pro																				
			55				60					65								
atg gcg atc atc ttc ctc atc gtg ggc att gcc ctg gcg ttg ctc atg	355																			
Met Ala Ile Ile Phe Leu Ile Val Gly Ile Ala Leu Ala Leu Leu Met																				
			70			75			80					85						
gtg ttg ggt ccg caa ttg gat gcc tta aac tcc ggc gat gaa acc gca	403																			
Val Leu Gly Pro Gln Leu Asp Ala Leu Asn Ser Gly Asp Glu Thr Ala																				
				90					95					100						
ctt acc ttg gga gta tcc cct gat cgc ctc cgc att ctc ctc ctg gtg	451																			
Leu Thr Leu Gly Val Ser Pro Asp Arg Leu Arg Ile Leu Leu Leu Val																				
			105					110					115							
atc acc tgc ctg ctg gtg gga tcc atg gtt gcc atg gcc ggc agc atc	499																			
Ile Thr Cys Leu Leu Val Gly Ser Met Val Ala Met Ala Gly Ser Ile																				
			120				125					130								
gga ttc atc ggc ctt gtc atc ccc cac ctg gcc agg cgt ttt gtt agt	547																			
Gly Phe Ile Gly Leu Val Ile Pro His Leu Ala Arg Arg Phe Val Ser																				
			135				140					145								
gga aaa cac cga ctc atg ctg cct gta tcc gcg ttg atg ggc gca att	595																			
Gly Lys His Arg Leu Met Leu Pro Val Ser Ala Leu Met Gly Ala Ile																				
			150			155			160				165							
ttg ctc atc tgg gct gat atc gcc gcc cgc acc ctg ctt gcg ccc caa	643																			
Leu Leu Ile Trp Ala Asp Ile Ala Ala Arg Thr Leu Leu Ala Pro Gln																				
				170				175					180							
gag att ccc atc ggc atc atc acc gca ctc atc gga gca ccc ttc ctc	691																			
Glu Ile Pro Ile Gly Ile Ile Thr Ala Leu Ile Gly Ala Pro Phe Leu																				
			185				190					195								
ctg att ctg gtt cgc cgg atg cac acc tac tgatttttaa ggaattatgc	741																			
Leu Ile Leu Val Arg Arg Met His Thr Tyr																				
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gta	744																			

<210> 490

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 490

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Met Ala Ala Ser Gly Leu Ile Phe Phe Val Ala Arg Ala Ala Gly Arg
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Ile Ser Ser Thr Arg Leu Leu Met Ser Gly Val Ala Ile Gly Tyr Met
          20           25           30
Leu Ser Ala Ala Thr Ser Phe Leu Ile Phe Ser Ser Asp Ser Ala Glu
          35           40           45
Gly Ser Arg Ser Val Leu Phe Trp Leu Leu Gly Ser Leu Gly Leu Ala
          50           55           60
Ala Trp Asn Gly Pro Met Ala Ile Ile Phe Leu Ile Val Gly Ile Ala
          65           70           75           80
Leu Ala Leu Leu Met Val Leu Gly Pro Gln Leu Asp Ala Leu Asn Ser
          85           90           95
Gly Asp Glu Thr Ala Leu Thr Leu Gly Val Ser Pro Asp Arg Leu Arg
          100          105          110
Ile Leu Leu Leu Val Ile Thr Cys Leu Leu Val Gly Ser Met Val Ala
          115          120          125
Met Ala Gly Ser Ile Gly Phe Ile Gly Leu Val Ile Pro His Leu Ala
          130          135          140
Arg Arg Phe Val Ser Gly Lys His Arg Leu Met Leu Pro Val Ser Ala
          145          150          155          160
Leu Met Gly Ala Ile Leu Leu Ile Trp Ala Asp Ile Ala Ala Arg Thr
          165          170          175
Leu Leu Ala Pro Gln Glu Ile Pro Ile Gly Ile Ile Thr Ala Leu Ile
          180          185          190
Gly Ala Pro Phe Leu Leu Ile Leu Val Arg Arg Met His Thr Tyr
          195          200          205

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<210> 491

<211> 1140

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1117)

<223> RXN03079

<400> 491

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ttgggtaaac aagtcataac aattttcatt aagggtcgtt ttg tcg cgc aca ggt 115
                                     Leu Ser Arg Thr Gly
                                     1           5
gtt tcg aaa aaa cca aag ctc acc gct cct gtt gtc atc atc ggc acc 163

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Val	Ser	Lys	Lys	Pro	Lys	Leu	Thr	Ala	Pro	Val	Val	Ile	Ile	Gly	Thr		
				10					15					20			
ctc	gtc	ttg	ttg	atc	atc	gcc	ttc	acc	gct	tcc	ctc	atg	ctg	ggt	ccc	211	
Leu	Val	Leu	Leu	Ile	Ile	Ala	Phe	Thr	Ala	Ser	Leu	Met	Leu	Gly	Pro		
			25					30					35				
gtg	acg	gtt	cca	ttg	aat	gag	ctt	gca	acc	aac	ccc	gtt	gtc	acc	gat	259	
Val	Thr	Val	Pro	Leu	Asn	Glu	Leu	Ala	Thr	Asn	Pro	Val	Val	Thr	Asp		
		40					45					50					
atc	cgt	gca	cca	cgc	att	atc	atc	gca	gca	ttg	gtg	ggt	gcg	gcg	ctg	307	
Ile	Arg	Ala	Pro	Arg	Ile	Ile	Ile	Ala	Ala	Leu	Val	Gly	Ala	Ala	Leu		
	55					60					65						
gct	gtc	tcc	ggt	gcg	atc	atg	cag	acg	gtg	ttt	cac	aac	ccg	ttg	gcg	355	
Ala	Val	Ser	Gly	Ala	Ile	Met	Gln	Thr	Val	Phe	His	Asn	Pro	Leu	Ala		
	70				75					80					85		
gat	ccc	ggc	att	gtg	ggt	gtg	tcc	tcc	ggt	gca	gct	gtt	gca	gct	gtc	403	
Asp	Pro	Gly	Ile	Val	Gly	Val	Ser	Ser	Gly	Ala	Ala	Val	Ala	Ala	Val		
				90					95						100		
ttg	gcg	att	gtc	acc	ggt	gcg	agt	ttc	ttt	ggc	caa	tgg	acc	gtt	cct	451	
Leu	Ala	Ile	Val	Thr	Gly	Ala	Ser	Phe	Phe	Gly	Gln	Trp	Thr	Val	Pro		
			105					110					115				
ttt	gcg	gcc	ttc	gtg	ggc	gca	ttg	gtc	acg	gtg	gct	gtg	gta	tat	ttg	499	
Phe	Ala	Ala	Phe	Val	Gly	Ala	Leu	Val	Thr	Val	Ala	Val	Val	Tyr	Leu		
		120					125					130					
atc	gct	agt	tcc	cgc	gcg	atg	gat	ggc	cgt	ggc	gca	gat	ccg	gcc	acg	547	
Ile	Ala	Ser	Ser	Arg	Ala	Met	Asp	Gly	Arg	Gly	Ala	Asp	Pro	Ala	Thr		
	135					140					145						
ttg	gta	ctg	gtc	ggc	atg	gct	atc	act	gcc	ttt	ttg	ggt	gct	gtt	att	595	
Leu	Val	Leu	Val	Gly	Met	Ala	Ile	Thr	Ala	Phe	Leu	Gly	Ala	Val	Ile		
	150				155					160					165		
tcc	agc	gcc	act	gcg	aac	gca	cca	caa	gat	tct	gag	ctt	cga	tcc	gtg	643	
Ser	Ser	Ala	Thr	Ala	Asn	Ala	Pro	Gln	Asp	Ser	Glu	Leu	Arg	Ser	Val		
				170					175					180			
acg	ttt	tgg	ctc	aac	ggc	gat	ctg	gta	tct	cgg	acg	tgg	gaa	cat	gtg	691	
Thr	Phe	Trp	Leu	Asn	Gly	Asp	Leu	Val	Ser	Arg	Thr	Trp	Glu	His	Val		
			185					190					195				
ggc	gtt	gca	ata	atc	ccc	att	atc	gtt	ggg	ttg	att	cta	gct	atc	ggc	739	
Gly	Val	Ala	Ile	Ile	Pro	Ile	Ile	Val	Gly	Leu	Ile	Leu	Ala	Ile	Gly		
		200					205					210					
ggt	tcc	cgc	gat	ctg	aac	ttg	ttg	ctg	ctg	ggt	gat	tcc	aca	gcg	caa	787	
Gly	Ser	Arg	Asp	Leu	Asn	Leu	Leu	Leu	Leu	Gly	Asp	Ser	Thr	Ala	Gln		
		215				220					225						
aca	tct	gga	ctc	aac	gtc	aac	cgc	gca	cgc	atc	att	ttg	cta	gca	ctt	835	
Thr	Ser	Gly	Leu	Asn	Val	Asn	Arg	Ala	Arg	Ile	Ile	Leu	Leu	Ala	Leu		
	230				235					240					245		
gcg	gca	ctg	ctc	acc	gcc	aca	gct	gtt	gcg	gtc	tcc	ggc	acc	att	acg	883	
Ala	Ala	Leu	Leu	Thr	Ala	Thr	Ala	Val	Ala	Val	Ser	Gly	Thr	Ile	Thr		

250	255	260	
ttt gtt. gga ttg gta gta ccc cac ctg gtg cgc att gtt tta ggt gcc			931
Phe Val Gly Leu Val Val Pro His Leu Val Arg Ile Val Leu Gly Ala			
265	270	275	
gat cac cga gcg tta ctc ccg gcc gcc gcg att ttg ggc gcc acg ttt			979
Asp His Arg Ala Leu Leu Pro Ala Ala Ala Ile Leu Gly Ala Thr Phe			
280	285	290	
gtt atc gtt tcc gac act gtt gcc cgc atg atc ttc tcc ccc atc gtc			1027
Val Ile Val Ser Asp Thr Val Ala Arg Met Ile Phe Ser Pro Ile Val			
295	300	305	
ttg caa aca ggc gtg gtg gtg gcg ttc att ggc tca cca att ttc ctt			1075
Leu Gln Thr Gly Val Val Val Ala Phe Ile Gly Ser Pro Ile Phe Leu			
310	315	320	325
tat tta ctg ctc agc atg cgc aag cga cgc gga ttg ggg ctg			1117
Tyr Leu Leu Leu Ser Met Arg Lys Arg Arg Gly Leu Gly Leu			
330	335		
taaaaaactca tgcctcaatt agt			1140
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<211> 339			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 492			
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Leu Met Leu Gly Pro Val Thr Val Pro Leu Asn Glu Leu Ala Thr Asn			
35	40	45	
Pro Val Val Thr Asp Ile Arg Ala Pro Arg Ile Ile Ile Ala Ala Leu			
50	55	60	
Val Gly Ala Ala Leu Ala Val Ser Gly Ala Ile Met Gln Thr Val Phe			
65	70	75	80
His Asn Pro Leu Ala Asp Pro Gly Ile Val Gly Val Ser Ser Gly Ala			
85	90	95	
Ala Val Ala Ala Val Leu Ala Ile Val Thr Gly Ala Ser Phe Phe Gly			
100	105	110	
Gln Trp Thr Val Pro Phe Ala Ala Phe Val Gly Ala Leu Val Thr Val			
115	120	125	
Ala Val Val Tyr Leu Ile Ala Ser Ser Arg Ala Met Asp Gly Arg Gly			
130	135	140	
Ala Asp Pro Ala Thr Leu Val Leu Val Gly Met Ala Ile Thr Ala Phe			
145	150	155	160

Leu Gly Ala Val Ile Ser Ser Ala Thr Ala Asn Ala Pro Gln Asp Ser
 165 170 175
 Glu Leu Arg Ser Val Thr Phe Trp Leu Asn Gly Asp Leu Val Ser Arg
 180 185 190
 Thr Trp Glu His Val Gly Val Ala Ile Ile Pro Ile Ile Val Gly Leu
 195 200 205
 Ile Leu Ala Ile Gly Gly Ser Arg Asp Leu Asn Leu Leu Leu Gly
 210 215 220
 Asp Ser Thr Ala Gln Thr Ser Gly Leu Asn Val Asn Arg Ala Arg Ile
 225 230 235 240
 Ile Leu Leu Ala Leu Ala Ala Leu Leu Thr Ala Thr Ala Val Ala Val
 245 250 255
 Ser Gly Thr Ile Thr Phe Val Gly Leu Val Val Pro His Leu Val Arg
 260 265 270
 Ile Val Leu Gly Ala Asp His Arg Ala Leu Leu Pro Ala Ala Ala Ile
 275 280 285
 Leu Gly Ala Thr Phe Val Ile Val Ser Asp Thr Val Ala Arg Met Ile
 290 295 300
 Phe Ser Pro Ile Val Leu Gln Thr Gly Val Val Val Ala Phe Ile Gly
 305 310 315 320
 Ser Pro Ile Phe Leu Tyr Leu Leu Leu Ser Met Arg Lys Arg Arg Gly
 325 330 335
 Leu Gly Leu

<210> 493
 <211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1117)
 <223> FRXA02865

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 Leu Ser Arg Thr Gly
 1 5
 gtt tcg aaa aaa cca aag ctc acc gct cct gtt gtc atc atc ggc acc 163
 Val Ser Lys Lys Pro Lys Leu Thr Ala Pro Val Val Ile Ile Gly Thr
 10 15 20
 ctc gtc ttg ttg atc atc gcc ttc acc gct tcc ctc atg ctg ggt ccc 211
 Leu Val Leu Leu Ile Ile Ala Phe Thr Ala Ser Leu Met Leu Gly Pro
 25 30 35

gtg acg gtt cca ttg aat gag ctt gca acc aac ccc gtt gtc acc gat	259
Val Thr Val Pro Leu Asn Glu Leu Ala Thr Asn Pro Val Val Thr Asp	
40 45 50	
atc cgt gca cca cgc att atc atc gca gca ttg gtg ggt gcg gcg ctg	307
Ile Arg Ala Pro Arg Ile Ile Ile Ala Ala Leu Val Gly Ala Ala Leu	
55 60 65	
gct gtc tcc ggt gcg atc atg cag acg gtg ttt cac aac ccg ttg gcg	355
Ala Val Ser Gly Ala Ile Met Gln Thr Val Phe His Asn Pro Leu Ala	
70 75 80 85	
gat ccc ggc att gtg ggt gtg tcc tcc ggt gca gct gtt gca gct gtc	403
Asp Pro Gly Ile Val Gly Val Ser Ser Gly Ala Ala Val Ala Ala Val	
90 95 100	
ttg gcg att gtc acc ggt gcg agt ttc ttt ggc caa tgg acc gtt cct	451
Leu Ala Ile Val Thr Gly Ala Ser Phe Phe Gly Gln Trp Thr Val Pro	
105 110 115	
ttt gcg gcc ttc gtg ggc gca ttg gtc acg gtg gct gtg gta tat ttg	499
Phe Ala Ala Phe Val Gly Ala Leu Val Thr Val Ala Val Val Tyr Leu	
120 125 130	
atc gct agt tcc cgc gcg atg gat ggc cgt ggc gca gat ccg gcc acg	547
Ile Ala Ser Ser Arg Ala Met Asp Gly Arg Gly Ala Asp Pro Ala Thr	
135 140 145	
ttg gta ctg gtc ggc atg gct atc act gcc ttt ttg ggt gct gtt att	595
Leu Val Leu Val Gly Met Ala Ile Thr Ala Phe Leu Gly Ala Val Ile	
150 155 160 165	
tcc agc gcc act gcg aac gca cca caa gat tct gag ctt cga tcc gtg	643
Ser Ser Ala Thr Ala Asn Ala Pro Gln Asp Ser Glu Leu Arg Ser Val	
170 175 180	
acg ttt tgg ctc aac ggc gat ctg gta tct cgg acg tgg gaa cat gtg	691
Thr Phe Trp Leu Asn Gly Asp Leu Val Ser Arg Thr Trp Glu His Val	
185 190 195	
ggc gtt gca ata atc ccc att atc gtt ggg ttg att cta gct atc ggc	739
Gly Val Ala Ile Ile Pro Ile Ile Val Gly Leu Ile Leu Ala Ile Gly	
200 205 210	
ggc tcc cgc gat ctg aac ttg ttg ctg ctg ggt gat tcc aca gcg caa	787
Gly Ser Arg Asp Leu Asn Leu Leu Leu Leu Gly Asp Ser Thr Ala Gln	
215 220 225	
aca tct gga ctc aac gtc aac cgc gca cgc atc att ttg cta gca ctt	835
Thr Ser Gly Leu Asn Val Asn Arg Ala Arg Ile Ile Leu Leu Ala Leu	
230 235 240 245	
gcg gca ctg ctc acc gcc aca gct gtt gcg gtc tcc ggc acc att acg	883
Ala Ala Leu Leu Thr Ala Thr Ala Val Ala Val Ser Gly Thr Ile Thr	
250 255 260	
ttt gtt gga ttg gta gta ccc cac ctg gtg cgc att gtt tta ggt gcc	931
Phe Val Gly Leu Val Val Pro His Leu Val Arg Ile Val Leu Gly Ala	
265 270 275	

gat cac cga gcg tta ctc ccg gcc gcc gcg att ttg ggc gcc acg ttt 979
Asp His Arg Ala Leu Leu Pro Ala Ala Ala Ile Leu Gly Ala Thr Phe
280 285 290

gtt atc gtt tcc gac act gtt gcc cgc atg atc ttc tcc ccc atc gtc 1027
Val Ile Val Ser Asp Thr Val Ala Arg Met Ile Phe Ser Pro Ile Val
295 300 305

ttg caa aca ggc gtg gtg gtg gcg ttc att ggc tca cca att ttc ctt 1075
Leu Gln Thr Gly Val Val Val Ala Phe Ile Gly Ser Pro Ile Phe Leu
310 315 320 325

tat tta ctg ctc agc atg cgc aag cga cgc gga ttg ggg ctg 1117
Tyr Leu Leu Leu Ser Met Arg Lys Arg Arg Gly Leu Gly Leu
330 335

taaaaactca tgcctcaatt agt 1140

<210> 494
<211> 339
<212> PRT
<213> Corynebacterium glutamicum

<400> 494
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35 40 45
Pro Val Val Thr Asp Ile Arg Ala Pro Arg Ile Ile Ile Ala Ala Leu
50 55 60
Val Gly Ala Ala Leu Ala Val Ser Gly Ala Ile Met Gln Thr Val Phe
65 70 75 80
His Asn Pro Leu Ala Asp Pro Gly Ile Val Gly Val Ser Ser Gly Ala
85 90 95
Ala Val Ala Ala Val Leu Ala Ile Val Thr Gly Ala Ser Phe Phe Gly
100 105 110
Gln Trp Thr Val Pro Phe Ala Ala Phe Val Gly Ala Leu Val Thr Val
115 120 125
Ala Val Val Tyr Leu Ile Ala Ser Ser Arg Ala Met Asp Gly Arg Gly
130 135 140
Ala Asp Pro Ala Thr Leu Val Leu Val Gly Met Ala Ile Thr Ala Phe
145 150 155 160
Leu Gly Ala Val Ile Ser Ser Ala Thr Ala Asn Ala Pro Gln Asp Ser
165 170 175
Glu Leu Arg Ser Val Thr Phe Trp Leu Asn Gly Asp Leu Val Ser Arg
180 185 190

Thr Trp Glu His Val Gly Val Ala Ile Ile Pro Ile Ile Val Gly Leu
 195 200 205
 Ile Leu Ala Ile Gly Gly Ser Arg Asp Leu Asn Leu Leu Leu Leu Gly
 210 215 220
 Asp Ser Thr Ala Gln Thr Ser Gly Leu Asn Val Asn Arg Ala Arg Ile
 225 230 235 240
 Ile Leu Leu Ala Leu Ala Ala Leu Leu Thr Ala Thr Ala Val Ala Val
 245 250 255
 Ser Gly Thr Ile Thr Phe Val Gly Leu Val Val Pro His Leu Val Arg
 260 265 270
 Ile Val Leu Gly Ala Asp His Arg Ala Leu Leu Pro Ala Ala Ala Ile
 275 280 285
 Leu Gly Ala Thr Phe Val Ile Val Ser Asp Thr Val Ala Arg Met Ile
 290 295 300
 Phe Ser Pro Ile Val Leu Gln Thr Gly Val Val Val Ala Phe Ile Gly
 305 310 315 320
 Ser Pro Ile Phe Leu Tyr Leu Leu Leu Ser Met Arg Lys Arg Arg Gly
 325 330 335
 Leu Gly Leu

<210> 495
 <211> 1695
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1672)
 <223> RXA00181

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 Met Ser Asp Asn Thr
 1 5
 tgg ttc atc ata gcc atc gtt atc tat atg ttg gtg atg gtg ctc atc 163
 Trp Phe Ile Ile Ala Ile Val Ile Tyr Met Leu Val Met Val Leu Ile
 10 15 20
 ggc tat tgg agt tac cgc aag aca gaa aaa tac gac gac tac atg ctc 211
 Gly Tyr Trp Ser Tyr Arg Lys Thr Glu Lys Tyr Asp Asp Tyr Met Leu
 25 30 35
 gcc ggc cgc ggg ctc aac cct ttt gtt gcc gca atg tcc gca ggt gcc 259
 Ala Gly Arg Gly Leu Asn Pro Phe Val Ala Ala Met Ser Ala Gly Ala
 40 45 50
 tca gat atg tca ggt tgg ctg ctc atg ggt ctg ccc ggc gcg ctg ttt 307

Ser	Asp	Met	Ser	Gly	Trp	Leu	Leu	Met	Gly	Leu	Pro	Gly	Ala	Leu	Phe	
55						60					65					
gtc	acc	ggc	atg	tcc	gag	ttg	tgg	atc	gca	gtc	gga	ctc	acc	att	ggc	355
Val	Thr	Gly	Met	Ser	Glu	Leu	Trp	Ile	Ala	Val	Gly	Leu	Thr	Ile	Gly	
70					75					80					85	
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Ala	Trp	Ala	Asn	Trp	Met	Trp	Val	Ala	Pro	Arg	Leu	Arg	Ser	Tyr	Ser	
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gaa	atc	tcg	gcc	aac	tca	atc	acc	ctg	cct	tca	ttc	ttt	gag	aac	cga	451
Glu	Ile	Ser	Ala	Asn	Ser	Ile	Thr	Leu	Pro	Ser	Phe	Phe	Glu	Asn	Arg	
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ctt	cgc	gat	aaa	tct	cgc	gcg	ctt	cgc	atc	att	gca	gca	cta	att	atc	499
Leu	Arg	Asp	Lys	Ser	Arg	Ala	Leu	Arg	Ile	Ile	Ala	Ala	Leu	Ile	Ile	
		120					125					130				
att	gtg	ttc	ttc	acc	ttc	tac	att	tct	tca	ggc	atg	gtt	gct	ggc	gga	547
Ile	Val	Phe	Phe	Thr	Phe	Tyr	Ile	Ser	Ser	Gly	Met	Val	Ala	Gly	Gly	
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gtg	tat	tgg	gag	tcc	acg	ttt	ggc	gga	gat	tat	cta	ctc	ggc	atg	gcc	595
Val	Tyr	Trp	Glu	Ser	Thr	Phe	Gly	Gly	Asp	Tyr	Leu	Leu	Gly	Met	Ala	
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Ile	Val	Ala	Gly	Val	Thr	Val	Leu	Tyr	Thr	Phe	Ile	Gly	Gly	Phe	Leu	
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Ala	Val	Ser	Tyr	Thr	Asp	Ala	Val	Gln	Gly	Thr	Ile	Met	Phe	Phe	Ser	
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Asp	Ile	Trp	Ser	Phe	Ala	Asn	Ser	Asn	Asp	Tyr	Gly	Pro	His	Thr	Asp	
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Ala	Ala	Ile	Ile	Gly	Asn	Leu	Gly	Trp	Gly	Leu	Gly	Tyr	Phe	Gly	Gln	
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cca	cac	att	gtg	gtt	cgt	ttc	atg	gca	ctt	cgc	aca	cca	gct	gaa	gca	931
Pro	His	Ile	Val	Val	Arg	Phe	Met	Ala	Leu	Arg	Thr	Pro	Ala	Glu	Ala	
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aag	caa	ggc	cgt	cgc	atc	ggc	att	tcc	tgg	atg	ata	atc	tgk	ctg	att	979
Lys	Gln	Gly	Arg	Arg	Ile	Gly	Ile	Ser	Trp	Met	Ile	Ile	Cys	Leu	Ile	
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Gly	Ala	Thr	Phe	Thr	Ala	Ile	Ile	Ser	Thr	Val	Phe	Phe	Ala	Gln	Asn	

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act gct gtt ctc gcg gcc atc atg tct acc atg tcg tca cag ctg ctg Thr Ala Val Leu Ala Ala Ile Met Ser Thr Met Ser Ser Gln Leu Leu 345 350 355			1171
gtc acc gca tct tcc ctg att gag gac ctg ctg aag gta gtt aaa aag Val Thr Ala Ser Ser Leu Ile Glu Asp Leu Leu Lys Val Val Lys Lys 360 365 370			1219
gac tcg ctg agc gaa cgc acc ctg atc atg ctg tct cgt gcc aca gtc Asp Ser Leu Ser Glu Arg Thr Leu Ile Met Leu Ser Arg Ala Thr Val 375 380 385			1267
atc att ctg gcg atc att gca gca gcc atg gct att aac ccg tct gat Ile Ile Leu Ala Ile Ile Ala Ala Ala Met Ala Ile Asn Pro Ser Asp 390 395 400 405			1315
tcc atc ctc gga ttg gtg gga ttt gcg tgg gca gga ttc ggc tct gca Ser Ile Leu Gly Leu Val Gly Phe Ala Trp Ala Gly Phe Gly Ser Ala 410 415 420			1363
ttt ggt ccg atc ata ctt gct agc ctt tat tgg aag cgt ctc aac gcc Phe Gly Pro Ile Ile Leu Ala Ser Leu Tyr Trp Lys Arg Leu Asn Ala 425 430 435			1411
gcc ggc gct atc tcc ggc atg att act ggt gct att gtc tcc atc gcg Ala Gly Ala Ile Ser Gly Met Ile Thr Gly Ala Ile Val Ser Ile Ala 440 445 450			1459
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gaa ccc tcc gaa gaa atc ctc aac gag ttt gaa acc gcc aag gat ctt Glu Pro Ser Glu Glu Ile Leu Asn Glu Phe Glu Thr Ala Lys Asp Leu 490 495 500			1603
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Asp Asp Tyr Met Leu Ala Gly Arg Gly Leu Asn Pro Phe Val Ala Ala
      35           40           45

Met Ser Ala Gly Ala Ser Asp Met Ser Gly Trp Leu Leu Met Gly Leu
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Pro Gly Ala Leu Phe Val Thr Gly Met Ser Glu Leu Trp Ile Ala Val
      65           70           75           80

Gly Leu Thr Ile Gly Ala Trp Ala Asn Trp Met Trp Val Ala Pro Arg
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Leu Arg Ser Tyr Ser Glu Ile Ser Ala Asn Ser Ile Thr Leu Pro Ser
      100          105          110

Phe Phe Glu Asn Arg Leu Arg Asp Lys Ser Arg Ala Leu Arg Ile Ile
      115          120          125

Ala Ala Leu Ile Ile Ile Val Phe Phe Thr Phe Tyr Ile Ser Ser Gly
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Met Val Ala Gly Gly Val Tyr Trp Glu Ser Thr Phe Gly Gly Asp Tyr
      145          150          155          160

Leu Leu Gly Met Ala Ile Val Ala Gly Val Thr Val Leu Tyr Thr Phe
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Ile Gly Gly Phe Leu Ala Val Ser Tyr Thr Asp Ala Val Gln Gly Thr
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Ile Met Phe Phe Ser Leu Ile Ile Val Pro Val Met Ala Tyr Phe Ala
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Leu Ala Asn Pro Met Asp Ile Trp Ser Phe Ala Asn Ser Asn Asp Tyr
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Gly Pro His Thr Asp Gly Ile Gly Asn Pro Thr Tyr Phe Ser Met Ile
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Ser Gly Ile Ser Ala Ala Ala Ile Ile Gly Asn Leu Gly Trp Gly Leu
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Gly Tyr Phe Gly Gln Pro His Ile Val Val Arg Phe Met Ala Leu Arg
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Thr Pro Ala Glu Ala Lys Gln Gly Arg Arg Ile Gly Ile Ser Trp Met
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Ile Ile Cys Leu Ile Gly Ala Thr Phe Thr Ala Ile Ile Ser Thr Val
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Phe Phe Ala Gln Asn Pro Asp Ala Asn Ile Thr Asp Thr Arg Ala Tyr
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 Glu Ser Ile Phe Leu Asp Leu Ala Arg Met Leu Phe His Pro Leu Ile
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 Ala Gly Leu Ile Leu Thr Ala Val Leu Ala Ala Ile Met Ser Thr Met
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 Ser Ser Gln Leu Leu Val Thr Ala Ser Ser Leu Ile Glu Asp Leu Leu
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 Lys Val Val Lys Lys Asp Ser Leu Ser Glu Arg Thr Leu Ile Met Leu
 370 375 380
 Ser Arg Ala Thr Val Ile Ile Leu Ala Ile Ile Ala Ala Ala Met Ala
 385 390 395 400
 Ile Asn Pro Ser Asp Ser Ile Leu Gly Leu Val Gly Phe Ala Trp Ala
 405 410 415
 Gly Phe Gly Ser Ala Phe Gly Pro Ile Ile Leu Ala Ser Leu Tyr Trp
 420 425 430
 Lys Arg Leu Asn Ala Ala Gly Ala Ile Ser Gly Met Ile Thr Gly Ala
 435 440 445
 Ile Val Ser Ile Ala Trp Gly Met Ser Pro Leu Ser Asp Thr Leu Tyr
 450 455 460
 Glu Ile Ile Pro Gly Phe Ala Leu Ala Thr Ile Val Met Val Val Val
 465 470 475 480
 Ser Leu Leu Thr Lys Glu Pro Ser Glu Glu Ile Leu Asn Glu Phe Glu
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 Met Thr Thr Ser Ser
 1 5
 aca gct tcg ccg atc gct gaa tta caa aac ctc agc ccg aag caa aga 163

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Lys	Ser	Glu	Ser	Arg	Arg	Ala	Ile	Ile	Ser	Ser	Tyr	Leu	Gly	Ser	Thr		
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Ile	Glu	Phe	Tyr	Asp	Phe	Leu	Leu	Tyr	Ala	Ala	Ala	Ser	Ala	Thr	Val		
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Leu	Val	Leu	Ser	Met	Leu	Ile	Met	Gly	Val	Ala	Ser	Thr	Cys	Ile	Gly		
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Leu	Val	Pro	Ser	Ala	Glu	Met	Ile	Gly	Ser	Met	Gly	Ala	Val	Ile	Leu		
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atc	atg	ctg	cgc	atc	tgc	caa	ggc	atc	gct	gtc	ggt	ggc	gaa	tgg	ggc	547	
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Gly	Ala	Ala	Leu	Met	Ala	Leu	Glu	His	Ser	Asp	Ser	Lys	Lys	Arg	Gly		
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Phe	Ala	Ala	Ser	Phe	Thr	Asn	Ala	Gly	Ala	Pro	Thr	Gly	Ala	Ala	Leu		
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Gly	Thr	Phe	Ala	Leu	Gly	Thr	Ala	Ser	Ala	Val	Leu	Thr	Gln	Glu	Gln		
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Phe	Leu	Ser	Trp	Gly	Trp	Arg	Ile	Pro	Phe	Leu	Leu	Ser	Phe	Val	Leu		
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Leu	Tyr	Ala	Phe	Ala	Val	Ala	Ser	Val	Phe	Ser	Val	Phe	Phe	Val	Ile					
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Leu	Ala	Leu	His	Ala	Met	Leu	Tyr	Gly	Pro	Leu	Ala	Ala	Phe	Ile	Ser					
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Glu	Gln	Phe	Gly	Thr	Ser	Ala	Arg	Tyr	Thr	Gly	Ala	Ser	Leu	Gly	Tyr					
	375					380					385									
cag	ttg	gcc	acg	ctc	atc	ggg	gca	gga	ttc	acc	cca	acc	atc	ctg	gct	1315				
Gln	Leu	Ala	Thr	Leu	Ile	Gly	Ala	Gly	Phe	Thr	Pro	Thr	Ile	Leu	Ala					
390					395					400					405					
agc	ctc	tac	gcg	gga	cca	ggc	ggc	gga	acc	tct	gtc	acc	cca	gtc	atc	1363				
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Val	Phe	Leu	Ala	Thr	Met	Ser	Leu	Val	Ser	Ile	Ile	Ala	Ile	Ala	Ile					
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acc	aga	gaa	tca	aaa	gac	cac	gat	ctt	tct	act	tac	gaa	cac			1453				
Thr	Arg	Glu	Ser	Lys	Asp	His	Asp	Leu	Ser	Thr	Tyr	Glu	His							
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 50 55 60
 Leu Ala Gly Thr Ile Ala Ala Tyr Gly Thr Phe Ala Ala Gly Tyr Leu
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 Ala Arg Pro Leu Gly Gly Ala Ile Phe Gly His Phe Gly Asp Arg Leu
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 Gly Arg Lys Lys Met Leu Val Leu Ser Met Leu Ile Met Gly Val Ala
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 Ser Thr Cys Ile Gly Leu Val Pro Ser Ala Glu Met Ile Gly Ser Met
 115 120 125
 Gly Ala Val Ile Leu Ile Met Leu Arg Ile Cys Gln Gly Ile Ala Val
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 Gly Gly Glu Trp Gly Gly Ala Ala Leu Met Ala Leu Glu His Ser Asp
 145 150 155 160
 Ser Lys Lys Arg Gly Phe Ala Ala Ser Phe Thr Asn Ala Gly Ala Pro
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 Thr Gly Ala Ala Leu Gly Thr Phe Ala Leu Gly Thr Ala Ser Ala Val
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 Leu Ser Phe Val Leu Leu Ile Val Gly Leu Val Ile Arg Ala Lys Val
 210 215 220
 Ser Glu Ser Pro Leu Phe Ala Ala Ala Ala Ala Glu Lys Ala Lys
 225 230 235 240
 Pro Thr Glu Arg Lys Val Pro Leu Leu Gln Val Leu Arg Arg Pro Lys
 245 250 255
 Ala Leu Ile Leu Thr Met Leu Gly Gly Ala Ser Gly Phe Gly Leu Gln
 260 265 270
 Val Leu Leu Ser Thr Phe Ser Ile Ser Tyr Ala Thr Gln Ser Gly Ile
 275 280 285
 Glu Arg Ser Ser Val Leu Tyr Ala Phe Ala Val Ala Ser Val Phe Ser
 290 295 300
 Val Phe Phe Val Ile Leu Phe Gly Arg Val Ser Asp Leu Phe Gly Arg
 305 310 315 320
 Arg Pro Val Met Ile Ile Ala Leu Val Leu Phe Val Ala Tyr Leu Pro
 325 330 335

Ala Phe Phe Arg Met Leu Thr Ser Asp Asn Trp Phe Ile Leu Leu Ser
 340 345 350

Ala Phe Thr Ile Ala Leu Ala Leu His Ala Met Leu Tyr Gly Pro Leu
 355 360 365

Ala Ala Phe Ile Ser Glu Gln Phe Gly Thr Ser Ala Arg Tyr Thr Gly
 370 375 380

Ala Ser Leu Gly Tyr Gln Leu Ala Thr Leu Ile Gly Ala Gly Phe Thr
 385 390 395 400

Pro Thr Ile Leu Ala Ser Leu Tyr Ala Gly Pro Gly Gly Gly Thr Ser
 405 410 415

Val Thr Pro Val Ile Val Phe Leu Ala Thr Met Ser Leu Val Ser Ile
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Tyr Glu His
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 Val Ser Pro Ile Arg
 1 5

tca aaa aag aaa atc aag aac gaa cca aga cta aca gtc gat gac gtc 163
 Ser Lys Lys Lys Ile Lys Asn Glu Pro Arg Leu Thr Val Asp Asp Val
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 Asn Val Val Pro Pro Lys Lys Ile Arg Pro Ala Ile Lys Gly Thr Val
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 Val Gly Asn Phe Met Glu Trp Tyr Asp Phe Gly Ile Tyr Gly Tyr Leu
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acg gtc acg atg acc gca gta ttt acc caa ggc ctg ccg caa gaa tgg 307
 Thr Val Thr Met Thr Ala Val Phe Thr Gln Gly Leu Pro Gln Glu Trp
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 Gln Leu Leu Ala Val Met Phe Gly Phe Ala Val Ser Tyr Leu Val Arg
 70 75 80 85

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Pro Leu Gly Gly Leu Val Leu Gly Pro Leu Gly Asp Lys Val Gly Arg	
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Gln Lys Val Leu Tyr Val Thr Met Ala Met Met Ala Val Ser Thr Ala	
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Leu Ile Gly Leu Leu Pro Thr Ala Ala Ser Ile Gly Ala Trp Ala Leu	
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Glu Tyr Ala Gly Ala Thr Thr Tyr Val Ala Glu Phe Ala Pro Asp Arg	
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Phe Ala Ala Gly Ala Ser Val Val Ala Ile Thr Thr Trp Val Thr Thr	
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His Phe Tyr Gly Ala Thr Ala Met Glu Asp Phe Gly Trp Arg Ile Pro	
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Phe Leu Thr Ala Ile Pro Leu Gly Ile Ile Ala Val Tyr Leu Arg Thr	
215 220 225	
cgt atc cct gag acc cct gcg ttt gag aac aac caa gac gag cca aat	835
Arg Ile Pro Glu Thr Pro Ala Phe Glu Asn Asn Gln Asp Glu Pro Asn	
230 235 240 245	
gca gtt gtt gaa aag gac act gaa gat cct tat gca cgc ctg ggc ctg	883
Ala Val Val Glu Lys Asp Thr Glu Asp Pro Tyr Ala Arg Leu Gly Leu	
250 255 260	
gct ggt gtt atc cgc cac cac tgg cgt cca ctg ctg att ggt att gcg	931
Ala Gly Val Ile Arg His His Trp Arg Pro Leu Leu Ile Gly Ile Ala	
265 270 275	
att gtg gca gcg acc aac acc gcc ggt tac gcg cta acc agt tac atg	979
Ile Val Ala Ala Thr Asn Thr Ala Gly Tyr Ala Leu Thr Ser Tyr Met	
280 285 290	
cct gtg tat cta gag gag cag atc ggt ctg cac tcc gca tcc gct gcc	1027
Pro Val Tyr Leu Glu Glu Gln Ile Gly Leu His Ser Ala Ser Ala Ala	
295 300 305	
gct gtg acc gtg ccg att ctg gtt gtt atg tcc ctg ctg ctg cca ttt	1075
Ala Val Thr Val Pro Ile Leu Val Val Met Ser Leu Leu Leu Pro Phe	
310 315 320 325	

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 Val Gly Met Trp Ser Asp Arg Val Gly Arg Lys Pro Val Tyr Ala Thr
 330 335 340

gct gtt gcg gca acg ctg atc ttg atg gtt cct gcc ttc ttg atc atg 1171
 Ala Val Ala Ala Thr Leu Ile Leu Met Val Pro Ala Phe Leu Ile Met
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aac acc gga acc atc ggc gcc gta ctg att gca ctg tcc atg gtt gct 1219
 Asn Thr Gly Thr Ile Gly Ala Val Leu Ile Ala Leu Ser Met Val Ala
 360 365 370

att cca acc ggt ttg tat gtg gca ctg tcc gca tct gcc ctg cca gcg 1267
 Ile Pro Thr Gly Leu Tyr Val Ala Leu Ser Ala Ser Ala Leu Pro Ala
 375 380 385

ctg ttc cca acc gcg tca cga ttc tct gga atg ggt att tcc tac aac 1315
 Leu Phe Pro Thr Ala Ser Arg Phe Ser Gly Met Gly Ile Ser Tyr Asn
 390 395 400 405

att tcc gtg tcg ttg ttc ggt ggt aca acc ccg ctg atc acc cag ttc 1363
 Ile Ser Val Ser Leu Phe Gly Gly Thr Thr Pro Leu Ile Thr Gln Phe
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ctg ctg cag aag act ggc ctg gat atc gtt cca gcg ctc tac atc atg 1411
 Leu Leu Gln Lys Thr Gly Leu Asp Ile Val Pro Ala Leu Tyr Ile Met
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 Phe Phe Ser Ala Ile Ala Gly Val Ala Leu Leu Phe Met Thr Glu Ser
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 Ser Gln Lys Pro Leu Leu Gly Ser Phe Pro Thr Val Glu Thr Lys Ser
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gag gcc gtg gag atc gtg aag aac cag gac gag gat cca aat att gat 1555
 Glu Ala Val Glu Ile Val Lys Asn Gln Asp Glu Asp Pro Asn Ile Asp
 470 475 480 485

ctt tcc cat atg ccg ttt cct gat gag gaa aac gta ggt gct gaa aag 1603
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<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 500

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Ile Lys Gly Thr Val Val Gly Asn Phe Met Glu Trp Tyr Asp Phe Gly
 35 40 45
 Ile Tyr Gly Tyr Leu Thr Val Thr Met Thr Ala Val Phe Thr Gln Gly
 50 55 60
 Leu Pro Gln Glu Trp Gln Leu Leu Ala Val Met Phe Gly Phe Ala Val
 65 70 75 80
 Ser Tyr Leu Val Arg Pro Leu Gly Gly Leu Val Leu Gly Pro Leu Gly
 85 90 95
 Asp Lys Val Gly Arg Gln Lys Val Leu Tyr Val Thr Met Ala Met Met
 100 105 110
 Ala Val Ser Thr Ala Leu Ile Gly Leu Leu Pro Thr Ala Ala Ser Ile
 115 120 125
 Gly Ala Trp Ala Leu Val Leu Leu Tyr Leu Leu Lys Met Val Gln Gly
 130 135 140
 Phe Ser Thr Gly Gly Glu Tyr Ala Gly Ala Thr Thr Tyr Val Ala Glu
 145 150 155 160
 Phe Ala Pro Asp Arg Arg Arg Gly Phe Phe Gly Ala Phe Leu Asp Met
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 Gly Ser Tyr Leu Gly Phe Ala Ala Gly Ala Ser Val Val Ala Ile Thr
 180 185 190
 Thr Trp Val Thr Thr His Phe Tyr Gly Ala Thr Ala Met Glu Asp Phe
 195 200 205
 Gly Trp Arg Ile Pro Phe Leu Thr Ala Ile Pro Leu Gly Ile Ile Ala
 210 215 220
 Val Tyr Leu Arg Thr Arg Ile Pro Glu Thr Pro Ala Phe Glu Asn Asn
 225 230 235 240
 Gln Asp Gly Pro Asn Ala Val Val Glu Lys Asp Thr Glu Asp Pro Tyr
 245 250 255
 Ala Arg Leu Gly Leu Ala Gly Val Ile Arg His His Trp Arg Pro Leu
 260 265 270
 Leu Ile Gly Ile Ala Ile Val Ala Ala Thr Asn Thr Ala Gly Tyr Ala
 275 280 285
 Leu Thr Ser Tyr Met Pro Val Tyr Leu Glu Glu Gln Ile Gly Leu His
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 Ser Ala Ser Ala Ala Ala Val Thr Val Pro Ile Leu Val Val Met Ser
 305 310 315 320
 Leu Leu Leu Pro Phe Val Gly Met Trp Ser Asp Arg Val Gly Arg Lys
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 Pro Val Tyr Ala Thr Ala Val Ala Ala Thr Leu Ile Leu Met Val Pro
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 Ala Phe Leu Ile Met Asn Thr Gly Thr Ile Gly Ala Val Leu Ile Ala

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gga cgc aaa gct acc ttg atc ggt tca ctg ctg acc atg ggc att gcc Gly Arg Lys Ala Thr Leu Ile Gly Ser Leu Leu Thr Met Gly Ile Ala 105 110 115			451
acc atc ttg atc ggc ctg ctg cct act tat ggt cag gtc gga atc att Thr Ile Leu Ile Gly Leu Leu Pro Thr Tyr Gly Gln Val Gly Ile Ile 120 125 130			499
gca ccg gcg ctg ttg gcg ctc atg cgt ttc tgc cag ggc ctg ggc ctt Ala Pro Ala Leu Leu Ala Leu Met Arg Phe Cys Gln Gly Leu Gly Leu 135 140 145			547
ggc ggt gaa tgg tct ggc gct gcg ttg ctg gct ggt gaa aac gcg gaa Gly Gly Glu Trp Ser Gly Ala Ala Leu Leu Ala Gly Glu Asn Ala Glu 150 155 160 165			595
aac act cac cgc gct cgt gct gca atg tgg cca cag ctg ggt gca ccg Asn Thr His Arg Ala Arg Ala Ala Met Trp Pro Gln Leu Gly Ala Pro 170 175 180			643
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ctt gcc cat cag gac ggc gat ctt cac ggc gcg ttc atg acc tgg ggt Leu Ala His Gln Asp Gly Asp Leu His Gly Ala Phe Met Thr Trp Gly 200 205 210			739
tgg cgt ctg cca ttc ctg tct tcg gcg atc atg atc gca gtt ggc ctg Trp Arg Leu Pro Phe Leu Ser Ser Ala Ile Met Ile Ala Val Gly Leu 215 220 225			787
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gat cag ggc aag aag gtg aag tct ccg ctc aag gag ctg ttc aag act Asp Gln Gly Lys Lys Val Lys Ser Pro Leu Lys Glu Leu Phe Lys Thr 250 255 260			883
tcc cct ggc cct gtt gtg cag gct act ttg atc atg ctg tcc act tat Ser Pro Gly Pro Val Val Gln Ala Thr Leu Ile Met Leu Ser Thr Tyr 265 270 275			931
acc ttg ttc tac ctg gtt acc acg tgg att ctg tcg tat ggc atc ggt Thr Leu Phe Tyr Leu Val Thr Thr Trp Ile Leu Ser Tyr Gly Ile Gly 280 285 290			979
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cag ttg cag ctg gcc acc atc gtg ttc ttc gcc atc atg atc cct gtg 1075
 Gln Leu Gln Leu Ala Thr Ile Val Phe Phe Ala Ile Met Ile Pro Val
 310 315 320 325
 tca ggc tgg ttg gct gat gtg tgg ggt cgt aaa aac acc ctg acc ttg 1123
 Ser Gly Trp Leu Ala Asp Val Trp Gly Arg Lys Asn Thr Leu Thr Leu
 330 335 340
 gct tct gtg ctg ctt ctc ggc ttt ggt ctg acg ttt aat ctg ctt ctc 1171
 Ala Ser Val Leu Leu Leu Gly Phe Gly Leu Thr Phe Asn Leu Leu Leu
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 gat cca gag acc gcc acc aag acc acc gtg ttc atc ttc ttg ttc gtg 1219
 Asp Pro Glu Thr Ala Thr Lys Thr Thr Val Phe Ile Phe Leu Phe Val
 360 365 370
 ggc atg agc atc atg ggt ctg atc ttt gga ccc atg tcg gca att ttg 1267
 Gly Met Ser Ile Met Gly Leu Ile Phe Gly Pro Met Ser Ala Ile Leu
 375 380 385
 ccg gag ctc ttc ccc acc aac gtc cgc tac acg ggc tcc gga atc gcc 1315
 Pro Glu Leu Phe Pro Thr Asn Val Arg Tyr Thr Gly Ser Gly Ile Ala
 390 395 400 405
 tac aat gtc tcc tcg atc ctc ggt gca gct att gca ccg ttc atc gca 1363
 Tyr Asn Val Ser Ser Ile Leu Gly Ala Ala Ile Ala Pro Phe Ile Ala
 410 415 420
 acg tgg ctg gtg tcc gag ttt tca gtg gcg tac gtc ggc tat tac ctc 1411
 Thr Trp Leu Val Ser Glu Phe Ser Val Ala Tyr Val Gly Tyr Tyr Leu
 425 430 435
 atc atc gtc acc gca att acc ttt gtt gcg gtg ctg acg atg aag gaa 1459
 Ile Ile Val Thr Ala Ile Thr Phe Val Ala Val Leu Thr Met Lys Glu
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 aac aaa aac cac gac ctc cga gag gtc taaaagattt ttgcttatcg 1506
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<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

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Ala Ala Ala Ser Thr Ile Gly Thr Thr Ile Glu Phe Tyr Asp Phe Tyr
 35 40 45

Ala Tyr Ala Ala Ala Ala Val Val Val Phe Pro Ser Leu Phe Phe Pro
 50 55 60

Ala Asn Asp Asn Pro Thr Val Asn Leu Leu Ala Ser Phe Ala Thr Phe
 65 70 75 80
 Gly Leu Ala Phe Val Ala Arg Pro Leu Gly Ser Ile Ile Phe Gly His
 85 90 95
 Phe Gly Asp Arg Val Gly Arg Lys Ala Thr Leu Ile Gly Ser Leu Leu
 100 105 110
 Thr Met Gly Ile Ala Thr Ile Leu Ile Gly Leu Leu Pro Thr Tyr Gly
 115 120 125
 Gln Val Gly Ile Ile Ala Pro Ala Leu Leu Ala Leu Met Arg Phe Cys
 130 135 140
 Gln Gly Leu Gly Leu Gly Gly Glu Trp Ser Gly Ala Ala Leu Leu Ala
 145 150 155 160
 Gly Glu Asn Ala Glu Asn Thr His Arg Ala Arg Ala Ala Met Trp Pro
 165 170 175
 Gln Leu Gly Ala Pro Phe Gly Phe Phe Leu Ala Asn Gly Phe Met Leu
 180 185 190
 Ile Leu Val Gly Val Leu Ala His Gln Asp Gly Asp Leu His Gly Ala
 195 200 205
 Phe Met Thr Trp Gly Trp Arg Leu Pro Phe Leu Ser Ser Ala Ile Met
 210 215 220
 Ile Ala Val Gly Leu Trp Val Arg Phe Ser Leu Glu Glu Thr Pro Val
 225 230 235 240
 Phe Lys Gln Ala Val Asp Gln Gly Lys Lys Val Lys Ser Pro Leu Lys
 245 250 255
 Glu Leu Phe Lys Thr Ser Pro Gly Pro Val Val Gln Ala Thr Leu Ile
 260 265 270
 Met Leu Ser Thr Tyr Thr Leu Phe Tyr Leu Val Thr Thr Trp Ile Leu
 275 280 285
 Ser Tyr Gly Ile Gly Asn Arg Ser Thr Gly Asn Gly Leu Ser Ile Pro
 290 295 300
 Tyr Phe Glu Phe Leu Gln Leu Gln Leu Ala Thr Ile Val Phe Phe Ala
 305 310 315 320
 Ile Met Ile Pro Val Ser Gly Trp Leu Ala Asp Val Trp Gly Arg Lys
 325 330 335
 Asn Thr Leu Thr Leu Ala Ser Val Leu Leu Leu Gly Phe Gly Leu Thr
 340 345 350
 Phe Asn Leu Leu Leu Asp Pro Glu Thr Ala Thr Lys Thr Thr Val Phe
 355 360 365
 Ile Phe Leu Phe Val Gly Met Ser Ile Met Gly Leu Ile Phe Gly Pro
 370 375 380

Met Ser Ala Ile Leu Pro Glu Leu Phe Pro Thr Asn Val Arg Tyr Thr
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Gly Ser Gly Ile Ala Tyr Asn Val Ser Ser Ile Leu Gly Ala Ala Ile
 405 410 415

Ala Pro Phe Ile Ala Thr Trp Leu Val Ser Glu Phe Ser Val Ala Tyr
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Val Gly Tyr Tyr Leu Ile Ile Val Thr Ala Ile Thr Phe Val Ala Val
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 <222> (101)..(847)
 <223> RXA00186

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 Met Gly Glu Lys Thr
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tct gtc gcg tat gtt cac gat gtt ctg atc aag ggc gtg cca gtg cgg 163
 Ser Val Ala Tyr Val His Asp Val Leu Ile Lys Gly Val Pro Val Arg
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ata tac aat ccg cac ccc aac gac ggg ccg ctt cct gtc ttt atc tac 211
 Ile Tyr Asn Pro His Pro Asn Asp Gly Pro Leu Pro Val Phe Ile Tyr
 25 30 35

ttc cat ggt ggc gga tgg gtt ttg ggg gac ctt gaa tca gtg gat tcc 259
 Phe His Gly Gly Gly Trp Val Leu Gly Asp Leu Glu Ser Val Asp Ser
 40 45 50

acc gtg cgc gat att gcc gtt gct tca ggc gcc ctg tgt atc agt gtg 307
 Thr Val Arg Asp Ile Ala Val Ala Ser Gly Ala Leu Cys Ile Ser Val
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gat tat cgc cgt gca ccg gaa cat cct ttt ctc gct gca ttg gat gat 355
 Asp Tyr Arg Arg Ala Pro Glu His Pro Phe Leu Ala Ala Leu Asp Asp
 70 75 80 85

tgc caa gtg gtc acg gaa gct gtc ctc aat ggt gaa ctc gcc agt gct 403
 Cys Gln Val Val Thr Glu Ala Val Leu Asn Gly Glu Leu Ala Ser Ala
 90 95 100

aac cag cat cta gtg gca gtc ggc ggg gac agc gcc ggt ggc aat att 451
 Asn Gln His Leu Val Ala Val Gly Gly Asp Ser Ala Gly Gly Asn Ile
 105 110 115

gcg gcg gtc atc gct caa cag ctg cgc gat cag atc acc cac caa gtt 499
 Ala Ala Val Ile Ala Gln Gln Leu Arg Asp Gln Ile Thr His Gln Val
 120 125 130

ctt gtg tat ccg gtg atg gac gta atc ttg ctg gtg att tgt tct atc 547
 Leu Val Tyr Pro Val Met Asp Val Ile Leu Leu Val Ile Cys Ser Ile
 135 140 145

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 Ile Thr Thr Gly Phe Ala Leu Leu Met His Pro Lys Ser Lys Asp Lys
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acg gag acg att tct gat gaa ttc ctc gca gag atc caa gcg gga agt 643
 Thr Glu Thr Ile Ser Asp Glu Phe Leu Ala Glu Ile Gln Ala Gly Ser
 170 175 180

gaa aag atc tcc att ctg cgt tgc acc cct gct gaa aaa gcc aat gcg 691
 Glu Lys Ile Ser Ile Leu Arg Ser Thr Pro Ala Glu Lys Ala Asn Ala
 185 190 195

agc cgt tgg atc atg tac ttc gtt ggc gga att ggc ctg ctc tac agc 739
 Ser Arg Trp Ile Met Tyr Phe Val Gly Gly Ile Gly Leu Leu Tyr Ser
 200 205 210

gtg ttc agc ctg tgg aca ggt ggc gta acc gga ctg acg ttg aac tcc 787
 Val Phe Ser Leu Trp Thr Gly Gly Val Thr Gly Leu Thr Leu Asn Ser
 215 220 225

ttc aac ttc ctg ttc ctg tca ctc ggc atg gtg ctc acc gct aat tac 835
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 Gly Pro Glu Tyr

<210> 504

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 504

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Pro Val Phe Ile Tyr Phe His Gly Gly Gly Trp Val Leu Gly Asp Leu
 35 40 45

Glu Ser Val Asp Ser Thr Val Arg Asp Ile Ala Val Ala Ser Gly Ala
 50 55 60

Leu Cys Ile Ser Val Asp Tyr Arg Arg Ala Pro Glu His Pro Phe Leu
 65 70 75 80

Ala Ala Leu Asp Asp Cys Gln Val Val Thr Glu Ala Val Leu Asn Gly
 85 90 95

Glu Leu Ala Ser Ala Asn Gln His Leu Val Ala Val Gly Gly Asp Ser
 100 105 110
 Ala Gly Gly Asn Ile Ala Ala Val Ile Ala Gln Gln Leu Arg Asp Gln
 115 120 125
 Ile Thr His Gln Val Leu Val Tyr Pro Val Met Asp Val Ile Leu Leu
 130 135 140
 Val Ile Cys Ser Ile Ile Thr Thr Gly Phe Ala Leu Leu Met His Pro
 145 150 155 160
 Lys Ser Lys Asp Lys Thr Glu Thr Ile Ser Asp Glu Phe Leu Ala Glu
 165 170 175
 Ile Gln Ala Gly Ser Glu Lys Ile Ser Ile Leu Arg Ser Thr Pro Ala
 180 185 190
 Glu Lys Ala Asn Ala Ser Arg Trp Ile Met Tyr Phe Val Gly Gly Ile
 195 200 205
 Gly Leu Leu Tyr Ser Val Phe Ser Leu Trp Thr Gly Gly Val Thr Gly
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<213> Corynebacterium glutamicum

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<222> (101)..(451)

<223> RXA00187

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 Val Ile Ser Gly Phe
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 Phe Thr Ser Ile Ser Thr Ala Thr Thr Trp Pro Val Ile Ala Phe Leu
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 Tyr Ser Gly Leu Leu Asn Ile Ala Val Pro Ser Gly Gly Ser Lys Phe
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atc atc gaa gcc ccg tac atc atc cca acc cca gtg gat ctt ggc gct 259
 Ile Ile Glu Ala Pro Tyr Ile Ile Pro Thr Pro Val Asp Leu Gly Ala
 40 45 50

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Asp Met Gly Leu Val Leu Gln Ala Tyr Gln Met Ser Asp Gly Ala Thr
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 aac ctg ctc att ccg ttc ttc gcg ctg cca tat ttg gcc aat ttc aag 355
 Asn Leu Leu Ile Pro Phe Phe Ala Leu Pro Tyr Leu Ala Asn Phe Lys
 70 75 80 85
 atc aaa ttc agc caa gtg gtg ggc tat aca gtt ccg cct gtc ctc gtt 403
 Ile Lys Phe Ser Gln Val Val Gly Tyr Thr Val Pro Pro Val Leu Val
 90 95 100
 gtt atc gcc gtg atc tgc att tac ctg ttc ctg cga gca tca atc att 451
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 105 110 115
 taaaaagatg cttctcg 468

<210> 506
 <211> 117
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 506
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 35 40 45
 Val Asp Leu Gly Ala Asp Met Gly Leu Val Leu Gln Ala Tyr Gln Met
 50 55 60
 Ser Asp Gly Ala Thr Asn Leu Leu Ile Pro Phe Phe Ala Leu Pro Tyr
 65 70 75 80
 Leu Ala Asn Phe Lys Ile Lys Phe Ser Gln Val Val Gly Tyr Thr Val
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	Met Ile Leu Gly Pro	
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aag gtg ttg ggt ctg att ggt tgg tcg gat cat ctt tcc act tac act	163	
Lys Val Leu Gly Leu Ile Gly Trp Ser Asp His Leu Ser Thr Tyr Thr		
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Thr Val Leu Ile Ala Ile Val Phe Ala Ser Met Pro Tyr Ser Met Lys		
	25 30 35	
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Phe Asp Arg Gly Val Arg Thr Gly Met Lys Thr Met Trp Ala Tyr Ser		
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Thr Ala Met Phe Val Gly Gln Trp Gly Leu Phe Ile Leu Leu Gly Leu		
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Phe Leu Phe Gln Pro Val Trp Gly Thr Asp Glu Trp Phe Gly Met Met		
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Leu Pro Val Gly Phe Val Gly Gly Phe Gly Thr Ala Ala Ala Val Gly		
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Thr Ala Leu Glu Ser Ser Gly Ala Glu Ala Ala Met Ser Leu Gly Phe		
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Thr Ser Ala Thr Val Gly Thr Phe Ala Ala Ile Val Gly Gly Ile Ile		
	120 125 130	
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Phe Thr Thr Trp Gly Ile Lys Lys Gly Lys Thr Ala Ala Met Pro Ala		
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Gln Leu Pro Trp Asp Leu Arg Ser Gly Tyr Ile Asp Lys Leu Ser Asp		
	150 155 160 165	
cgt ccg tcg att ggt aag gcg agt acg aat ccg tct gcg att gag cct	643	
Arg Pro Ser Ile Gly Lys Ala Ser Thr Asn Pro Ser Ala Ile Glu Pro		
	170 175 180	
ttg gcg ctg cat act ggc att att ttg ttg act gtt gcg gtt gcg tat	691	
Leu Ala Leu His Thr Gly Ile Ile Leu Leu Thr Val Ala Val Ala Tyr		
	185 190 195	
tcc att aat cag tgg ttg ggt agc atg ttc cca acc gtg cag att ccg	739	
Ser Ile Asn Gln Trp Leu Gly Ser Met Phe Pro Thr Val Gln Ile Pro		
	200 205 210	
ttg ttt gcg atg tca ttt gtg gtc ggc att gtg ggc atg gga att atg	787	
Leu Phe Ala Met Ser Phe Val Val Gly Ile Val Gly Met Gly Ile Met		
	215 220 225	

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cgt ttg ttg aag aag cct gag tat ttg gat cgc gac acc gtg aat tcc      835
Arg Leu Leu Lys Lys Pro Glu Tyr Leu Asp Arg Asp Thr Val Asn Ser
230                               235                               240                               245

gtg tcg ggc gcg gcg acg gat tac ctc att gcg ttt ggt att gcc tcg      883
Val Ser Gly Ala Ala Thr Asp Tyr Leu Ile Ala Phe Gly Ile Ala Ser
                               250                               255                               260

att gct cct gct gcg att gct gat tac tgg gtt cct ctt gtg gtg ctg      931
Ile Ala Pro Ala Ala Ile Ala Asp Tyr Trp Val Pro Leu Val Val Leu
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Phe Val Leu Gly Thr Ile Asn Cys Cys Phe Phe Phe Phe Trp Val Ala
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ggt tgg gct act gcc gcg gtt gct acc ggt atc gcg ttg ctg aag atc      1075
Gly Trp Ala Thr Ala Ala Val Ala Thr Gly Ile Ala Leu Leu Lys Ile
310                               315                               320                               325

gtg gat ccg aag ttg aag tcg gga gcg ctt aat gag tac ggc gtg gct      1123
Val Asp Pro Lys Leu Lys Ser Gly Ala Leu Asn Glu Tyr Gly Val Ala
                               330                               335                               340

tat atc ggt ttt gct cca ttt gaa atc ggc atg acc atc atc gcg ccg      1171
Tyr Ile Gly Phe Ala Pro Phe Glu Ile Gly Met Thr Ile Ile Ala Pro
                               345                               350                               355

atc gcg gtg ctc gca ggc ttt acc atg ggg ttg ggt tgg gcg tcg ttg      1219
Ile Ala Val Leu Ala Gly Phe Thr Met Gly Leu Gly Trp Ala Ser Leu
                               360                               365                               370

att gtt gcg atc gtg att ttt ggc ctc gcg tgg ggt ctg aag tgg ttg      1267
Ile Val Ala Ile Val Ile Phe Gly Leu Ala Trp Gly Leu Lys Trp Leu
                               375                               380                               385

ccg gag cgc gga cat gtc cgc ggc gag ggt aag ccg caa taaaggttgg      1316
Pro Glu Arg Gly His Val Arg Gly Glu Gly Lys Pro Gln
390                               395                               400

aagcgcgcggg tct                                                    1329

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<210> 508

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

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Met Ile Leu Gly Pro Lys Val Leu Gly Leu Ile Gly Trp Ser Asp His
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Leu Ser Thr Tyr Thr Thr Val Leu Ile Ala Ile Val Phe Ala Ser Met
 20                               25                               30

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Pro Tyr Ser Met Lys Phe Asp Arg Gly Val Arg Thr Gly Met Lys Thr
 35                               40                               45

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Met Trp Ala Tyr Ser Thr Ala Met Phe Val Gly Gln Trp Gly Leu Phe
 50 55 60
 Ile Leu Leu Gly Leu Phe Leu Phe Gln Pro Val Trp Gly Thr Asp Glu
 65 70 75 80
 Trp Phe Gly Met Met Leu Pro Val Gly Phe Val Gly Gly Phe Gly Thr
 85 90 95
 Ala Ala Ala Val Gly Thr Ala Leu Glu Ser Ser Gly Ala Glu Ala Ala
 100 105 110
 Met Ser Leu Gly Phe Thr Ser Ala Thr Val Gly Thr Phe Ala Ala Ile
 115 120 125
 Val Gly Gly Ile Ile Phe Thr Thr Trp Gly Ile Lys Lys Gly Lys Thr
 130 135 140
 Ala Ala Met Pro Ala Gln Leu Pro Trp Asp Leu Arg Ser Gly Tyr Ile
 145 150 155 160
 Asp Lys Leu Ser Asp Arg Pro Ser Ile Gly Lys Ala Ser Thr Asn Pro
 165 170 175
 Ser Ala Ile Glu Pro Leu Ala Leu His Thr Gly Ile Ile Leu Leu Thr
 180 185 190
 Val Ala Val Ala Tyr Ser Ile Asn Gln Trp Leu Gly Ser Met Phe Pro
 195 200 205
 Thr Val Gln Ile Pro Leu Phe Ala Met Ser Phe Val Val Gly Ile Val
 210 215 220
 Gly Met Gly Ile Met Arg Leu Leu Lys Lys Pro Glu Tyr Leu Asp Arg
 225 230 235 240
 Asp Thr Val Asn Ser Val Ser Gly Ala Ala Thr Asp Tyr Leu Ile Ala
 245 250 255
 Phe Gly Ile Ala Ser Ile Ala Pro Ala Ala Ile Ala Asp Tyr Trp Val
 260 265 270
 Pro Leu Val Val Leu Phe Val Leu Gly Thr Ile Asn Cys Cys Phe Phe
 275 280 285
 Phe Phe Trp Val Ala Pro Arg Phe Phe Gly Glu Lys Trp Leu Glu Arg
 290 295 300
 Ala Ile Phe Gly Trp Gly Trp Ala Thr Ala Ala Val Ala Thr Gly Ile
 305 310 315 320
 Ala Leu Leu Lys Ile Val Asp Pro Lys Leu Lys Ser Gly Ala Leu Asn
 325 330 335
 Glu Tyr Gly Val Ala Tyr Ile Gly Phe Ala Pro Phe Glu Ile Gly Met
 340 345 350
 Thr Ile Ile Ala Pro Ile Ala Val Leu Ala Gly Phe Thr Met Gly Leu
 355 360 365

Gly Trp Ala Ser Leu Ile Val Ala Ile Val Ile Phe Gly Leu Ala Trp
 370 375 380

Gly Leu Lys Trp Leu Pro Glu Arg Gly His Val Arg Gly Glu Gly Lys
 385 390 395 400

Pro Gln

<210> 509

<211> 1776

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1753)

<223> RXA02171

<400> 509

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tcaggctgct attcgccaga agatggaagg ttaatcagat atg aat tcc act att 115
 Met Asn Ser Thr Ile
 1 5

ctc ctt gca caa gac gct gtt tct gag ggc gtc ggt aat ccg att ctt 163
 Leu Leu Ala Gln Asp Ala Val Ser Glu Gly Val Gly Asn Pro Ile Leu
 10 15 20

aac atc agt gtc ttc gtc gtc ttc att att gtg acg atg acc gtg gtg 211
 Asn Ile Ser Val Phe Val Val Phe Ile Ile Val Thr Met Thr Val Val
 25 30 35

ctt cgc gtg ggc aag agc acc agc gaa tcc acc gac ttc tac acc ggt 259
 Leu Arg Val Gly Lys Ser Thr Ser Glu Ser Thr Asp Phe Tyr Thr Gly
 40 45 50

ggg gct tcc ttc tcc gga acc cag aac ggt ctg gct atc gca ggt gac 307
 Gly Ala Ser Phe Ser Gly Thr Gln Asn Gly Leu Ala Ile Ala Gly Asp
 55 60 65

tac ctg tct gca gcg tcc ttc ctc gga atc gtt ggt gca att tca ctc 355
 Tyr Leu Ser Ala Ala Ser Phe Leu Gly Ile Val Gly Ala Ile Ser Leu
 70 75 80 85

aac ggt tac gac gga ttc ctt tac tcc atc ggc ttc ttc gtc gca tgg 403
 Asn Gly Tyr Asp Gly Phe Leu Tyr Ser Ile Gly Phe Phe Val Ala Trp
 90 95 100

ctt gtt gca ctg ctg ctc gtg gca gag cca ctt cgt aac gtg ggc cgc 451
 Leu Val Ala Leu Leu Leu Val Ala Glu Pro Leu Arg Asn Val Gly Arg
 105 110 115

ttc acc atg gct gac gtg ctg tcc ttc cga ctg cgt cag aaa cca gtc 499
 Phe Thr Met Ala Asp Val Leu Ser Phe Arg Leu Arg Gln Lys Pro Val
 120 125 130

cgc gtc gct gcg gcc tgc ggt acc ctc gcg gtt acc ctc ttt tac ttg 547
 Arg Val Ala Ala Ala Cys Gly Thr Leu Ala Val Thr Leu Phe Tyr Leu

135	140	145	
atc gct cag atg gct ggt gca ggt tgc ctt gtg tcc gtt ctg ctg gac Ile Ala Gln Met Ala Gly Ala Gly Ser Leu Val Ser Val Leu Leu Asp 150 155 160 165			595
atc cac gag ttc aag tgg cag gca gtt gtt gtc ggt atc gtt ggc att Ile His Glu Phe Lys Trp Gln Ala Val Val Val Gly Ile Val Gly Ile 170 175 180			643
gtc atg atc gcc tac gtt ctt ctt ggc ggt atg aag ggc acc aca tac Val Met Ile Ala Tyr Val Leu Leu Gly Gly Met Lys Gly Thr Thr Tyr 185 190 195			691
gtt cag atg att aag gca gtt ctg ctg gtc ggt ggc gtt gcc att atg Val Gln Met Ile Lys Ala Val Leu Leu Val Gly Gly Val Ala Ile Met 200 205 210			739
acc gtt ctg acc ttc gtc aag gtg tct ggt ggc ctg acc acc ctt tta Thr Val Leu Thr Phe Val Lys Val Ser Gly Gly Leu Thr Thr Leu Leu 215 220 225			787
aat gac gct gtt gag aag cac gcc gct tca gat tac gct gcc acc aag Asn Asp Ala Val Glu Lys His Ala Ala Ser Asp Tyr Ala Ala Thr Lys 230 235 240 245			835
ggg tac gat cca acc cag atc ctg gag cct ggt ctg cag tac ggt gca Gly Tyr Asp Pro Thr Gln Ile Leu Glu Pro Gly Leu Gln Tyr Gly Ala 250 255 260			883
act ctg acc act cag ctg gac ttc att tcc ttg gct ctc gct ctg tgt Thr Leu Thr Thr Gln Leu Asp Phe Ile Ser Leu Ala Leu Ala Leu Cys 265 270 275			931
ctt gga acc gct ggt ctg cca cac gtt ctg atg cgc ttc tac acc gtt Leu Gly Thr Ala Gly Leu Pro His Val Leu Met Arg Phe Tyr Thr Val 280 285 290			979
cct acc gcc aag gaa gca cgt aag tct gtg acc tgg gct atc gtc ctc Pro Thr Ala Lys Glu Ala Arg Lys Ser Val Thr Trp Ala Ile Val Leu 295 300 305			1027
att ggt gcg ttc tac ctg atg acc ctg gtc ctt ggt tac ggc gct gcg Ile Gly Ala Phe Tyr Leu Met Thr Leu Val Leu Gly Tyr Gly Ala Ala 310 315 320 325			1075
gca ctg gtc ggt cca gac cgc gtc att gcc gca cca ggt gct gct aat Ala Leu Val Gly Pro Asp Arg Val Ile Ala Ala Pro Gly Ala Ala Asn 330 335 340			1123
gct gct gct cct ctg ctg gcc ttc gag ctt ggt ggt tcc atc ttc atg Ala Ala Ala Pro Leu Leu Ala Phe Glu Leu Gly Gly Ser Ile Phe Met 345 350 355			1171
gcg ctg att tcc gca gtt gcg ttc gct acc gtt ctc gcc gtg gtc gca Ala Leu Ile Ser Ala Val Ala Phe Ala Thr Val Leu Ala Val Val Ala 360 365 370			1219
ggt ctt gca att acc gca tcc gct gct gtt ggt cac gac atc tac aac Gly Leu Ala Ile Thr Ala Ser Ala Ala Val Gly His Asp Ile Tyr Asn 375 380 385			1267

gct gtt atc cgc aac ggt cag tcc acc gaa gcg gag cag gtc cga gta 1315
 Ala Val Ile Arg Asn Gly Gln Ser Thr Glu Ala Glu Gln Val Arg Val
 390 395 400 405
 tcc cgc atc acc gtt gtc gtc att ggc ctg att tcc att gtc ctg gga 1363
 Ser Arg Ile Thr Val Val Val Ile Gly Leu Ile Ser Ile Val Leu Gly
 410 415 420
 att ctt gca atg acc cag aac gtt gcg ttc ctc gtg gcc ctg gcc ttc 1411
 Ile Leu Ala Met Thr Gln Asn Val Ala Phe Leu Val Ala Leu Ala Phe
 425 430 435
 gca gtt gca gca tcc gct aac ctg cca acc atc ctg tac tcc ctg tac 1459
 Ala Val Ala Ala Ser Ala Asn Leu Pro Thr Ile Leu Tyr Ser Leu Tyr
 440 445 450
 tgg aag aag ttc aac acc acc ggc gct gtg gcc gct atc tac acc ggt 1507
 Trp Lys Lys Phe Asn Thr Thr Gly Ala Val Ala Ala Ile Tyr Thr Gly
 455 460 465
 ctc atc tcc gcg ctg ctg ctg atc ttc ctg tcc cca gca gtc tcc ggt 1555
 Leu Ile Ser Ala Leu Leu Leu Ile Phe Leu Ser Pro Ala Val Ser Gly
 470 475 480 485
 aat gac agc gca atg gtt cca ggt gca gac tgg gca atc ttc cca ctg 1603
 Asn Asp Ser Ala Met Val Pro Gly Ala Asp Trp Ala Ile Phe Pro Leu
 490 495 500
 aag aac cca ggc ctc gtc tcc atc cca ctg gca ttc atc gct ggt tgg 1651
 Lys Asn Pro Gly Leu Val Ser Ile Pro Leu Ala Phe Ile Ala Gly Trp
 505 510 515
 atc ggc act ttg gtt ggc aag cca gac aac atg gat gat ctt gct gcc 1699
 Ile Gly Thr Leu Val Gly Lys Pro Asp Asn Met Asp Asp Leu Ala Ala
 520 525 530
 gaa atg gaa gtt cgt tcc ctc acc ggt gtc ggt gtt gaa aag gct gtt 1747
 Glu Met Glu Val Arg Ser Leu Thr Gly Val Gly Val Glu Lys Ala Val
 535 540 545
 gat cac taaatctagt ttctgaagtt att 1776
 Asp His
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<210> 510

<211> 551

<212> PRT

<213> Corynebacterium glutamicum

<400> 510

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Thr Met Thr Val Val Leu Arg Val Gly Lys Ser Thr Ser Glu Ser Thr
 35 40 45

Asp Phe Tyr Thr Gly Gly Ala Ser Phe Ser Gly Thr Gln Asn Gly Leu
 50 55 60
 Ala Ile Ala Gly Asp Tyr Leu Ser Ala Ala Ser Phe Leu Gly Ile Val
 65 70 75 80
 Gly Ala Ile Ser Leu Asn Gly Tyr Asp Gly Phe Leu Tyr Ser Ile Gly
 85 90 95
 Phe Phe Val Ala Trp Leu Val Ala Leu Leu Val Ala Glu Pro Leu
 100 105 110
 Arg Asn Val Gly Arg Phe Thr Met Ala Asp Val Leu Ser Phe Arg Leu
 115 120 125
 Arg Gln Lys Pro Val Arg Val Ala Ala Ala Cys Gly Thr Leu Ala Val
 130 135 140
 Thr Leu Phe Tyr Leu Ile Ala Gln Met Ala Gly Ala Gly Ser Leu Val
 145 150 155 160
 Ser Val Leu Leu Asp Ile His Glu Phe Lys Trp Gln Ala Val Val Val
 165 170 175
 Gly Ile Val Gly Ile Val Met Ile Ala Tyr Val Leu Leu Gly Gly Met
 180 185 190
 Lys Gly Thr Thr Tyr Val Gln Met Ile Lys Ala Val Leu Leu Val Gly
 195 200 205
 Gly Val Ala Ile Met Thr Val Leu Thr Phe Val Lys Val Ser Gly Gly
 210 215 220
 Leu Thr Thr Leu Leu Asn Asp Ala Val Glu Lys His Ala Ala Ser Asp
 225 230 235 240
 Tyr Ala Ala Thr Lys Gly Tyr Asp Pro Thr Gln Ile Leu Glu Pro Gly
 245 250 255
 Leu Gln Tyr Gly Ala Thr Leu Thr Thr Gln Leu Asp Phe Ile Ser Leu
 260 265 270
 Ala Leu Ala Leu Cys Leu Gly Thr Ala Gly Leu Pro His Val Leu Met
 275 280 285
 Arg Phe Tyr Thr Val Pro Thr Ala Lys Glu Ala Arg Lys Ser Val Thr
 290 295 300
 Trp Ala Ile Val Leu Ile Gly Ala Phe Tyr Leu Met Thr Leu Val Leu
 305 310 315 320
 Gly Tyr Gly Ala Ala Ala Leu Val Gly Pro Asp Arg Val Ile Ala Ala
 325 330 335
 Pro Gly Ala Ala Asn Ala Ala Ala Pro Leu Leu Ala Phe Glu Leu Gly
 340 345 350
 Gly Ser Ile Phe Met Ala Leu Ile Ser Ala Val Ala Phe Ala Thr Val
 355 360 365
 Leu Ala Val Val Ala Gly Leu Ala Ile Thr Ala Ser Ala Ala Val Gly

745

aat cca aag aat att gca gcg agc cac gat cag gtg ctt cta tct ggt	259
Asn Pro Lys Asn Ile Ala Ala Ser His Asp Gln Val Leu Leu Ser Gly	
40 45 50	
tgg ggc aaa ttt gtg cgt tgg ctc ttg gta ttg ttg tcc att ttg gtc	307
Trp Gly Lys Phe Val Arg Trp Leu Leu Val Leu Leu Ser Ile Leu Val	
55 60 65	
atc atc att ggc atc aac ctc atc ttg gac ggt gtc tac gga ttt ggt	355
Ile Ile Ile Gly Ile Asn Leu Ile Leu Asp Gly Val Tyr Gly Phe Gly	
70 75 80 85	
act ttt tca acc acc cag atg tac caa gtt gcg aaa gat cca ctc att	403
Thr Phe Ser Thr Thr Gln Met Tyr Gln Val Ala Lys Asp Pro Leu Ile	
90 95 100	
ggg gtg ctg atc ggt atc ttg gct acg gcc ttg gtg caa tca tca acc	451
Gly Val Leu Ile Gly Ile Leu Ala Thr Ala Leu Val Gln Ser Ser Thr	
105 110 115	
acc acc aca acg ttg acg gtg act gca gtt ggt acg ggc att gtg tcg	499
Thr Thr Thr Thr Leu Thr Val Thr Ala Val Gly Thr Gly Ile Val Ser	
120 125 130	
gtg cct gtg gcg att ccg atc att ctt ggc gca aat atc ggt acg acg	547
Val Pro Val Ala Ile Pro Ile Ile Leu Gly Ala Asn Ile Gly Thr Thr	
135 140 145	
atc acc gcg atg ctc gtt gcg ttt tct tat gtg ggt gaa cgc agg gag	595
Ile Thr Ala Met Leu Val Ala Phe Ser Tyr Val Gly Glu Arg Arg Glu	
150 155 160 165	
ttt aag cga gct ttt acg gtt gcc gcc atg cat gtg tgg ttt aac gtg	643
Phe Lys Arg Ala Phe Thr Val Ala Ala Met His Val Trp Phe Asn Val	
170 175 180	
ctc gtc att ctt gtt cta ttt gtt gtg gaa ttg ctc ttt cat cca ttc	691
Leu Val Ile Leu Val Leu Phe Val Val Glu Leu Leu Phe His Pro Phe	
185 190 195	
cgc aca att agt ggt gcg atc gca acg gag atc aca ctg aca act ggt	739
Arg Thr Ile Ser Gly Ala Ile Ala Thr Glu Ile Thr Leu Thr Thr Gly	
200 205 210	
ggc tct ttg cct acc agt ggt gtg atg acc aag att ttt gat ccc cca	787
Gly Ser Leu Pro Thr Ser Gly Val Met Thr Lys Ile Phe Asp Pro Pro	
215 220 225	
acc caa ctt ctg ggt atg aat ggt ctt atc ggt tcg atc ggc aat cct	835
Thr Gln Leu Leu Gly Met Asn Gly Leu Ile Gly Ser Ile Gly Asn Pro	
230 235 240 245	
agt att tcg gcg att gta tgt ctt gtg gtg ggc acc att ctt att ctg	883
Ser Ile Ser Ala Ile Val Cys Leu Val Val Gly Thr Ile Leu Ile Leu	
250 255 260	
att tcg gtg cgt gcc atg agt tct cag atc cga acc att acg gca gcg	931
Ile Ser Val Arg Ala Met Ser Ser Gln Ile Arg Thr Ile Thr Ala Ala	
265 270 275	
acc gta acc tca att atg gac aag gtg atc aat cca gag aac agc ccc	979

Thr Val Thr Ser Ile Met Asp Lys Val Ile Asn Pro Glu Asn Ser Pro
 280 285 290

aag gcg acg att ctt tcc aat ttc tgg agc ttc att ctt gga gtt ttg 1027
 Lys Ala Thr Ile Leu Ser Asn Phe Trp Ser Phe Ile Leu Gly Val Leu
 295 300 305

ttc acg ctc atg gtc act gcc tcg tca gtg acc gtg gct tcc atg cag 1075
 Phe Thr Leu Met Val Thr Ala Ser Ser Val Thr Val Ala Ser Met Gln
 310 315 320 325

cca gtg gct gcc tct ggt gtc gtt aag caa aag cca ttg ctg ggc gtc 1123
 Pro Val Ala Ala Ser Gly Val Val Lys Gln Lys Pro Leu Leu Gly Val
 330 335 340

att ttg ggt gcc aac gtg ggc acc acg gtg acc gca atg ttt gct act 1171
 Ile Leu Gly Ala Asn Val Gly Thr Thr Val Thr Ala Met Phe Ala Thr
 345 350 355

ttc gcg att gtc agc gat cag ggt gag ttc gct att cag gct gcg ttg 1219
 Phe Ala Ile Val Ser Asp Gln Gly Glu Phe Ala Ile Gln Ala Ala Leu
 360 365 370

atc cac ctc att gtg aac ttc acc ggc gca tta cta gtg ctg tgt att 1267
 Ile His Leu Ile Val Asn Phe Thr Gly Ala Leu Leu Val Leu Cys Ile
 375 380 385

ccg cag ctt gcc aat gtg att att cac ttg gcc gag aaa act gcg aac 1315
 Pro Gln Leu Ala Asn Val Ile Ile His Leu Ala Glu Lys Thr Ala Asn
 390 395 400 405

ctc act gcc cgc agt tac 1333
 Leu Thr Ala Arg Ser Tyr
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 <211> 411
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 512
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Pro Pro Ile Pro Glu Arg Lys Gly Pro Ala Ala Ala Phe Leu Pro Gly
 20 25 30

Thr Phe His Pro Ile Asn Pro Lys Asn Ile Ala Ala Ser His Asp Gln
 35 40 45

Val Leu Leu Ser Gly Trp Gly Lys Phe Val Arg Trp Leu Leu Val Leu
 50 55 60

Leu Ser Ile Leu Val Ile Ile Ile Gly Ile Asn Leu Ile Leu Asp Gly
 65 70 75 80

Val Tyr Gly Phe Gly Thr Phe Ser Thr Thr Gln Met Tyr Gln Val Ala
 85 90 95

Lys Asp Pro Leu Ile Gly Val Leu Ile Gly Ile Leu Ala Thr Ala Leu

100					105					110					
Val	Gln	Ser	Ser	Thr	Thr	Thr	Thr	Thr	Leu	Thr	Val	Thr	Ala	Val	Gly
		115						120					125		
Thr	Gly	Ile	Val	Ser	Val	Pro	Val	Ala	Ile	Pro	Ile	Ile	Leu	Gly	Ala
	130					135					140				
Asn	Ile	Gly	Thr	Thr	Ile	Thr	Ala	Met	Leu	Val	Ala	Phe	Ser	Tyr	Val
145					150					155					160
Gly	Glu	Arg	Arg	Glu	Phe	Lys	Arg	Ala	Phe	Thr	Val	Ala	Ala	Met	His
				165					170					175	
Val	Trp	Phe	Asn	Val	Leu	Val	Ile	Leu	Val	Leu	Phe	Val	Val	Glu	Leu
			180					185					190		
Leu	Phe	His	Pro	Phe	Arg	Thr	Ile	Ser	Gly	Ala	Ile	Ala	Thr	Glu	Ile
		195					200					205			
Thr	Leu	Thr	Thr	Gly	Gly	Ser	Leu	Pro	Thr	Ser	Gly	Val	Met	Thr	Lys
	210					215					220				
Ile	Phe	Asp	Pro	Pro	Thr	Gln	Leu	Leu	Gly	Met	Asn	Gly	Leu	Ile	Gly
225					230					235					240
Ser	Ile	Gly	Asn	Pro	Ser	Ile	Ser	Ala	Ile	Val	Cys	Leu	Val	Val	Gly
			245						250					255	
Thr	Ile	Leu	Ile	Leu	Ile	Ser	Val	Arg	Ala	Met	Ser	Ser	Gln	Ile	Arg
		260						265					270		
Thr	Ile	Thr	Ala	Ala	Thr	Val	Thr	Ser	Ile	Met	Asp	Lys	Val	Ile	Asn
	275						280					285			
Pro	Glu	Asn	Ser	Pro	Lys	Ala	Thr	Ile	Leu	Ser	Asn	Phe	Trp	Ser	Phe
	290					295					300				
Ile	Leu	Gly	Val	Leu	Phe	Thr	Leu	Met	Val	Thr	Ala	Ser	Ser	Val	Thr
305					310					315					320
Val	Ala	Ser	Met	Gln	Pro	Val	Ala	Ala	Ser	Gly	Val	Val	Lys	Gln	Lys
				325					330					335	
Pro	Leu	Leu	Gly	Val	Ile	Leu	Gly	Ala	Asn	Val	Gly	Thr	Thr	Val	Thr
		340						345					350		
Ala	Met	Phe	Ala	Thr	Phe	Ala	Ile	Val	Ser	Asp	Gln	Gly	Glu	Phe	Ala
		355					360					365			
Ile	Gln	Ala	Ala	Leu	Ile	His	Leu	Ile	Val	Asn	Phe	Thr	Gly	Ala	Leu
	370					375					380				
Leu	Val	Leu	Cys	Ile	Pro	Gln	Leu	Ala	Asn	Val	Ile	Ile	His	Leu	Ala
385					390					395					400
Glu	Lys	Thr	Ala	Asn	Leu	Thr	Ala	Arg	Ser	Tyr					
				405					410						

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<211> 1440
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1417)
 <223> RXA00941

<400> 513

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                                   Met Asn Leu Thr Arg
                                   1      5

aat gac agg ctc gat cga ctg ccc gta act tcc aaa cat aaa aag att      163
Asn Asp Arg Leu Asp Arg Leu Pro Val Thr Ser Lys His Lys Lys Ile
                                   10      15      20

ctt ggc ggc tca ggt atc ggc tgg gca ttg gat gcc atg gat gtc gga      211
Leu Gly Gly Ser Gly Ile Gly Trp Ala Leu Asp Ala Met Asp Val Gly
                                   25      30      35

ctg atc tct ttc gtc atg gct gcg ttg gcc act cat tgg ggc cta tcc      259
Leu Ile Ser Phe Val Met Ala Leu Ala Thr His Trp Gly Leu Ser
                                   40      45      50

cct act gaa act tcc ctg ctc gga tcc atc ggt ttc gtt ggc atg gcc      307
Pro Thr Glu Thr Ser Leu Leu Gly Ser Ile Gly Phe Val Gly Met Ala
                                   55      60      65

atc ggc gct tcg ctg ggc ggt ttg ctg gcg gac aag ttg ggg cgt cga      355
Ile Gly Ala Ser Leu Gly Gly Leu Leu Ala Asp Lys Leu Gly Arg Arg
                                   70      75      80      85

caa gtt ttt gcg ttg tct ttg cta gtt tat ggc gtt gcc act ggc gcg      403
Gln Val Phe Ala Leu Ser Leu Leu Val Tyr Gly Val Ala Thr Gly Ala
                                   90      95      100

tcg gcg ctt tca gtg tcg ctg gca atg ttg atg gcg ctg cgc ttc gtc      451
Ser Ala Leu Ser Val Ser Leu Ala Met Leu Met Ala Leu Arg Phe Val
                                   105      110      115

gtt gga ctt ggc ctg ggc gct gaa ctc ccc gtt gca tcc act ctg att      499
Val Gly Leu Gly Leu Gly Ala Glu Leu Pro Val Ala Ser Thr Leu Ile
                                   120      125      130

tcc gag ttt tct cca cga aaa gtt cgt ggc cgc atg gtc gtt atc ctg      547
Ser Glu Phe Ser Pro Arg Lys Val Arg Gly Arg Met Val Val Ile Leu
                                   135      140      145

gag gcg ttt tgg gcg ctg ggc tgg atc atg gct gca atc gtc gga acc      595
Glu Ala Phe Trp Ala Leu Gly Trp Ile Met Ala Ala Ile Val Gly Thr
                                   150      155      160      165

ttt gtc gtg gca gga tcc gat aat ggt tgg cgt tgg gcg tta gct ctt      643
Phe Val Val Ala Gly Ser Asp Asn Gly Trp Arg Trp Ala Leu Ala Leu
                                   170      175      180

ggc tgt gtc cct gca att tac gcg gtg tat gtc cgt ctc gga ctt cca      691

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Gly	Cys	Val	Pro	Ala	Ile	Tyr	Ala	Val	Tyr	Val	Arg	Leu	Gly	Leu	Pro	
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gaa	tca	gta	cgt	ttc	ctg	gag	aag	aaa	ggc	cgg	cac	gac	gaa	gca	gaa	739
Glu	Ser	Val	Arg	Phe	Leu	Glu	Lys	Lys	Gly	Arg	His	Asp	Glu	Ala	Glu	
		200					205					210				
gcc	atc	gtt	gtt	tcc	ttc	gaa	gaa	gct	gcc	gct	gcc	gaa	ggt	aaa	gct	787
Ala	Ile	Val	Val	Ser	Phe	Glu	Glu	Ala	Ala	Ala	Ala	Glu	Gly	Lys	Ala	
		215					220					225				
gcc	gat	gcc	acc	acc	gct	gtg	gtt	cat	gac	aac	gct	gcc	gag	ggt	tcc	835
Ala	Asp	Ala	Thr	Thr	Ala	Val	Val	His	Asp	Asn	Ala	Ala	Glu	Gly	Ser	
		230				235				240					245	
gta	tcc	atc	tgg	tca	gct	gct	ttg	cgc	aag	cgc	acc	gtc	gcg	ctg	tgg	883
Val	Ser	Ile	Trp	Ser	Ala	Ala	Leu	Arg	Lys	Arg	Thr	Val	Ala	Leu	Trp	
				250					255					260		
atc	gtg	tgg	ttc	tgc	atc	aac	ttg	tcc	tac	tac	gga	gcc	ttc	att	tgg	931
Ile	Val	Trp	Phe	Cys	Ile	Asn	Leu	Ser	Tyr	Tyr	Gly	Ala	Phe	Ile	Trp	
			265					270					275			
att	cca	tgc	ctg	ctg	gtt	gcc	gac	ggg	ttc	acc	ctc	gtg	aag	tct	ttc	979
Ile	Pro	Ser	Leu	Leu	Val	Ala	Asp	Gly	Phe	Thr	Leu	Val	Lys	Ser	Phe	
		280					285					290				
caa	ttc	act	ctg	atc	atc	acc	ttg	gct	cag	ctt	cca	ggc	tat	gcg	gtt	1027
Gln	Phe	Thr	Leu	Ile	Ile	Thr	Leu	Ala	Gln	Leu	Pro	Gly	Tyr	Ala	Val	
		295					300				305					
gca	gcg	tgg	ttg	att	gaa	aag	tgg	ggc	cgt	cgc	agc	aca	ttg	gcc	acg	1075
Ala	Ala	Trp	Leu	Ile	Glu	Lys	Trp	Gly	Arg	Arg	Ser	Thr	Leu	Ala	Thr	
		310				315				320					325	
ttc	ctg	gtt	ggt	tct	gct	atc	tct	gca	gcg	ctc	tac	ggc	ttg	gca	aat	1123
Phe	Leu	Val	Gly	Ser	Ala	Ile	Ser	Ala	Ala	Leu	Tyr	Gly	Leu	Ala	Asn	
				330					335					340		
gtg	gag	tgg	cag	atc	ctg	gtc	gca	ggg	tgt	tta	cta	tcc	ttc	ttc	aac	1171
Val	Glu	Trp	Gln	Ile	Leu	Val	Ala	Gly	Cys	Leu	Leu	Ser	Phe	Phe	Asn	
			345					350					355			
ctg	ggc	gca	tgg	ggc	gca	ctg	tat	gcc	att	ggg	ccg	gag	ctt	tat	ccc	1219
Leu	Gly	Ala	Trp	Gly	Ala	Leu	Tyr	Ala	Ile	Gly	Pro	Glu	Leu	Tyr	Pro	
		360					365					370				
act	aat	gtc	cgt	gga	act	gga	acg	ggg	gct	gcc	gcg	gga	ttc	ggg	cgc	1267
Thr	Asn	Val	Arg	Gly	Thr	Gly	Thr	Gly	Ala	Ala	Ala	Gly	Phe	Gly	Arg	
		375					380					385				
att	gct	tcc	atc	atc	gct	ccg	ctc	att	gtt	ccg	cca	gtg	att	gct	ttt	1315
Ile	Ala	Ser	Ile	Ile	Ala	Pro	Leu	Ile	Val	Pro	Pro	Val	Ile	Ala	Phe	
		390				395				400					405	
ggg	gga	cca	att	gct	ttg	ttc	gct	ctc	ttt	gcc	acc	gcg	ttt	gcg	atc	1363
Gly	Gly	Pro	Ile	Ala	Leu	Phe	Ala	Leu	Phe	Ala	Thr	Ala	Phe	Ala	Ile	
				410					415					420		
gca	gcg	att	gcg	gcg	ttt	acg	ctg	cct	gag	cag	aag	ggg	aag	tct	ctc	1411
Ala	Ala	Ile	Ala	Ala	Phe	Thr	Leu	Pro	Glu	Gln	Lys	Gly	Lys	Ser	Leu	

425

430

435

gct gat tagtgagatc cttccaccag ttt
Ala Asp

1440

<210> 514

<211> 439

<212> PRT

<213> Corynebacterium glutamicum

<400> 514

Met Asn Leu Thr Arg Asn Asp Arg Leu Asp Arg Leu Pro Val Thr Ser
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Lys His Lys Lys Ile Leu Gly Gly Ser Gly Ile Gly Trp Ala Leu Asp
20 25 30

Ala Met Asp Val Gly Leu Ile Ser Phe Val Met Ala Ala Leu Ala Thr
35 40 45

His Trp Gly Leu Ser Pro Thr Glu Thr Ser Leu Leu Gly Ser Ile Gly
50 55 60

Phe Val Gly Met Ala Ile Gly Ala Ser Leu Gly Gly Leu Leu Ala Asp
65 70 75 80

Lys Leu Gly Arg Arg Gln Val Phe Ala Leu Ser Leu Leu Val Tyr Gly
85 90 95

Val Ala Thr Gly Ala Ser Ala Leu Ser Val Ser Leu Ala Met Leu Met
100 105 110

Ala Leu Arg Phe Val Val Gly Leu Gly Leu Gly Ala Glu Leu Pro Val
115 120 125

Ala Ser Thr Leu Ile Ser Glu Phe Ser Pro Arg Lys Val Arg Gly Arg
130 135 140

Met Val Val Ile Leu Glu Ala Phe Trp Ala Leu Gly Trp Ile Met Ala
145 150 155 160

Ala Ile Val Gly Thr Phe Val Val Ala Gly Ser Asp Asn Gly Trp Arg
165 170 175

Trp Ala Leu Ala Leu Gly Cys Val Pro Ala Ile Tyr Ala Val Tyr Val
180 185 190

Arg Leu Gly Leu Pro Glu Ser Val Arg Phe Leu Glu Lys Lys Gly Arg
195 200 205

His Asp Glu Ala Glu Ala Ile Val Val Ser Phe Glu Glu Ala Ala Ala
210 215 220

Ala Glu Gly Lys Ala Ala Asp Ala Thr Thr Ala Val Val His Asp Asn
225 230 235 240

Ala Ala Glu Gly Ser Val Ser Ile Trp Ser Ala Ala Leu Arg Lys Arg
245 250 255

<210> 515
<211> 1704
<212> DNA
<213> *Corynebacterium glutamicum*

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ttaagcaagg gagtgaatta cagaaaagga ttgttcagca atg agc aca cct gac    115
                                         Met Ser Thr Pro Asp
                                           1           5

att aaa gaa ggc tcg gca gaa tca ccg ggc gaa gta atg gtc gtt gga    163
Ile Lys Glu Gly Ser Ala Glu Ser Pro Gly Glu Val Met Val Val Gly
                        10                      15                     20

gac agg cga gag tgg cgt cga caa gca acc ggc atc att gcc ggc ctc    211
Asp Arg Arg   Glu Trp Arg Arg Gln Ala Thr Gly Ile Ile  Ala Gly Leu
                    25                30                 35
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gtc tta gcc gcc ctg gtc tat ctt ctc ttc ccc tcg aac tcc gtg gaa Val Leu Ala Ala Leu Val Tyr Leu Leu Phe Pro Ser Asn Ser Val Glu	259
40 45 50	
acc gtc atg caa tcc agt ggc gtc gat cca gaa act gaa tac acc aac Thr Val Met Gln Ser Ser Gly Val Asp Pro Glu Thr Glu Tyr Thr Asn	307
55 60 65	
aac gcg atg cgt ctt act gct gca gtc aca atc ttg atg gca gtg tgg Asn Ala Met Arg Leu Thr Ala Ala Val Thr Ile Leu Met Ala Val Trp	355
70 75 80 85	
tgg atg aca gaa gca atc cca cta gca gca acc gca ctt atc ccg ttg Trp Met Thr Glu Ala Ile Pro Leu Ala Ala Thr Ala Leu Ile Pro Leu	403
90 95 100	
gtt gca ttc cct gct ttc cag gtt gtg gac ttt ggg aag gca aca gct Val Ala Phe Pro Ala Phe Gln Val Val Asp Phe Gly Lys Ala Thr Ala	451
105 110 115	
ccg tat gcc aac cct acg agc ttc ctc ttc ttg ggc ggc ttt ctt atg Pro Tyr Ala Asn Pro Thr Ser Phe Leu Phe Leu Gly Gly Phe Leu Met	499
120 125 130	
gca ctt ggc ctg cag aaa tgg aac cta cac cga cgt atg gct cta gcg Ala Leu Gly Leu Gln Lys Trp Asn Leu His Arg Arg Met Ala Leu Ala	547
135 140 145	
gtc gtg cta gct gtt ggt act aag cca aag caa ttg gtc ttg ggt ttt Val Val Leu Ala Val Gly Thr Lys Pro Lys Gln Leu Val Leu Gly Phe	595
150 155 160 165	
atg gtg gca act gga ttt ttg tcc atg tgg gtg tct aac act gca acg Met Val Ala Thr Gly Phe Leu Ser Met Trp Val Ser Asn Thr Ala Thr	643
170 175 180	
gcc gtg gtt atg tta ccg atc ggt atg tcg gta ctg gca ctg acc gct Ala Val Val Met Leu Pro Ile Gly Met Ser Val Leu Ala Leu Thr Ala	691
185 190 195	
gag act gtg ggc gga atg aaa aac caa aag aaa ttc gcc act gga ctc Glu Thr Val Gly Gly Met Lys Asn Gln Lys Lys Phe Ala Thr Gly Leu	739
200 205 210	
atg ctg tcc att gct tat tct gct tcc atc ggt tca ctc ggc acc tta Met Leu Ser Ile Ala Tyr Ser Ala Ser Ile Gly Ser Leu Gly Thr Leu	787
215 220 225	
att ggc acg cca ccc aat gcc ttg ctt gct gcg tat atg tct gaa tcg Ile Gly Thr Pro Pro Asn Ala Leu Leu Ala Ala Tyr Met Ser Glu Ser	835
230 235 240 245	
cat gat atc cac atc gga ttt ggt cag tgg atg att ctt ggt gta cca His Asp Ile His Ile Gly Phe Gly Gln Trp Met Ile Leu Gly Val Pro	883
250 255 260	
att gct gtc gtc ttc acc atc atc gcg tgg ctt gtg ttg acc acc gtg Ile Ala Val Val Phe Thr Ile Ile Ala Trp Leu Val Leu Thr Thr Val	931
265 270 275	

ttc aag cca gaa atg aaa gaa atc cct ggc gga cgt gaa ctg atc aaa	979
Phe Lys Pro Glu Met Lys Glu Ile Pro Gly Gly Arg Glu Leu Ile Lys	
280 285 290	
cggt gaa atc gct gaa atg ggg ccg tgg act gca cct cag gtc aca gtg	1027
Arg Glu Ile Ala Glu Met Gly Pro Trp Thr Ala Pro Gln Val Thr Val	
295 300 305	
gggt gtt att ttt gcg gca gct gca ctg gct tgg gtc ttc att cca tta	1075
Gly Val Ile Phe Ala Ala Ala Leu Ala Trp Val Phe Ile Pro Leu	
310 315 320 325	
act cta gat tgg acc ggt tcc cag ctc tct atc aat gac tcc ctc att	1123
Thr Leu Asp Trp Thr Gly Ser Gln Leu Ser Ile Asn Asp Ser Leu Ile	
330 335 340	
ggc atc gct gcc ggc ctg ctg atg ttt atc gtt ccc gct aac ttt aaa	1171
Gly Ile Ala Ala Gly Leu Leu Met Phe Ile Val Pro Ala Asn Phe Lys	
345 350 355	
acc ggc gaa cgc att ctt gat tgg cgt act gca ggc gaa ctt cca tgg	1219
Thr Gly Glu Arg Ile Leu Asp Trp Arg Thr Ala Gly Glu Leu Pro Trp	
360 365 370	
gat gtt ctc ttg ctt ttt ggt ggc ggg ctt tca ctt tct gcg atg ttt	1267
Asp Val Leu Leu Leu Phe Gly Gly Leu Ser Leu Ser Ala Met Phe	
375 380 385	
acc agc acg gga ctt tcc cta tgg atc ggt gaa cta gct aag gga ctt	1315
Thr Ser Thr Gly Leu Ser Leu Trp Ile Gly Glu Leu Ala Lys Gly Leu	
390 395 400 405	
gat gcc ctt cca atc ttc att ctc atc ttc gcc att gct gtc ctg gtg	1363
Asp Ala Leu Pro Ile Phe Ile Leu Ile Phe Ala Ile Ala Val Leu Val	
410 415 420	
ttg ttc ctg acc gag ttc acc tcc aac acc gca aca gcg gca acc ttc	1411
Leu Phe Leu Thr Glu Phe Thr Ser Asn Thr Ala Thr Ala Ala Thr Phe	
425 430 435	
ctg cca atc atg ggt ggc gtc gcc gta ggt atc gga ctg acc gca ggt	1459
Leu Pro Ile Met Gly Gly Val Ala Val Gly Ile Gly Leu Thr Ala Gly	
440 445 450	
ggc gag cag aat gtt ctg ctg ctg acc atc cca gtc gca ctg tcc gca	1507
Gly Glu Gln Asn Val Leu Leu Leu Thr Ile Pro Val Ala Leu Ser Ala	
455 460 465	
acc tgt gcg ttc atg ctt cca gtg gca acg cct cca aac gcg att gca	1555
Thr Cys Ala Phe Met Leu Pro Val Ala Thr Pro Pro Asn Ala Ile Ala	
470 475 480 485	
ttc ggc tcc ggc tac att aag atc ggc gaa atg gtc aag ggt ggt ctg	1603
Phe Gly Ser Gly Tyr Ile Lys Ile Gly Glu Met Val Lys Gly Gly Leu	
490 495 500	
tgg ctg aac atc atc gca gtc atc ctc att acg att ttc acc tac ttc	1651
Trp Leu Asn Ile Ile Ala Val Ile Leu Ile Thr Ile Phe Thr Tyr Phe	
505 510 515	
gta gcg atc cca ctc ttt ggc atc atg ctt taaaagttaa caggcccgca	1701

Val Ala Ile Pro Leu Phe Gly Ile Met Leu
 520 525

gtc

1704

<210> 516
 <211> 527
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 516

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Ile Ile Ala Gly Leu Val Leu Ala Ala Leu Val Tyr Leu Leu Phe Pro
 35 40 45

Ser Asn Ser Val Glu Thr Val Met Gln Ser Ser Gly Val Asp Pro Glu
 50 55 60

Thr Glu Tyr Thr Asn Asn Ala Met Arg Leu Thr Ala Ala Val Thr Ile
 65 70 75 80

Leu Met Ala Val Trp Trp Met Thr Glu Ala Ile Pro Leu Ala Ala Thr
 85 90 95

Ala Leu Ile Pro Leu Val Ala Phe Pro Ala Phe Gln Val Val Asp Phe
 100 105 110

Gly Lys Ala Thr Ala Pro Tyr Ala Asn Pro Thr Ser Phe Leu Phe Leu
 115 120 125

Gly Gly Phe Leu Met Ala Leu Gly Leu Gln Lys Trp Asn Leu His Arg
 130 135 140

Arg Met Ala Leu Ala Val Val Leu Ala Val Gly Thr Lys Pro Lys Gln
 145 150 155 160

Leu Val Leu Gly Phe Met Val Ala Thr Gly Phe Leu Ser Met Trp Val
 165 170 175

Ser Asn Thr Ala Thr Ala Val Val Met Leu Pro Ile Gly Met Ser Val
 180 185 190

Leu Ala Leu Thr Ala Glu Thr Val Gly Gly Met Lys Asn Gln Lys Lys
 195 200 205

Phe Ala Thr Gly Leu Met Leu Ser Ile Ala Tyr Ser Ala Ser Ile Gly
 210 215 220

Ser Leu Gly Thr Leu Ile Gly Thr Pro Pro Asn Ala Leu Leu Ala Ala
 225 230 235 240

Tyr Met Ser Glu Ser His Asp Ile His Ile Gly Phe Gly Gln Trp Met
 245 250 255

Ile Leu Gly Val Pro Ile Ala Val Val Phe Thr Ile Ile Ala Trp Leu

260					265					270					
Val	Leu	Thr	Thr	Val	Phe	Lys	Pro	Glu	Met	Lys	Glu	Ile	Pro	Gly	Gly
	275						280					285			
Arg	Glu	Leu	Ile	Lys	Arg	Glu	Ile	Ala	Glu	Met	Gly	Pro	Trp	Thr	Ala
	290					295					300				
Pro	Gln	Val	Thr	Val	Gly	Val	Ile	Phe	Ala	Ala	Ala	Ala	Leu	Ala	Trp
	305					310					315				320
Val	Phe	Ile	Pro	Leu	Thr	Leu	Asp	Trp	Thr	Gly	Ser	Gln	Leu	Ser	Ile
			325						330					335	
Asn	Asp	Ser	Leu	Ile	Gly	Ile	Ala	Ala	Gly	Leu	Leu	Met	Phe	Ile	Val
			340					345					350		
Pro	Ala	Asn	Phe	Lys	Thr	Gly	Glu	Arg	Ile	Leu	Asp	Trp	Arg	Thr	Ala
		355					360					365			
Gly	Glu	Leu	Pro	Trp	Asp	Val	Leu	Leu	Leu	Phe	Gly	Gly	Gly	Leu	Ser
	370					375					380				
Leu	Ser	Ala	Met	Phe	Thr	Ser	Thr	Gly	Leu	Ser	Leu	Trp	Ile	Gly	Glu
	385					390					395				400
Leu	Ala	Lys	Gly	Leu	Asp	Ala	Leu	Pro	Ile	Phe	Ile	Leu	Ile	Phe	Ala
			405						410					415	
Ile	Ala	Val	Leu	Val	Leu	Phe	Leu	Thr	Glu	Phe	Thr	Ser	Asn	Thr	Ala
			420					425					430		
Thr	Ala	Ala	Thr	Phe	Leu	Pro	Ile	Met	Gly	Gly	Val	Ala	Val	Gly	Ile
			435				440					445			
Gly	Leu	Thr	Ala	Gly	Gly	Glu	Gln	Asn	Val	Leu	Leu	Leu	Thr	Ile	Pro
	450					455					460				
Val	Ala	Leu	Ser	Ala	Thr	Cys	Ala	Phe	Met	Leu	Pro	Val	Ala	Thr	Pro
	465					470					475				480
Pro	Asn	Ala	Ile	Ala	Phe	Gly	Ser	Gly	Tyr	Ile	Lys	Ile	Gly	Glu	Met
			485						490					495	
Val	Lys	Gly	Gly	Leu	Trp	Leu	Asn	Ile	Ile	Ala	Val	Ile	Leu	Ile	Thr
			500					505					510		
Ile	Phe	Thr	Tyr	Phe	Val	Ala	Ile	Pro	Leu	Phe	Gly	Ile	Met	Leu	
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<211> 1028

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1005)

<223> FRXA00449

<400> 517

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ttc gcc act gga ctc atg ctg tcc att gct tat tct gct tcc atc ggt	96
Phe Ala Thr Gly Leu Met Leu Ser Ile Ala Tyr Ser Ala Ser Ile Gly	
20 25 30	
tca ctc ggc acc tta att ggc acg cca ccc aat gcc ttg ctt gct gcg	144
Ser Leu Gly Thr Leu Ile Gly Thr Pro Pro Asn Ala Leu Leu Ala Ala	
35 40 45	
tat atg tct gaa tcg cat gat atc cac atc gga ttt ggt cag tgg atg	192
Tyr Met Ser Glu Ser His Asp Ile His Ile Gly Phe Gly Gln Trp Met	
50 55 60	
att ctt ggt gta cca att gct gtc gtc ttc acc atc atc gcg tgg ctt	240
Ile Leu Gly Val Pro Ile Ala Val Val Phe Thr Ile Ile Ala Trp Leu	
65 70 75 80	
gtg ttg acc acc gtg ttc aag cca gaa atg aaa gaa atc cct ggc gga	288
Val Leu Thr Thr Val Phe Lys Pro Glu Met Lys Glu Ile Pro Gly Gly	
85 90 95	
cgt gaa ctg atc aaa cgt gaa atc gct gaa atg ggg ccg tgg act gca	336
Arg Glu Leu Ile Lys Arg Glu Ile Ala Glu Met Gly Pro Trp Thr Ala	
100 105 110	
cct cag gtc aca gtg ggt gtt att ttt gcg gca gct gca ctg gct tgg	384
Pro Gln Val Thr Val Gly Val Ile Phe Ala Ala Ala Ala Leu Ala Trp	
115 120 125	
gtc ttc att cca tta act cta gat tgg acc ggt tcc cag ctc tct atc	432
Val Phe Ile Pro Leu Thr Leu Asp Trp Thr Gly Ser Gln Leu Ser Ile	
130 135 140	
aat gac tcc ctc att ggc atc gct gcc ggc ctg ctg atg ttt atc gtt	480
Asn Asp Ser Leu Ile Gly Ile Ala Ala Gly Leu Leu Met Phe Ile Val	
145 150 155 160	
ccc gct aac ttt aaa acc ggc gaa cgc att ctt gat tgg cgt act gca	528
Pro Ala Asn Phe Lys Thr Gly Glu Arg Ile Leu Asp Trp Arg Thr Ala	
165 170 175	
ggc gaa ctt cca tgg gat gtt ctc ttg ctt ttt ggt ggc ggg ctt tca	576
Gly Glu Leu Pro Trp Asp Val Leu Leu Leu Phe Gly Gly Gly Leu Ser	
180 185 190	
ctt tct gcg atg ttt acc agc acg gga ctt tcc cta tgg atc ggt gaa	624
Leu Ser Ala Met Phe Thr Ser Thr Gly Leu Ser Leu Trp Ile Gly Glu	
195 200 205	
cta gct aag gga ctt gat gcc ctt cca atc ttc att ctc atc ttc gcc	672
Leu Ala Lys Gly Leu Asp Ala Leu Pro Ile Phe Ile Leu Ile Phe Ala	
210 215 220	
att gct gtc ctg gtg ttg ttc ctg acc gag ttc acc tcc aac acc gca	720
Ile Ala Val Leu Val Leu Phe Leu Thr Glu Phe Thr Ser Asn Thr Ala	
225 230 235 240	

aca gcg gca acc ttc ctg cca atc atg ggt ggc gtc gcc gta ggt atc 768
 Thr Ala Ala Thr Phe Leu Pro Ile Met Gly Gly Val Ala Val Gly Ile
 245 250 255
 gga ctg acc gca ggt ggc gag cag aat gtt ctg ctg ctg acc atc cca 816
 Gly Leu Thr Ala Gly Gly Glu Gln Asn Val Leu Leu Leu Thr Ile Pro
 260 265 270
 gtc gca ctg tcc gca acc tgt gcg ttc atg ctt cca gtg gca acg cct 864
 Val Ala Leu Ser Ala Thr Cys Ala Phe Met Leu Pro Val Ala Thr Pro
 275 280 285
 cca aac gcg att gca ttc ggc tcc ggc tac att aag atc ggc gaa atg 912
 Pro Asn Ala Ile Ala Phe Gly Ser Gly Tyr Ile Lys Ile Gly Glu Met
 290 295 300
 gtc aag ggt ggt ctg tgg ctg aac atc atc gca gtc atc ctc att acg 960
 Val Lys Gly Gly Leu Trp Leu Asn Ile Ile Ala Val Ile Leu Ile Thr
 305 310 315 320
 att ttc acc tac ttc gta gcg atc cca ctc ttt ggc atc atg ctt 1005
 Ile Phe Thr Tyr Phe Val Ala Ile Pro Leu Phe Gly Ile Met Leu
 325 330 335
 taaaagttaa caggcccgca gtc 1028

<210> 518
 <211> 335
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 518
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 Phe Ala Thr Gly Leu Met Leu Ser Ile Ala Tyr Ser Ala Ser Ile Gly
 20 25 30
 Ser Leu Gly Thr Leu Ile Gly Thr Pro Pro Asn Ala Leu Leu Ala Ala
 35 40 45
 Tyr Met Ser Glu Ser His Asp Ile His Ile Gly Phe Gly Gln Trp Met
 50 55 60
 Ile Leu Gly Val Pro Ile Ala Val Val Phe Thr Ile Ile Ala Trp Leu
 65 70 75 80
 Val Leu Thr Thr Val Phe Lys Pro Glu Met Lys Glu Ile Pro Gly Gly
 85 90 95
 Arg Glu Leu Ile Lys Arg Glu Ile Ala Glu Met Gly Pro Trp Thr Ala
 100 105 110
 Pro Gln Val Thr Val Gly Val Ile Phe Ala Ala Ala Ala Leu Ala Trp
 115 120 125
 Val Phe Ile Pro Leu Thr Leu Asp Trp Thr Gly Ser Gln Leu Ser Ile
 130 135 140
 Asn Asp Ser Leu Ile Gly Ile Ala Ala Gly Leu Leu Met Phe Ile Val

145	150								155								160			
Pro	Ala	Asn	Phe	Lys	Thr	Gly	Glu	Arg	Ile	Leu	Asp	Trp	Arg	Thr	Ala					
				165					170					175						
Gly	Glu	Leu	Pro	Trp	Asp	Val	Leu	Leu	Leu	Phe	Gly	Gly	Gly	Leu	Ser					
			180					185					190							
Leu	Ser	Ala	Met	Phe	Thr	Ser	Thr	Gly	Leu	Ser	Leu	Trp	Ile	Gly	Glu					
		195					200					205								
Leu	Ala	Lys	Gly	Leu	Asp	Ala	Leu	Pro	Ile	Phe	Ile	Leu	Ile	Phe	Ala					
	210					215					220									
Ile	Ala	Val	Leu	Val	Leu	Phe	Leu	Thr	Glu	Phe	Thr	Ser	Asn	Thr	Ala					
225					230					235					240					
Thr	Ala	Ala	Thr	Phe	Leu	Pro	Ile	Met	Gly	Gly	Val	Ala	Val	Gly	Ile					
				245					250					255						
Gly	Leu	Thr	Ala	Gly	Gly	Glu	Gln	Asn	Val	Leu	Leu	Leu	Thr	Ile	Pro					
			260					265					270							
Val	Ala	Leu	Ser	Ala	Thr	Cys	Ala	Phe	Met	Leu	Pro	Val	Ala	Thr	Pro					
		275					280					285								
Pro	Asn	Ala	Ile	Ala	Phe	Gly	Ser	Gly	Tyr	Ile	Lys	Ile	Gly	Glu	Met					
	290					295					300									
Val	Lys	Gly	Gly	Leu	Trp	Leu	Asn	Ile	Ile	Ala	Val	Ile	Leu	Ile	Thr					
305					310					315					320					
Ile	Phe	Thr	Tyr	Phe	Val	Ala	Ile	Pro	Leu	Phe	Gly	Ile	Met	Leu						
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<210> 519
<211> 448
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS  
<222> (101)..(448)  
<223> FRXA01755
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ttaagcaagg gagtgaatta cagaaaagga ttgttcagca atg agc aca cct gac    115
                                     Met Ser Thr Pro Asp
                                           1           5

att aaa gaa ggc tcg gca gaa tca ccg ggc gaa gta atg gtc gtt gga    163
Ile Lys Glu Gly Ser Ala Glu Ser Pro Gly Glu Val Met Val Val Gly
                        10                      15                    20

gac agg cga gag tgg cgt cga caa gca acc ggc atc att gcc ggc ctc    211
Asp Arg Arg Glu Trp Arg Arg Gln Ala Thr Gly Ile Ile Ala Gly Leu
                        25                      30                    35
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gtc tta gcc gcc ctg gtc tat ctt ctc ttc ccc tcg aac tcc gtg gaa 259
Val Leu Ala Ala Leu Val Tyr Leu Leu Phe Pro Ser Asn Ser Val Glu
      40                      45                      50

acc gtc atg caa tcc agt ggc gtc gat cca gaa act gaa tac acc aac 307
Thr Val Met Gln Ser Ser Gly Val Asp Pro Glu Thr Glu Tyr Thr Asn
      55                      60                      65

aac gcg atg cgt ctt act gct gca gtc aca atc ttg atg gca gtg tgg 355
Asn Ala Met Arg Leu Thr Ala Ala Val Thr Ile Leu Met Ala Val Trp
      70                      75                      80                      85

tgg atg aca gaa gca atc cca cta gca gca acc gca ctt atc ccg ttg 403
Trp Met Thr Glu Ala Ile Pro Leu Ala Ala Thr Ala Leu Ile Pro Leu
      90                      95                      100

gtt gca ttc cct gct ttc cag gtt gtg gac ttt ggg aag gca gca 448
Val Ala Phe Pro Ala Phe Gln Val Val Asp Phe Gly Lys Ala Ala
      105                      110                      115

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<210> 520
 <211> 116
 <212> PRT
 <213> Corynebacterium glutamicum

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Val Met Val Val Gly Asp Arg Arg Glu Trp Arg Arg Gln Ala Thr Gly
      20              25              30

Ile Ile Ala Gly Leu Val Leu Ala Ala Leu Val Tyr Leu Leu Phe Pro
      35              40              45

Ser Asn Ser Val Glu Thr Val Met Gln Ser Ser Gly Val Asp Pro Glu
      50              55              60

Thr Glu Tyr Thr Asn Asn Ala Met Arg Leu Thr Ala Ala Val Thr Ile
      65              70              75              80

Leu Met Ala Val Trp Trp Met Thr Glu Ala Ile Pro Leu Ala Ala Thr
      85              90              95

Ala Leu Ile Pro Leu Val Ala Phe Pro Ala Phe Gln Val Val Asp Phe
      100              105              110

Gly Lys Ala Ala
      115

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<210> 521
 <211> 912
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(889)
 <223> RXA00269

<400> 521

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accgaagcct aagcaaccag tagcagtggg ggcttaagac atg tta tcc atc aac 115
Met Leu Ser Ile Asn
1 5

gga att tct aag acg ttc ttc ccc ggc act gtg aat gag cgc cgc gcg 163
Gly Ile Ser Lys Thr Phe Phe Pro Gly Thr Val Asn Glu Arg Arg Ala
10 15 20

ttg cag cag ctc aaa ctc gat atg gct gag ggc gat ttt gtc acc gtc 211
Leu Gln Gln Leu Lys Leu Asp Met Ala Glu Gly Asp Phe Val Thr Val
25 30 35

atc ggt tct aac ggt gcg ggt aaa tcc acg ctg ctc aac gct gtt tct 259
Ile Gly Ser Asn Gly Ala Gly Lys Ser Thr Leu Leu Asn Ala Val Ser
40 45 50

ggc cgt ttg ctt gtt gat tcc ggc gag att tcc atc gac ggc aac aag 307
Gly Arg Leu Leu Val Asp Ser Gly Glu Ile Ser Ile Asp Gly Asn Lys
55 60 65

gta aac aag atg tca gag cac aag cgt gcc cgc tac atc ggc cgc gtt 355
Val Asn Lys Met Ser Glu His Lys Arg Ala Arg Tyr Ile Gly Arg Val
70 75 80 85

ttc cag gat cct ctg gcc ggc acc gcg ccg aat ctc acc att gaa gag 403
Phe Gln Asp Pro Leu Ala Gly Thr Ala Pro Asn Leu Thr Ile Glu Glu
90 95 100

aat ctg gcc atc gcg ttg ctg cgc ggc aag cgc cgt gga ttg ggc ttt 451
Asn Leu Ala Ile Ala Leu Leu Arg Gly Lys Arg Arg Gly Leu Gly Phe
105 110 115

gca ctg acc tcg aag cgc cgt gag caa ttc aag cag gaa ctt gag cgc 499
Ala Leu Thr Ser Lys Arg Arg Glu Gln Phe Lys Gln Glu Leu Glu Arg
120 125 130

ctt gag ctg ggt ctg gaa aac agg ctc act gcc aaa gtt ggt ttg ctc 547
Leu Glu Leu Gly Leu Glu Asn Arg Leu Thr Ala Lys Val Gly Leu Leu
135 140 145

tct ggc ggt cag cgt cag gca ttg tcc ctg ctg atg gct ggt ttt act 595
Ser Gly Gly Gln Arg Gln Ala Leu Ser Leu Met Ala Gly Phe Thr
150 155 160 165

caa cct aaa atc atg ctg ttg gat gag cac acc gca gcg ctt gat cca 643
Gln Pro Lys Ile Met Leu Leu Asp Glu His Thr Ala Ala Leu Asp Pro
170 175 180

cag cgt gca gag ctt gtg acc acc ttg acc gaa aag atc gtg gca gat 691
Gln Arg Ala Glu Leu Val Thr Thr Leu Thr Glu Lys Ile Val Ala Asp
185 190 195

gga aat ctg act acg ctt atg gtc acg cac aac atg gaa cag gca att 739
Gly Asn Leu Thr Thr Leu Met Val Thr His Asn Met Glu Gln Ala Ile
200 205 210

cgc ctg ggc aat cgc ctg atc atg atg cat gaa ggc cag att gtc tac 787

Arg Leu Gly Asn Arg Leu Ile Met Met His Glu Gly Gln Ile Val Tyr
 215 220 225

cag gca gat cag gct acc aag tcg aag ttg act gtg cgc gat ttg ctg 835
 Gln Ala Asp Gln Ala Thr Lys Ser Lys Leu Thr Val Arg Asp Leu Leu
 230 235 240 245

cag gag ttc gcc aac atc aag ggc gca aca ttg tct gac aag gcg ttc 883
 Gln Glu Phe Ala Asn Ile Lys Gly Ala Thr Leu Ser Asp Lys Ala Phe
 250 255 260

ctc ggc taaaaagagc ttgctttacg acg 912
 Leu Gly

<210> 522

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 522

Met Leu Ser Ile Asn Gly Ile Ser Lys Thr Phe Phe Pro Gly Thr Val
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Asn Glu Arg Arg Ala Leu Gln Gln Leu Lys Leu Asp Met Ala Glu Gly
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Asp Phe Val Thr Val Ile Gly Ser Asn Gly Ala Gly Lys Ser Thr Leu
 35 40 45

Leu Asn Ala Val Ser Gly Arg Leu Leu Val Asp Ser Gly Glu Ile Ser
 50 55 60

Ile Asp Gly Asn Lys Val Asn Lys Met Ser Glu His Lys Arg Ala Arg
 65 70 75 80

Tyr Ile Gly Arg Val Phe Gln Asp Pro Leu Ala Gly Thr Ala Pro Asn
 85 90 95

Leu Thr Ile Glu Glu Asn Leu Ala Ile Ala Leu Leu Arg Gly Lys Arg
 100 105 110

Arg Gly Leu Gly Phe Ala Leu Thr Ser Lys Arg Arg Glu Gln Phe Lys
 115 120 125

Gln Glu Leu Glu Arg Leu Glu Leu Gly Leu Glu Asn Arg Leu Thr Ala
 130 135 140

Lys Val Gly Leu Leu Ser Gly Gly Gln Arg Gln Ala Leu Ser Leu Leu
 145 150 155 160

Met Ala Gly Phe Thr Gln Pro Lys Ile Met Leu Leu Asp Glu His Thr
 165 170 175

Ala Ala Leu Asp Pro Gln Arg Ala Glu Leu Val Thr Thr Leu Thr Glu
 180 185 190

Lys Ile Val Ala Asp Gly Asn Leu Thr Thr Leu Met Val Thr His Asn
 195 200 205

Met Glu Gln Ala Ile Arg Leu Gly Asn Arg Leu Ile Met Met His Glu
 210 215 220

Gly Gln Ile Val Tyr Gln Ala Asp Gln Ala Thr Lys Ser Lys Leu Thr
 225 230 235 240

Val Arg Asp Leu Leu Gln Glu Phe Ala Asn Ile Lys Gly Ala Thr Leu
 245 250 255

Ser Asp Lys Ala Phe Leu Gly
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<210> 523

<211> 817

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(817)

<223> RXA00369

<400> 523

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ggcgctcgcg ttgacgggtgc gcagccagaa ggagtttttag gtg tca tcg atc aaa 115
 Val Ser Ser Ile Lys
 1 5

ttg cgc gat tta agc gtg agc ttc cgc gac gga acc ttc ggg ctg caa 163
 Leu Arg Asp Leu Ser Val Ser Phe Arg Asp Gly Thr Phe Gly Leu Gln
 10 15 20

gat atc aat ttg aaa att gag ccg gaa gaa ttt gtg gtg ctc atc ggg 211
 Asp Ile Asn Leu Lys Ile Glu Pro Glu Glu Phe Val Val Leu Ile Gly
 25 30 35

ccg tcg ggg tcc ggt aaa acc acc atg ttg ggc acc atc gcg ggg ttt 259
 Pro Ser Gly Ser Gly Lys Thr Thr Met Leu Gly Thr Ile Ala Gly Phe
 40 45 50

gtg gag cca agt tcc ggc agt gtg ctc atc gcc ggc gaa gaa atg acg 307
 Val Glu Pro Ser Ser Gly Ser Val Leu Ile Ala Gly Glu Glu Met Thr
 55 60 65

cat gtc ccg ccg gag cgc cgt cgc atg ggc atg gtg ttt cag cag cat 355
 His Val Pro Pro Glu Arg Arg Arg Met Gly Met Val Phe Gln Gln His
 70 75 80 85

gcg gtg tgg ccg cat atg tcg gtc gcc aag aat gtg gga tac ccg ctg 403
 Ala Val Trp Pro His Met Ser Val Ala Lys Asn Val Gly Tyr Pro Leu
 90 95 100

gcg cga agt ggt cag aag ggg gcg tcg ata agc aaa cgc gtg gag cgc 451
 Ala Arg Ser Gly Gln Lys Gly Ala Ser Ile Ser Lys Arg Val Glu Arg
 105 110 115

acg ctc gcg ctg gtg ggg ctt gag ggg ttc ggc agt cgc aga ccg gcc 499
 Thr Leu Ala Leu Val Gly Leu Glu Gly Phe Gly Ser Arg Arg Pro Ala
 120 125 130

agc ctg tct ggt ggt caa cgt cag cgg gtg gcg ctt gcg cgc gcc atc 547
 Ser Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Leu Ala Arg Ala Ile
 135 140 145

 atc gcc gac ccc acc gtg ctg ctt ctc gac gag gcc ctc tcc gcc ctc 595
 Ile Ala Asp Pro Thr Val Leu Leu Leu Asp Glu Ala Leu Ser Ala Leu
 150 155 160 165

 gac gaa ccg ctg cga gac gct tta cga cgc gaa ctc gta tct ttg acc 643
 Asp Glu Pro Leu Arg Asp Ala Leu Arg Arg Glu Leu Val Ser Leu Thr
 170 175 180

 cgg cgc gaa ggc ctc act act gtg cac gtg acg cat gac cgc gcc gaa 691
 Arg Arg Glu Gly Leu Thr Thr Val His Val Thr His Asp Arg Ala Glu
 185 190 195

 gcg atc tcc atc gct gac cgc atc gtc gta ctc ggc aac ggt cga atc 739
 Ala Ile Ser Ile Ala Asp Arg Ile Val Val Leu Gly Asn Gly Arg Ile
 200 205 210

 caa cag gta gcc acc cct act gag ctc ctt tcc gcc ccc gct act gcc 787
 Gln Gln Val Ala Thr Pro Thr Glu Leu Leu Ser Ala Pro Ala Thr Ala
 215 220 225

 gat gtt gcc cga ttc atc gtc gac gcc acc 817
 Asp Val Ala Arg Phe Ile Val Asp Ala Thr
 230 235

<210> 524

<211> 239

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 524

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 Thr Phe Gly Leu Gln Asp Ile Asn Leu Lys Ile Glu Pro Glu Glu Phe
 20 25 30

 Val Val Leu Ile Gly Pro Ser Gly Ser Gly Lys Thr Thr Met Leu Gly
 35 40 45

 Thr Ile Ala Gly Phe Val Glu Pro Ser Ser Gly Ser Val Leu Ile Ala
 50 55 60

 Gly Glu Glu Met Thr His Val Pro Pro Glu Arg Arg Arg Met Gly Met
 65 70 75 80

 Val Phe Gln Gln His Ala Val Trp Pro His Met Ser Val Ala Lys Asn
 85 90 95

 Val Gly Tyr Pro Leu Ala Arg Ser Gly Gln Lys Gly Ala Ser Ile Ser
 100 105 110

 Lys Arg Val Glu Arg Thr Leu Ala Leu Val Gly Leu Glu Gly Phe Gly
 115 120 125

 Ser Arg Arg Pro Ala Ser Leu Ser Gly Gly Gln Arg Gln Arg Val Ala

130				135				140							
Leu 145	Ala	Arg	Ala	Ile	Ile 150	Ala	Asp	Pro	Thr	Val 155	Leu	Leu	Leu	Asp	Glu 160
Ala	Leu	Ser	Ala	Leu 165	Asp	Glu	Pro	Leu	Arg 170	Asp	Ala	Leu	Arg	Arg 175	Glu
Leu	Val	Ser	Leu 180	Thr	Arg	Arg	Glu	Gly 185	Leu	Thr	Thr	Val	His 190	Val	Thr
His	Asp	Arg 195	Ala	Glu	Ala	Ile	Ser 200	Ile	Ala	Asp	Arg	Ile 205	Val	Val	Leu
Gly 210	Asn	Gly	Arg	Ile	Gln 215	Gln	Val	Ala	Thr	Pro	Thr 220	Glu	Leu	Leu	Ser
Ala 225	Pro	Ala	Thr	Ala	Asp 230	Val	Ala	Arg	Phe	Ile 235	Val	Asp	Ala	Thr	

<210> 525
<211> 1653
<212> DNA
<213> *Corynebacterium glutamicum*

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<223> RXA02073
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												Met	Ile	Ser	Arg	Leu
												1				5
ctc caa ttg gct aag aaa gta tgg ccg gaa ctt gga gcc tcc acg ctc															163	
Leu	Gln	Leu	Ala	Lys	Lys	Val	Trp	Pro	Glu	Leu	Gly	Ala	Ser	Thr	Leu	
				10					15					20		
ctg cga ctg ctc aat cag cta ctc acc gca gca ctc att gtg ttc ccc															211	
Leu	Arg	Leu	Leu	Asn	Gln	Leu	Leu	Thr	Ala	Ala	Leu	Ile	Val	Phe	Pro	
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gcc tgg gtg cta agc cgc aaa cca gac atc tcc ctg ctc gcc gtc gcc															259	
Ala	Trp	Val	Leu	Ser	Arg	Lys	Pro	Asp	Ile	Ser	Leu	Leu	Ala	Val	Ala	
		40					45					50				
atc atc atg gcg ctc atc gcg ctg aca gca gct gtc tgt cgc tgg ggt															307	
Ile	Ile	Met	Ala	Leu	Ile	Ala	Leu	Thr	Ala	Ala	Val	Cys	Arg	Trp	Gly	
	55					60					65					
gag cag gta tgc ggc cac cgc gct gcc ttt ggg ctg ctt gcc cac atg															355	
Glu	Gln	Val	Cys	Gly	His	Arg	Ala	Ala	Phe	Gly	Leu	Leu	Ala	His	Met	
70					75					80				85		
cgc gtt atg ctt tac gac gcc ctc gtc cac aaa ggt tcc ccc tcg ccg															403	
Arg	Val	Met	Leu	Tyr	Asp	Ala	Leu	Val	His	Lys	Gly	Ser	Pro	Ser	Pro	
				90					95					100		

atc cac ggc agc ggt tcg atc atg tct gtt gcc acc cgt gac att aac	451
Ile His Gly Ser Gly Ser Ile Met Ser Val Ala Thr Arg Asp Ile Asn	
105 110 115	
tcc atc gaa gta ttc ttc gcg cac acc att ggg cct aca gtc acc gca	499
Ser Ile Glu Val Phe Phe Ala His Thr Ile Gly Pro Thr Val Thr Ala	
120 125 130	
gtg ctg ctc agt gcg gga ggc gtg atc acg ctg gca acg ctc gat ccc	547
Val Leu Leu Ser Ala Gly Gly Val Ile Thr Leu Ala Thr Leu Asp Pro	
135 140 145	
gtt gct ggt cta att ggt tta ctc ggt gtc ctc atc gcg tgg ttg atc	595
Val Ala Gly Leu Ile Gly Leu Leu Gly Val Leu Ile Ala Trp Leu Ile	
150 155 160 165	
ccc ttg att gga aaa caa tcc tca agc agt gaa gcc aca tca cgt gga	643
Pro Leu Ile Gly Lys Gln Ser Ser Ser Ser Glu Ala Thr Ser Arg Gly	
170 175 180	
cac atc gcc cag cac ctc acc gaa gat gcc gcc ggc agg ctt gaa atc	691
His Ile Ala Gln His Leu Thr Glu Asp Ala Ala Gly Arg Leu Glu Ile	
185 190 195	
aac tca cat gga gcg caa gcc aca cgg tta aat gcg ctc gag gtg aaa	739
Asn Ser His Gly Ala Gln Ala Thr Arg Leu Asn Ala Leu Glu Val Lys	
200 205 210	
gag caa caa ctg gaa caa gtt gtg acc cga cag ggc ttg atc gtc ggt	787
Glu Gln Gln Leu Glu Gln Val Val Thr Arg Gln Gly Leu Ile Val Gly	
215 220 225	
atc cgt cag ggc gca gca ctt tta tgg ccg tgg ata tca gct gtg ttg	835
Ile Arg Gln Gly Ala Ala Leu Leu Trp Pro Trp Ile Ser Ala Val Leu	
230 235 240 245	
ttg gtt gct ctg gtt cct cat gtg ggc att gtt gca gcc gcg att atc	883
Leu Val Ala Leu Val Pro His Val Gly Ile Val Ala Ala Ala Ile Ile	
250 255 260	
ctg ggc atc tcc cct gcg ttg gat gca gtt gag gga ttt gct cgc acc	931
Leu Gly Ile Ser Pro Ala Leu Asp Ala Val Glu Gly Phe Ala Arg Thr	
265 270 275	
atg cct acc gcg tta aac agt gcg cag cgg tat ttc cag atc atc gat	979
Met Pro Thr Ala Leu Asn Ser Ala Gln Arg Tyr Phe Gln Ile Ile Asp	
280 285 290	
gcc cct gtt gct atc gct gaa cct gac gag ccg aag cct ttg ccc aaa	1027
Ala Pro Val Ala Ile Ala Glu Pro Asp Glu Pro Lys Pro Leu Pro Lys	
295 300 305	
ggc ccg ctt aag ctg cga att tct aga gtt cca gtc agc gca aag ggc	1075
Gly Pro Leu Lys Leu Arg Ile Ser Arg Val Pro Val Ser Ala Lys Gly	
310 315 320 325	
acc gtg tct tta gag gtt gca gct ggt gaa cac atc ggc atc atc gga	1123
Thr Val Ser Leu Glu Val Ala Ala Gly Glu His Ile Gly Ile Ile Gly	
330 335 340	

tcc agc ggt agt gga aaa tcc act ttg gcc aaa ctc atc ctc aag ctg 1171
 Ser Ser Gly Ser Gly Lys Ser Thr Leu Ala Lys Leu Ile Leu Lys Leu
 345 350 355

gcg caa cta cgg tct gga acc atc acc atc ggt ggt gtt gat atc gca 1219
 Ala Gln Leu Arg Ser Gly Thr Ile Thr Ile Gly Gly Val Asp Ile Ala
 360 365 370

gag gtt tca tcg gcg gag ctt cgc aaa tcc gtc acg ctg gtt gag cag 1267
 Glu Val Ser Ser Ala Glu Leu Arg Lys Ser Val Thr Leu Val Glu Gln
 375 380 385

aaa tct gtg ctg ttt aga gca agc gtg ctg gag aat tta cgg atg ggc 1315
 Lys Ser Val Leu Phe Arg Ala Ser Val Leu Glu Asn Leu Arg Met Gly
 390 395 400 405

aat cca gag ctg tct gaa gat gaa gca agg gaa gcc ttg agg ttg gcg 1363
 Asn Pro Glu Leu Ser Glu Asp Glu Ala Arg Glu Ala Leu Arg Leu Ala
 410 415 420

tcg ata agc gaa ctg cct tta gat gct gac gcc ctg cgc cta tct ggc 1411
 Ser Ile Ser Glu Leu Pro Leu Asp Ala Asp Ala Leu Arg Leu Ser Gly
 425 430 435

gga cag caa caa cgg ctc tgc ctg gcg cgt gct ttg gca cgc acc cct 1459
 Gly Gln Gln Gln Arg Leu Cys Leu Ala Arg Ala Leu Ala Arg Thr Pro
 440 445 450

cag gta ctg att gtc gat gaa gcc acc agc cac caa gat gcg ctc aat 1507
 Gln Val Leu Ile Val Asp Glu Ala Thr Ser His Gln Asp Ala Leu Asn
 455 460 465

caa gcg gat ctt tcc cag act ctg gcc acg ctt aaa gac acc acg gtg 1555
 Gln Ala Asp Leu Ser Gln Thr Leu Ala Thr Leu Lys Asp Thr Thr Val
 470 475 480 485

atc atc att gcg cac cgc aca gct gca tta acc cat gtg gat cgg ata 1603
 Ile Ile Ile Ala His Arg Thr Ala Ala Leu Thr His Val Asp Arg Ile
 490 495 500

att gac ctg gaa gaa atc aaa aat ccc tgatccttaa cgcggatcag 1650
 Ile Asp Leu Glu Glu Ile Lys Asn Pro
 505 510

ggg 1653

<210> 526

<211> 510

<212> PRT

<213> Corynebacterium glutamicum

<400> 526

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Gly Ala Ser Thr Leu Leu Arg Leu Leu Asn Gln Leu Leu Thr Ala Ala
 20 25 30

Leu Ile Val Phe Pro Ala Trp Val Leu Ser Arg Lys Pro Asp Ile Ser
 35 40 45

Leu Leu Ala Val Ala Ile Ile Met Ala Leu Ile Ala Leu Thr Ala Ala
 50 55 60
 Val Cys Arg Trp Gly Glu Gln Val Cys Gly His Arg Ala Ala Phe Gly
 65 70 75 80
 Leu Leu Ala His Met Arg Val Met Leu Tyr Asp Ala Leu Val His Lys
 85 90 95
 Gly Ser Pro Ser Pro Ile His Gly Ser Gly Ser Ile Met Ser Val Ala
 100 105 110
 Thr Arg Asp Ile Asn Ser Ile Glu Val Phe Phe Ala His Thr Ile Gly
 115 120 125
 Pro Thr Val Thr Ala Val Leu Leu Ser Ala Gly Gly Val Ile Thr Leu
 130 135 140
 Ala Thr Leu Asp Pro Val Ala Gly Leu Ile Gly Leu Leu Gly Val Leu
 145 150 155 160
 Ile Ala Trp Leu Ile Pro Leu Ile Gly Lys Gln Ser Ser Ser Ser Glu
 165 170 175
 Ala Thr Ser Arg Gly His Ile Ala Gln His Leu Thr Glu Asp Ala Ala
 180 185 190
 Gly Arg Leu Glu Ile Asn Ser His Gly Ala Gln Ala Thr Arg Leu Asn
 195 200 205
 Ala Leu Glu Val Lys Glu Gln Gln Leu Glu Gln Val Val Thr Arg Gln
 210 215 220
 Gly Leu Ile Val Gly Ile Arg Gln Gly Ala Ala Leu Leu Trp Pro Trp
 225 230 235 240
 Ile Ser Ala Val Leu Leu Val Ala Leu Val Pro His Val Gly Ile Val
 245 250 255
 Ala Ala Ala Ile Ile Leu Gly Ile Ser Pro Ala Leu Asp Ala Val Glu
 260 265 270
 Gly Phe Ala Arg Thr Met Pro Thr Ala Leu Asn Ser Ala Gln Arg Tyr
 275 280 285
 Phe Gln Ile Ile Asp Ala Pro Val Ala Ile Ala Glu Pro Asp Glu Pro
 290 295 300
 Lys Pro Leu Pro Lys Gly Pro Leu Lys Leu Arg Ile Ser Arg Val Pro
 305 310 315 320
 Val Ser Ala Lys Gly Thr Val Ser Leu Glu Val Ala Ala Gly Glu His
 325 330 335
 Ile Gly Ile Ile Gly Ser Ser Gly Ser Gly Lys Ser Thr Leu Ala Lys
 340 345 350
 Leu Ile Leu Lys Leu Ala Gln Leu Arg Ser Gly Thr Ile Thr Ile Gly
 355 360 365

Gly Val Asp Ile Ala Glu Val Ser Ser Ala Glu Leu Arg Lys Ser Val
 370 375 380

Thr Leu Val Glu Gln Lys Ser Val Leu Phe Arg Ala Ser Val Leu Glu
 385 390 395 400

Asn Leu Arg Met Gly Asn Pro Glu Leu Ser Glu Asp Glu Ala Arg Glu
 405 410 415

Ala Leu Arg Leu Ala Ser Ile Ser Glu Leu Pro Leu Asp Ala Asp Ala
 420 425 430

Leu Arg Leu Ser Gly Gly Gln Gln Gln Arg Leu Cys Leu Ala Arg Ala
 435 440 445

Leu Ala Arg Thr Pro Gln Val Leu Ile Val Asp Glu Ala Thr Ser His
 450 455 460

Gln Asp Ala Leu Asn Gln Ala Asp Leu Ser Gln Thr Leu Ala Thr Leu
 465 470 475 480

Lys Asp Thr Thr Val Ile Ile Ile Ala His Arg Thr Ala Ala Leu Thr
 485 490 495

His Val Asp Arg Ile Ile Asp Leu Glu Glu Ile Lys Asn Pro
 500 505 510

<210> 527

<211> 1142

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1119)

<223> RXA01399

<400> 527

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gct gca att atc cct ccc ctg ctt gct gct cgc gga gtt aaa aca gcc	96
Ala Ala Ile Ile Pro Pro Leu Leu Ala Ala Arg Gly Val Lys Thr Ala	
20 25 30	
gaa gcc cgg cgc gct gaa tcc agc gaa gcc tac ttg agt tcc ttg gat	144
Glu Ala Arg Arg Ala Glu Ser Ser Glu Ala Tyr Leu Ser Ser Leu Asp	
35 40 45	
cag gtg ctg tcc aac cag gcg gcg ctt cgt gtt cgt ggt gaa atg ccg	192
Gln Val Leu Ser Asn Gln Ala Ala Leu Arg Val Arg Gly Glu Met Pro	
50 55 60	
gcc gct ctg tcc aag gcg gat gtg gct gcg cgt tcc tat tct tct tca	240
Ala Ala Leu Ser Lys Ala Asp Val Ala Ala Arg Ser Tyr Ser Ser Ser	
65 70 75 80	
ctg gag gca ggc gcg aaa gac act gcc att gcc gca gcg agt tcc ctg	288
Leu Glu Ala Gly Ala Lys Asp Thr Ala Ile Gly Ala Ala Ser Ser Leu	

85										90										95									
tgg	att	cac	ggt	ttc	act	gtc	att	ggt	gtg	ctc	atg	ggt	tcc	gcg	tca														336
Trp	Ile	His	Gly	Phe	Thr	Val	Ile	Gly	Val	Leu	Met	Val	Ser	Ala	Ser														
			100						105				110																
ctg	tat	gca	gat	gga	agc	cat	tca	ccg	cag	tgg	ttt	ggt	gtg	ttg	gtg														384
Leu	Tyr	Ala	Asp	Gly	Ser	His	Ser	Pro	Gln	Trp	Phe	Gly	Val	Leu	Val														
			115					120					125																
ctg	ctt	tca	ctc	gca	gct	ttc	gag	gct	gtc	tct	ggt	ctc	ccc	gat	gct														432
Leu	Leu	Ser	Leu	Ala	Ala	Phe	Glu	Ala	Val	Ser	Val	Leu	Pro	Asp	Ala														
			130				135						140																
gcg	att	gct	cgt	acc	cgc	gcc	gca	gat	gcc	acc	agg	agg	ctt	gcg	gaa														480
Ala	Ile	Ala	Arg	Thr	Arg	Ala	Ala	Asp	Ala	Thr	Arg	Arg	Leu	Ala	Glu														
						150				155					160														
atc	tcg	gcg	ctg	cca	gaa	tct	gtc	tct	ctt	gag	ctt	cgc	acg	gcc	tct														528
Ile	Ser	Ala	Leu	Pro	Glu	Ser	Val	Ser	Leu	Glu	Leu	Arg	Thr	Ala	Ser														
				165					170					175															
gac	cag	ccc	gta	tta	cgc	gcc	gag	aat	cta	ggt	tat	gga	tgg	gac	agc														576
Asp	Gln	Pro	Val	Leu	Arg	Ala	Glu	Asn	Leu	Val	Tyr	Gly	Trp	Asp	Ser														
			180					185					190																
gac	cta	ggc	acg	agc	aac	ctg	gat	ctc	acc	ttt	ggt	tca	cga	cat	gaa														624
Asp	Leu	Gly	Thr	Ser	Asn	Leu	Asp	Leu	Thr	Phe	Gly	Ser	Arg	His	Glu														
			195				200					205																	
atc	atc	gca	ccc	tct	gga	act	ggc	aaa	acg	acc	ctg	ctg	ctc	aca	ctt														672
Ile	Ile	Ala	Pro	Ser	Gly	Thr	Gly	Lys	Thr	Thr	Leu	Leu	Leu	Thr	Leu														
			210				215					220																	
gcg	ggg	ctg	ttg	gaa	cct	cgt	gga	ggc	caa	gtg	ctt	atc	gac	ggc	acc														720
Ala	Gly	Leu	Leu	Glu	Pro	Arg	Gly	Gly	Gln	Val	Leu	Ile	Asp	Gly	Thr														
			225				230			235				240															
aat	cct	tcc	gag	ttg	aaa	aac	gcc	gtg	ctg	ttc	agt	cca	gaa	gat	gcc														768
Asn	Pro	Ser	Glu	Leu	Lys	Asn	Ala	Val	Leu	Phe	Ser	Pro	Glu	Asp	Ala														
				245				250					255																
cac	att	ttt	ggc	acc	act	gtc	cga	gat	aac	tta	gca	ctc	gga	gca	ccg														816
His	Ile	Phe	Ala	Thr	Thr	Val	Arg	Asp	Asn	Leu	Ala	Leu	Gly	Ala	Pro														
			260					265					270																
gaa	gca	acc	gac	gcg	gaa	atg	aca	tcg	atc	ctg	gaa	cat	ggt	ggt	ttg														864
Glu	Ala	Thr	Asp	Ala	Glu	Met	Thr	Ser	Ile	Leu	Glu	His	Val	Gly	Leu														
			275				280					285																	
tca	gag	tgg	ggt	caa	ggt	tta	ccc	gat	ggt	ctt	ggc	act	gtc	ctt	gat														912
Ser	Glu	Trp	Val	Gln	Gly	Leu	Pro	Asp	Gly	Leu	Gly	Thr	Val	Leu	Asp														
			290				295					300																	
tca	ggt	ggc	gat	agt	ctc	tcg	gga	ggt	cag	cgc	cgc	cgc	ctg	ctc	ctt														960
Ser	Gly	Ala	Asp	Ser	Leu	Ser	Gly	Gly	Gln	Arg	Arg	Arg	Leu	Leu	Leu														
			305				310			315					320														
gcc	cgc	gta	cta	cta	agt	gat	gca	cca	att	ctg	ctt	ttg	gat	gaa	ccc														1008
Ala	Arg	Val	Leu	Leu	Ser	Asp	Ala	Pro	Ile	Leu	Leu	Leu	Asp	Glu	Pro														
				325				330						335															

acc gag cac ctc gac act gca ggc tcc tct gaa atc ttg tct atg ctg 1056
 Thr Glu His Leu Asp Thr Ala Gly Ser Ser Glu Ile Leu Ser Met Leu
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gcc tcc gat gaa ctc cct ggt aaa aga gct agg aga acc gta gtg att 1104
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<210> 528

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 528

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Gln Val Leu Ser Asn Gln Ala Ala Leu Arg Val Arg Gly Glu Met Pro
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Ala Ala Leu Ser Lys Ala Asp Val Ala Ala Arg Ser Tyr Ser Ser Ser
 65 70 75 80

Leu Glu Ala Gly Ala Lys Asp Thr Ala Ile Gly Ala Ala Ser Ser Leu
 85 90 95

Trp Ile His Gly Phe Thr Val Ile Gly Val Leu Met Val Ser Ala Ser
 100 105 110

Leu Tyr Ala Asp Gly Ser His Ser Pro Gln Trp Phe Gly Val Leu Val
 115 120 125

Leu Leu Ser Leu Ala Ala Phe Glu Ala Val Ser Val Leu Pro Asp Ala
 130 135 140

Ala Ile Ala Arg Thr Arg Ala Ala Asp Ala Thr Arg Arg Leu Ala Glu
 145 150 155 160

Ile Ser Ala Leu Pro Glu Ser Val Ser Leu Glu Leu Arg Thr Ala Ser
 165 170 175

Asp Gln Pro Val Leu Arg Ala Glu Asn Leu Val Tyr Gly Trp Asp Ser
 180 185 190

Asp Leu Gly Thr Ser Asn Leu Asp Leu Thr Phe Gly Ser Arg His Glu
 195 200 205

Ile Ile Ala Pro Ser Gly Thr Gly Lys Thr Thr Leu Leu Leu Thr Leu
 210 215 220

Ala Gly Leu Leu Glu Pro Arg Gly Gly Gln Val Leu Ile Asp Gly Thr
225 230 235 240

Asn Pro Ser Glu Leu Lys Asn Ala Val Leu Phe Ser Pro Glu Asp Ala
245 250 255

His Ile Phe Ala Thr Thr Val Arg Asp Asn Leu Ala Leu Gly Ala Pro
260 265 270

Glu Ala Thr Asp Ala Glu Met Thr Ser Ile Leu Glu His Val Gly Leu
275 280 285

Ser Glu Trp Val Gln Gly Leu Pro Asp Gly Leu Gly Thr Val Leu Asp
290 295 300

Ser Gly Ala Asp Ser Leu Ser Gly Gly Gln Arg Arg Arg Leu Leu Leu
305 310 315 320

Ala Arg Val Leu Leu Ser Asp Ala Pro Ile Leu Leu Leu Asp Glu Pro
325 330 335

Thr Glu His Leu Asp Thr Ala Gly Ser Ser Glu Ile Leu Ser Met Leu
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Val Arg His Val Arg
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<211> 1368

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1345)

<223> RXA01339

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Met Thr Thr Glu Ser
1 5

ata gtt gcg cac aat gct gca ggt aca gca cct cag aat gtg tcc tct 163
Ile Val Ala His Asn Ala Ala Gly Thr Ala Pro Gln Asn Val Ser Ser
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gct aag aag aag tac ctc agc gtt gcc caa ggc gtt gcc ctt atc tac 211
Ala Lys Lys Lys Tyr Leu Ser Val Ala Gln Gly Val Ala Leu Ile Tyr
25 30 35

gga acc aac atc ggc gcc ggt gtg ctc agc ctc cca tac gct gcc cgc 259
Gly Thr Asn Ile Gly Ala Gly Val Leu Ser Leu Pro Tyr Ala Ala Arg
40 45 50

aac ggt ggt ttc ctc gcc ctg gtt gtt gcc ctg ctc att gcg gga aca	307
Asn Gly Gly Phe Leu Ala Leu Val Val Ala Leu Leu Ile Ala Gly Thr	
55 60 65	
ctg acc acc atc tcc atg ctc tac atc gcc gaa gta tcc ctg cgc acc	355
Leu Thr Thr Ile Ser Met Leu Tyr Ile Ala Glu Val Ser Leu Arg Thr	
70 75 80 85	
aag aag cca ctg cag ctt tcc ggc ctg gca gaa aaa tac ctg ggg cag	403
Lys Lys Pro Leu Gln Leu Ser Gly Leu Ala Glu Lys Tyr Leu Gly Gln	
90 95 100	
tgg ggc cgc tgg ctg gtg ttc att gcc att gtg gtc aac agc gtg ggt	451
Trp Gly Arg Trp Leu Val Phe Ile Ala Ile Val Val Asn Ser Val Gly	
105 110 115	
gca ctg att gcc tac gca tca gga tcc ggc att ttg ata ggc aac ctc	499
Ala Leu Ile Ala Tyr Ala Ser Gly Ser Gly Ile Leu Ile Gly Asn Leu	
120 125 130	
acc ggc ctg cca cca atc gtg ggc acc ctt gga ttc ttt gtt tta ggc	547
Thr Gly Leu Pro Pro Ile Val Gly Thr Leu Gly Phe Phe Val Leu Gly	
135 140 145	
acc ttg atc atg tgg aaa ggc ctg cac acg gca agc ttc gtg gag gca	595
Thr Leu Ile Met Trp Lys Gly Leu His Thr Ala Ser Phe Val Glu Ala	
150 155 160 165	
ttg atc acc act ggc atg gca acg atc atc atc gtg ctg tgt gga tgg	643
Leu Ile Thr Thr Gly Met Ala Thr Ile Ile Ile Val Leu Cys Gly Trp	
170 175 180	
aca gtg ctt ggc cct gga att tcc gca gac aac ctg atc gtg ttc cac	691
Thr Val Leu Gly Pro Gly Ile Ser Ala Asp Asn Leu Ile Val Phe His	
185 190 195	
cca ttc ttc atc gtt ccg atc atg aac ctc gcg gtc ttt acc ttc ctt	739
Pro Phe Phe Ile Val Pro Ile Met Asn Leu Ala Val Phe Thr Phe Leu	
200 205 210	
gcc caa tat gtg gtt cca gaa atc gca cga gga gtt aac cct gcc acc	787
Ala Gln Tyr Val Val Pro Glu Ile Ala Arg Gly Val Asn Pro Ala Thr	
215 220 225	
ccg aag gca gtg cca cgc gcg atc atc atc gcc atg gtc gca act ggt	835
Pro Lys Ala Val Pro Arg Ala Ile Ile Ile Gly Met Val Ala Thr Gly	
230 235 240 245	
gtc acc ctg gca gct gta cca ttc gcg gca cta ggg ctt ctg ggc aca	883
Val Thr Leu Ala Ala Val Pro Phe Ala Ala Leu Gly Leu Leu Gly Thr	
250 255 260	
ggc gtc agt gaa gtt gtc acc atc tcc tgg ggc gaa gca ctc gcc cca	931
Gly Val Ser Glu Val Val Thr Ile Ser Trp Gly Glu Ala Leu Ala Pro	
265 270 275	
gtg gcc tat tac atg gcc aat gcc ttc gca cta ttg gcc atg ttc act	979
Val Ala Tyr Tyr Met Ala Asn Ala Phe Ala Leu Leu Ala Met Phe Thr	
280 285 290	
tca ttc atc gcc att gga ttc acc gcg atg cgc aac gta cta gat att	1027

Ser Phe Ile Ala Ile Gly Phe Thr Ala Met Arg Asn Val Leu Asp Ile
 295 300 305

ggc cac tgg cca caa cac gga tgg cag cga tcc gtt gct gtc gga cta 1075
 Gly His Trp Pro Gln His Gly Trp Gln Arg Ser Val Ala Val Gly Leu
 310 315 320 325

act gtt ctt cca cca ctg gca att tca ctt gcg gga tta ggc gga ttc 1123
 Thr Val Leu Pro Pro Leu Ala Ile Ser Leu Ala Gly Leu Gly Gly Phe
 330 335 340

gtg gca gca ctg agc tac gcc gga gga ttt gcc gga gca atc atg tcc 1171
 Val Ala Ala Leu Ser Tyr Ala Gly Gly Phe Ala Gly Ala Ile Met Ser
 345 350 355

atc atc ccc gtg ctg ttg ctg cgc aac tcc cgc aag agt ggc gac caa 1219
 Ile Ile Pro Val Leu Leu Leu Arg Asn Ser Arg Lys Ser Gly Asp Gln
 360 365 370

gaa cca gtg tgg aaa gcc acc tgg caa gcg cac ccc atc ttc cag atc 1267
 Glu Pro Val Trp Lys Ala Thr Trp Gln Ala His Pro Ile Phe Gln Ile
 375 380 385

ctg ttg att gtg gtg tac tcc ctg gcg ttt gtg tac tcg gtt ctc gcg 1315
 Leu Leu Ile Val Val Tyr Ser Leu Ala Phe Val Tyr Ser Val Leu Ala
 390 395 400 405

atc gtc gga tta atg cct gcg ggt tgg gca tagtcacttc ctgttggtggc 1365
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<212> PRT

<213> Corynebacterium glutamicum

<400> 530

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Gln Asn Val Ser Ser Ala Lys Lys Lys Tyr Leu Ser Val Ala Gln Gly
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Val Ala Leu Ile Tyr Gly Thr Asn Ile Gly Ala Gly Val Leu Ser Leu
 35 40 45

Pro Tyr Ala Ala Arg Asn Gly Gly Phe Leu Ala Leu Val Val Ala Leu
 50 55 60

Leu Ile Ala Gly Thr Leu Thr Thr Ile Ser Met Leu Tyr Ile Ala Glu
 65 70 75 80

Val Ser Leu Arg Thr Lys Lys Pro Leu Gln Leu Ser Gly Leu Ala Glu
 85 90 95

Lys Tyr Leu Gly Gln Trp Gly Arg Trp Leu Val Phe Ile Ala Ile Val
 100 105 110

Val Asn Ser Val Gly Ala Leu Ile Ala Tyr Ala Ser Gly Ser Gly Ile
 115 120 125
 Leu Ile Gly Asn Leu Thr Gly Leu Pro Pro Ile Val Gly Thr Leu Gly
 130 135 140
 Phe Phe Val Leu Gly Thr Leu Ile Met Trp Lys Gly Leu His Thr Ala
 145 150 155 160
 Ser Phe Val Glu Ala Leu Ile Thr Thr Gly Met Ala Thr Ile Ile Ile
 165 170 175
 Val Leu Cys Gly Trp Thr Val Leu Gly Pro Gly Ile Ser Ala Asp Asn
 180 185 190
 Leu Ile Val Phe His Pro Phe Phe Ile Val Pro Ile Met Asn Leu Ala
 195 200 205
 Val Phe Thr Phe Leu Ala Gln Tyr Val Val Pro Glu Ile Ala Arg Gly
 210 215 220
 Val Asn Pro Ala Thr Pro Lys Ala Val Pro Arg Ala Ile Ile Ile Gly
 225 230 235 240
 Met Val Ala Thr Gly Val Thr Leu Ala Ala Val Pro Phe Ala Ala Leu
 245 250 255
 Gly Leu Leu Gly Thr Gly Val Ser Glu Val Val Thr Ile Ser Trp Gly
 260 265 270
 Glu Ala Leu Ala Pro Val Ala Tyr Tyr Met Ala Asn Ala Phe Ala Leu
 275 280 285
 Leu Ala Met Phe Thr Ser Phe Ile Ala Ile Gly Phe Thr Ala Met Arg
 290 295 300
 Asn Val Leu Asp Ile Gly His Trp Pro Gln His Gly Trp Gln Arg Ser
 305 310 315 320
 Val Ala Val Gly Leu Thr Val Leu Pro Pro Leu Ala Ile Ser Leu Ala
 325 330 335
 Gly Leu Gly Gly Phe Val Ala Ala Leu Ser Tyr Ala Gly Gly Phe Ala
 340 345 350
 Gly Ala Ile Met Ser Ile Ile Pro Val Leu Leu Leu Arg Asn Ser Arg
 355 360 365
 Lys Ser Gly Asp Gln Glu Pro Val Trp Lys Ala Thr Trp Gln Ala His
 370 375 380
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 <212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1429)

<223> RXA02527

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Ile	Ala	Thr	Ile	Val	Ala	Ile	Ile	Leu	Lys	Pro	Met	Pro	Met	Gly	Ala	
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gtg	aca	att	atc	ggc	atg	atc	gcc	gcg	gtg	ttg	act	ggt	ttg	gtg	ccg	211
Val	Thr	Ile	Ile	Gly	Met	Ile	Ala	Ala	Val	Leu	Thr	Gly	Leu	Val	Pro	
				25				30					35			

ttg	acg	gcg	tct	tct	gat	gat	ccc	ggc	gcg	gtg	tat	ggc	ctt	att	ggt	259
Leu	Thr	Ala	Ser	Ser	Asp	Asp	Pro	Gly	Ala	Val	Tyr	Gly	Leu	Ile	Gly	
			40				45					50				

ttc	agt	aac	ggc	acc	att	tgg	ctg	att	gtg	atg	gcg	ttc	ctg	att	tcg	307
Phe	Ser	Asn	Gly	Thr	Ile	Trp	Leu	Ile	Val	Met	Ala	Phe	Leu	Ile	Ser	
	55					60				65						

cgt	gga	ttc	atc	aag	acg	ggg	ctt	gga	cgt	cga	ata	gcg	ttg	ttc	ttt	355
Arg	Gly	Phe	Ile	Lys	Thr	Gly	Leu	Gly	Arg	Arg	Ile	Ala	Leu	Phe	Phe	
70				75					80					85		

gtg	tct	aaa	gtc	ggc	gga	aaa	atg	ctg	ggt	gtg	acc	tat	ggt	ttg	gcg	403
Val	Ser	Lys	Val	Gly	Gly	Lys	Met	Leu	Gly	Val	Thr	Tyr	Gly	Leu	Ala	
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ctc	gct	gat	ttg	gtg	ttg	gct	cct	gcg	att	cca	tca	gca	act	gcc	cga	451
Leu	Ala	Asp	Leu	Val	Leu	Ala	Pro	Ala	Ile	Pro	Ser	Ala	Thr	Ala	Arg	
			105				110						115			

ggt	ggt	ggc	att	atg	gct	ccg	att	atg	aag	tcg	gtg	gca	ttg	act	tat	499
Gly	Gly	Gly	Ile	Met	Ala	Pro	Ile	Met	Lys	Ser	Val	Ala	Leu	Thr	Tyr	
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gat	tcc	act	cct	ggc	cca	act	cgt	cgc	agg	gct	ggc	gcg	ttc	ttg	gcg	547
Asp	Ser	Thr	Pro	Gly	Pro	Thr	Arg	Arg	Arg	Ala	Gly	Ala	Phe	Leu	Ala	
	135					140					145					

ctg	aat	gtg	gga	cag	gta	aat	gcg	att	acg	tgc	gcg	atg	ttt	cta	act	595
Leu	Asn	Val	Gly	Gln	Val	Asn	Ala	Ile	Thr	Cys	Ala	Met	Phe	Leu	Thr	
150				155					160					165		

gca	atg	gca	gga	aac	ccc	ttg	atc	gcc	tct	ttg	gct	tcg	cag	atg	gat	643
Ala	Met	Ala	Gly	Asn	Pro	Leu	Ile	Ala	Ser	Leu	Ala	Ser	Gln	Met	Asp	
				170				175						180		

gtc	aat	atc	acg	tgg	aca	aac	tgg	gct	gtg	ggt	gcg	att	gtg	cct	ggt	691
Val	Asn	Ile	Thr	Trp	Thr	Asn	Trp	Ala	Val	Gly	Ala	Ile	Val	Pro	Gly	
	185						190						195			

ctg gtg gcg ctt att gtg gtg ccg tgg gtg gta tac aag atc tat cca	739
Leu Val Ala Leu Ile Val Val Pro Trp Val Val Tyr Lys Ile Tyr Pro	
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cct gag ttg aag gac acc cct gag gtc aag aaa atg gct tct gat gag	787
Pro Glu Leu Lys Asp Thr Pro Glu Val Lys Lys Met Ala Ser Asp Glu	
215 220 225	
ctc aag caa ttg ggt ggg ttt act tat ggt gag aag gtg ctg gcg gga	835
Leu Lys Gln Leu Gly Gly Phe Thr Tyr Gly Glu Lys Val Leu Ala Gly	
230 235 240 245	
acc ttt gtt gtg ttg ctg ctg ctc tgg aca ggt ggc gat ttg gtc ttg	883
Thr Phe Val Val Leu Leu Leu Trp Thr Gly Gly Asp Leu Val Leu	
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gga atc tcg gca act acc acc gct ttc gtt ggc gtc atc atc ttg cta	931
Gly Ile Ser Ala Thr Thr Thr Ala Phe Val Gly Val Ile Ile Leu Leu	
265 270 275	
gtg gct cac gtg ctg acg tgg gag gac atc att caa gaa aag act gcg	979
Val Ala His Val Leu Thr Trp Glu Asp Ile Ile Gln Glu Lys Thr Ala	
280 285 290	
tgg gac acc atg gtg tgg ttc gcg gtg cta tac atg atg gca aca gcg	1027
Trp Asp Thr Met Val Trp Phe Ala Val Leu Tyr Met Met Ala Thr Ala	
295 300 305	
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Leu Ser Gln Tyr Gly Phe Ile Ala Trp Ile Ser Glu Val Ile Ala Ser	
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Ser Leu Gly Gly Met Asn Trp Val Val Ala Leu Val Val Leu Val Leu	
330 335 340	
att tac ttc ttc agt cac tat ttc ttt gcc tcg gca aca gcg cat att	1171
Ile Tyr Phe Phe Ser His Tyr Phe Phe Ala Ser Ala Thr Ala His Ile	
345 350 355	
tct gcg atg tac ttg gcc ttc ctg ggt gct gcg att gcg att ggt gca	1219
Ser Ala Met Tyr Leu Ala Phe Leu Gly Ala Ala Ile Ala Ile Gly Ala	
360 365 370	
ccc ccg ttg atg gcg gcc ctg gtg ttg gcg tac acc tcc aat ttg ttc	1267
Pro Pro Leu Met Ala Ala Leu Val Leu Ala Tyr Thr Ser Asn Leu Phe	
375 380 385	
tct tca ctc act cag tat tct ggt ggt cct tcg cca aca ttg ttt ggt	1315
Ser Ser Leu Thr Gln Tyr Ser Gly Gly Pro Ser Pro Thr Leu Phe Gly	
390 395 400 405	
ttg aac tac atc acg gtg ggt gag tgg tgg cgg acc tcg gca att gct	1363
Leu Asn Tyr Ile Thr Val Gly Glu Trp Trp Arg Thr Ser Ala Ile Ala	
410 415 420	
ggc gcg gta tcg att aca atc tgg ttg gtt atc ggt ggt ttg tgg atg	1411
Gly Ala Val Ser Ile Thr Ile Trp Leu Val Ile Gly Gly Leu Trp Met	
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 Asn Val Ile Gly Leu Trp
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1452

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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Tyr Gly Leu Ile Gly Phe Ser Asn Gly Thr Ile Trp Leu Ile Val Met
 50 55 60
 Ala Phe Leu Ile Ser Arg Gly Phe Ile Lys Thr Gly Leu Gly Arg Arg
 65 70 75 80
 Ile Ala Leu Phe Phe Val Ser Lys Val Gly Gly Lys Met Leu Gly Val
 85 90 95
 Thr Tyr Gly Leu Ala Leu Ala Asp Leu Val Leu Ala Pro Ala Ile Pro
 100 105 110
 Ser Ala Thr Ala Arg Gly Gly Gly Ile Met Ala Pro Ile Met Lys Ser
 115 120 125
 Val Ala Leu Thr Tyr Asp Ser Thr Pro Gly Pro Thr Arg Arg Arg Ala
 130 135 140
 Gly Ala Phe Leu Ala Leu Asn Val Gly Gln Val Asn Ala Ile Thr Cys
 145 150 155 160
 Ala Met Phe Leu Thr Ala Met Ala Gly Asn Pro Leu Ile Ala Ser Leu
 165 170 175
 Ala Ser Gln Met Asp Val Asn Ile Thr Trp Thr Asn Trp Ala Val Gly
 180 185 190
 Ala Ile Val Pro Gly Leu Val Ala Leu Ile Val Val Pro Trp Val Val
 195 200 205
 Tyr Lys Ile Tyr Pro Pro Glu Leu Lys Asp Thr Pro Glu Val Lys Lys
 210 215 220
 Met Ala Ser Asp Glu Leu Lys Gln Leu Gly Gly Phe Thr Tyr Gly Glu
 225 230 235 240
 Lys Val Leu Ala Gly Thr Phe Val Val Leu Leu Leu Leu Trp Thr Gly
 245 250 255
 Gly Asp Leu Val Leu Gly Ile Ser Ala Thr Thr Thr Ala Phe Val Gly
 260 265 270

Val Ile Ile Leu Leu Val Ala His Val Leu Thr Trp Glu Asp Ile Ile
 275 280 285

Gln Glu Lys Thr Ala Trp Asp Thr Met Val Trp Phe Ala Val Leu Tyr
 290 295 300

Met Met Ala Thr Ala Leu Ser Gln Tyr Gly Phe Ile Ala Trp Ile Ser
 305 310 315 320

Glu Val Ile Ala Ser Ser Leu Gly Gly Met Asn Trp Val Val Ala Leu
 325 330 335

Val Val Leu Val Leu Ile Tyr Phe Phe Ser His Tyr Phe Phe Ala Ser
 340 345 350

Ala Thr Ala His Ile Ser Ala Met Tyr Leu Ala Phe Leu Gly Ala Ala
 355 360 365

Ile Ala Ile Gly Ala Pro Pro Leu Met Ala Ala Leu Val Leu Ala Tyr
 370 375 380

Thr Ser Asn Leu Phe Ser Ser Leu Thr Gln Tyr Ser Gly Gly Pro Ser
 385 390 395 400

Pro Thr Leu Phe Gly Leu Asn Tyr Ile Thr Val Gly Glu Trp Trp Arg
 405 410 415

Thr Ser Ala Ile Ala Gly Ala Val Ser Ile Thr Ile Trp Leu Val Ile
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Gly Gly Leu Trp Met Asn Val Ile Gly Leu Trp
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 <213> Corynebacterium glutamicum

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 <223> RXN00298

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 Met Ser Ser Asn Ile
 1 5

gct atc acg acc gag cct gaa ggg aaa aat aaa aag ggt ctc aaa tca 163
 Ala Ile Thr Thr Glu Pro Glu Gly Lys Asn Lys Lys Gly Leu Lys Ser
 10 15 20

gac ccg ttc att ttt tcc att tct gtc ggt ttt atc gtg gtg ttt gtc 211
 Asp Pro Phe Ile Phe Ser Ile Ser Val Gly Phe Ile Val Val Phe Val
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atc gcc aca att gcg cta ggc gag aaa gct cga aca acc ttt tcc gcg 259

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Ile	Ala	Gly	Trp	Leu	Leu	Glu	Asn	Leu	Gly	Trp	Met	Tyr	Ile	Gly	Gly		
	55					60				65							
gtc	tcc	ttg	gtt	ttc	att	ttc	ctc	atg	ggg	atc	ttt	gcg	tcc	cgg	tat	355	
Val	Ser	Leu	Val	Phe	Ile	Phe	Leu	Met	Gly	Ile	Phe	Ala	Ser	Arg	Tyr		
	70				75					80					85		
ggc	cgg	gta	aaa	ctt	ggt	gat	gac	gat	gat	gac	ccc	gag	cac	acc	cta	403	
Gly	Arg	Val	Lys	Leu	Gly	Asp	Asp	Asp	Asp	Asp	Pro	Glu	His	Thr	Leu		
				90					95					100			
atc	gtg	tgg	ttc	tgt	atg	ctt	ttt	gct	ggc	ggg	gtc	ggg	gca	gtc	tta	451	
Ile	Val	Trp	Phe	Cys	Met	Leu	Phe	Ala	Gly	Gly	Val	Gly	Ala	Val	Leu		
			105					110						115			
atg	ttt	tgg	ggg	gtt	gcc	gaa	ccg	att	aac	cac	gcg	ttc	aac	gtg	cca	499	
Met	Phe	Trp	Gly	Val	Ala	Glu	Pro	Ile	Asn	His	Ala	Phe	Asn	Val	Pro		
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atg	gct	aat	gaa	gaa	tcc	atg	agt	gaa	gcc	gca	att	gtg	cag	gct	ttt	547	
Met	Ala	Asn	Glu	Glu	Ser	Met	Ser	Glu	Ala	Ala	Ile	Val	Gln	Ala	Phe		
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gct	tat	act	ttc	tat	cac	ttc	ggg	att	cac	atg	tgg	gta	atc	atg	gca	595	
Ala	Tyr	Thr	Phe	Tyr	His	Phe	Gly	Ile	His	Met	Trp	Val	Ile	Met	Ala		
	150				155					160					165		
ctc	cca	gga	tta	tca	ttg	gga	tac	ttt	att	tac	aaa	cgt	aag	cta	cct	643	
Leu	Pro	Gly	Leu	Ser	Leu	Gly	Tyr	Phe	Ile	Tyr	Lys	Arg	Lys	Leu	Pro		
			170					175						180			
ccc	cgt	cta	tcc	tct	gtg	ttt	tct	ccg	atc	ttg	ggg	aag	cac	att	tat	691	
Pro	Arg	Leu	Ser	Ser	Val	Phe	Ser	Pro	Ile	Leu	Gly	Lys	His	Ile	Tyr		
			185					190					195				
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Ser	Thr	Pro	Gly	Lys	Leu	Ile	Asp	Val	Leu	Ala	Ile	Val	Gly	Thr	Thr		
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Phe	Gly	Ile	Ala	Val	Ser	Val	Gly	Leu	Gly	Val	Leu	Gln	Ile	Asn	Ala		
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ggg	atg	aac	aaa	cta	tgg	agc	acc	ccg	caa	gta	tcg	tgg	gtt	cag	ctt	835	
Gly	Met	Asn	Lys	Leu	Trp	Ser	Thr	Pro	Gln	Val	Ser	Trp	Val	Gln	Leu		
	230				235				240					245			
ttg	atc	atc	ttg	atc	atc	acc	gcg	gtt	gca	tgt	att	tcc	gtt	gct	tcc	883	
Leu	Ile	Ile	Leu	Ile	Ile	Thr	Ala	Val	Ala	Cys	Ile	Ser	Val	Ala	Ser		
			250					255						260			
ggg	ttg	gat	aag	ggc	att	aag	tta	ctg	tcc	aac	att	aat	att	gca	atg	931	
Gly	Leu	Asp	Lys	Gly	Ile	Lys	Leu	Leu	Ser	Asn	Ile	Asn	Ile	Ala	Met		
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gcc	gtt	gcg	ttg	atg	ttc	ttc	atc	ttg	ttc	act	ggg	cca	acc	ctc	aca	979	
Ala	Val	Ala	Leu	Met	Phe	Phe	Ile	Leu	Phe	Thr	Gly	Pro	Thr	Leu	Thr		

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Leu Leu Arg Phe Leu Val	Glu Ser Phe Gly Ile Tyr	Ala Ser Trp Met	
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cct aat ctg atg ttt tgg act	gac tct ttc caa gat aac cca	ggc tgg	1075
Pro Asn Leu Met Phe Trp	Thr Asp Ser Phe Gln Asp	Asn Pro Gly Trp	
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cag ggc aaa tgg acg gtg ttc	tat tgg gca tgg act att	tgt tgg tgc	1123
Gln Gly Lys Trp Thr Val	Phe Tyr Trp Ala Trp Thr	Ile Cys Trp Ser	
330	335	340	
cca tat gtc ggc atg ttc gtg	gcg cgt att tgc cgt gga	cgt acc gtc	1171
Pro Tyr Val Gly Met Phe	Val Ala Arg Ile Ser Arg	Gly Arg Thr Val	
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cgt gaa ttt atc ggt ggg gtt	cta gct ctg cca gcg atc ttt	ggc gta	1219
Arg Glu Phe Ile Gly Gly	Val Leu Ala Leu Pro Ala	Ile Phe Gly Val	
360	365	370	
gtt tgg ttc tct atc ttt ggt	cgt gca ggc atc gaa gtg	gaa ctg agt	1267
Val Trp Phe Ser Ile Phe	Gly Arg Ala Gly Ile Glu	Val Glu Leu Ser	
375	380	385	
aac cca ggt ttc ttg acc cag	cca act gtt gtt gaa ggt	gac gtg cca	1315
Asn Pro Gly Phe Leu Thr	Gln Pro Thr Val Val Glu	Gly Asp Val Pro	
390	395	400 405	
gca gcg ctt ttt aat gtg ctg	caa gag tat ccg ctg act	gga att gtc	1363
Ala Ala Leu Phe Asn Val	Leu Gln Glu Tyr Pro Leu	Thr Gly Ile Val	
410	415	420	
tcc gcg ttt gca ctt gta att	att gtg att ttc ttt atc	acc tcc atc	1411
Ser Ala Phe Ala Leu Val	Ile Ile Val Ile Phe Phe	Ile Thr Ser Ile	
425	430	435	
gat tcc gca gcg cta gtt aac	gat atg ttc gct acc ggt	gca gaa aat	1459
Asp Ser Ala Ala Leu Val	Asn Asp Met Phe Ala Thr	Gly Ala Glu Asn	
440	445	450	
caa aca ccg act agt tac cgc	gtg atg tgg gcc tgc acc	att ggg gcg	1507
Gln Thr Pro Thr Ser Tyr	Arg Val Met Trp Ala Cys	Thr Ile Gly Ala	
455	460	465	
gtc gca ggt tcc ttg ctg atc	att tcc cca tcc tct ggt	att gcc acg	1555
Val Ala Gly Ser Leu Leu	Ile Ile Ser Pro Ser Ser	Gly Ile Ala Thr	
470	475	480 485	
ctg caa gaa gtg gtt atc atc	gtg gct ttc cca ttc ttc	ctc gtg caa	1603
Leu Gln Glu Val Val Ile	Ile Val Ala Phe Pro Phe	Phe Leu Val Gln	
490	495	500	
ttt gtc atg atg ttt tct ttg	ctt aaa ggc atg agt gaa	gat gct gct	1651
Phe Val Met Met Phe Ser	Leu Leu Lys Gly Met Ser	Glu Asp Ala Ala	
505	510	515	
gcg gtt cgt cgt gtg cag act	cgt cag tgg gaa aag act	gat aca cca	1699
Ala Val Arg Arg Val Gln	Thr Arg Gln Trp Glu Lys	Thr Asp Thr Pro	
520	525	530	

gaa aaa ctt gaa gag cat tcg tcc caa cca gcc ccg ggc tat gat gac 1747
 Glu Lys Leu Glu Glu His Ser Ser Gln Pro Ala Pro Gly Tyr Asp Asp
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 gag ggc aac ccc ttg cca atg cct gcc ctc gaa cat gat gag gac ggt 1795
 Glu Gly Asn Pro Leu Pro Met Pro Ala Leu Glu His Asp Glu Asp Gly
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 aac att gtt atc cca ggc aac gta gtc att gaa ggt gat ctt ggg gta 1843
 Asn Ile Val Ile Pro Gly Asn Val Val Ile Glu Gly Asp Leu Gly Val
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 Val Gly Asp Val Val Asp Asp Pro Glu Glu Ala Gln Glu Met Gly Ser
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 cgt ttt aag atc gtc gag caa act cgg ccc cag tcc agg gac gaa tac 1939
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 Asp Ile
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 35 40 45

 Thr Thr Phe Ser Ala Ile Ala Gly Trp Leu Leu Glu Asn Leu Gly Trp
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 Met Tyr Ile Gly Gly Val Ser Leu Val Phe Ile Phe Leu Met Gly Ile
 65 70 75 80

 Phe Ala Ser Arg Tyr Gly Arg Val Lys Leu Gly Asp Asp Asp Asp Asp
 85 90 95

 Pro Glu His Thr Leu Ile Val Trp Phe Cys Met Leu Phe Ala Gly Gly
 100 105 110

 Val Gly Ala Val Leu Met Phe Trp Gly Val Ala Glu Pro Ile Asn His
 115 120 125

 Ala Phe Asn Val Pro Met Ala Asn Glu Glu Ser Met Ser Glu Ala Ala
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 145 150 155 160

Trp Val Ile Met Ala Leu Pro Gly Leu Ser Leu Gly Tyr Phe Ile Tyr
 165 170 175
 Lys Arg Lys Leu Pro Pro Arg Leu Ser Ser Val Phe Ser Pro Ile Leu
 180 185 190
 Gly Lys His Ile Tyr Ser Thr Pro Gly Lys Leu Ile Asp Val Leu Ala
 195 200 205
 Ile Val Gly Thr Thr Phe Gly Ile Ala Val Ser Val Gly Leu Gly Val
 210 215 220
 Leu Gln Ile Asn Ala Gly Met Asn Lys Leu Trp Ser Thr Pro Gln Val
 225 230 235 240
 Ser Trp Val Gln Leu Leu Ile Ile Leu Ile Ile Thr Ala Val Ala Cys
 245 250 255
 Ile Ser Val Ala Ser Gly Leu Asp Lys Gly Ile Lys Leu Leu Ser Asn
 260 265 270
 Ile Asn Ile Ala Met Ala Val Ala Leu Met Phe Phe Ile Leu Phe Thr
 275 280 285
 Gly Pro Thr Leu Thr Leu Leu Arg Phe Leu Val Glu Ser Phe Gly Ile
 290 295 300
 Tyr Ala Ser Trp Met Pro Asn Leu Met Phe Trp Thr Asp Ser Phe Gln
 305 310 315 320
 Asp Asn Pro Gly Trp Gln Gly Lys Trp Thr Val Phe Tyr Trp Ala Trp
 325 330 335
 Thr Ile Cys Trp Ser Pro Tyr Val Gly Met Phe Val Ala Arg Ile Ser
 340 345 350
 Arg Gly Arg Thr Val Arg Glu Phe Ile Gly Gly Val Leu Ala Leu Pro
 355 360 365
 Ala Ile Phe Gly Val Val Trp Phe Ser Ile Phe Gly Arg Ala Gly Ile
 370 375 380
 Glu Val Glu Leu Ser Asn Pro Gly Phe Leu Thr Gln Pro Thr Val Val
 385 390 395 400
 Glu Gly Asp Val Pro Ala Ala Leu Phe Asn Val Leu Gln Glu Tyr Pro
 405 410 415
 Leu Thr Gly Ile Val Ser Ala Phe Ala Leu Val Ile Ile Val Ile Phe
 420 425 430
 Phe Ile Thr Ser Ile Asp Ser Ala Ala Leu Val Asn Asp Met Phe Ala
 435 440 445
 Thr Gly Ala Glu Asn Gln Thr Pro Thr Ser Tyr Arg Val Met Trp Ala
 450 455 460
 Cys Thr Ile Gly Ala Val Ala Gly Ser Leu Leu Ile Ile Ser Pro Ser
 465 470 475 480

Ser Gly Ile Ala Thr Leu Gln Glu Val Val Ile Ile Val Ala Phe Pro
 485 490 495

Phe Phe Leu Val Gln Phe Val Met Met Phe Ser Leu Leu Lys Gly Met
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Ser Glu Asp Ala Ala Ala Val Arg Arg Val Gln Thr Arg Gln Trp Glu
 515 520 525

Lys Thr Asp Thr Pro Glu Lys Leu Glu Glu His Ser Ser Gln Pro Ala
 530 535 540

Pro Gly Tyr Asp Asp Glu Gly Asn Pro Leu Pro Met Pro Ala Leu Glu
 545 550 555 560

His Asp Glu Asp Gly Asn Ile Val Ile Pro Gly Asn Val Val Ile Glu
 565 570 575

Gly Asp Leu Gly Val Val Gly Asp Val Val Asp Asp Pro Glu Glu Ala
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Gln Glu Met Gly Ser Arg Phe Lys Ile Val Glu Gln Thr Arg Pro Gln
 595 600 605

Ser Arg Asp Glu Tyr Asp Ile
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 Met Ser Ser Asn Ile 5
 1 5

gct atc acg acc gag cct gaa ggg aaa aat aaa aag ggt ctc aaa tca 163
 Ala Ile Thr Thr Glu Pro Glu Gly Lys Asn Lys Lys Gly Leu Lys Ser 20
 10 15 20

gac ccg ttc att ttt tcc att tct gtc ggt ttt atc gtg gtg ttt gtc 211
 Asp Pro Phe Ile Phe Ser Ile Ser Val Gly Phe Ile Val Val Phe Val 35
 25 30 35

atc gcc aca att gcg cta ggc gag aaa gct cga aca acc ttt tcc gcg 259
 Ile Ala Thr Ile Ala Leu Gly Glu Lys Ala Arg Thr Thr Phe Ser Ala 50
 40 45 50

att gcc gcc tgg ctc tta gaa aat tta ggg tgg atg tat atc ggg ggt 307
 Ile Ala Gly Trp Leu Leu Glu Asn Leu Gly Trp Met Tyr Ile Gly Gly 65
 55 60 65

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Val Ser Leu Val Phe Ile Phe Leu Met Gly Ile Phe Ala Ser Arg Tyr	
70 75 80 85	
ggc cgg gta aaa ctt ggt gat gac gat gat gac ccc gag cac acc cta	403
Gly Arg Val Lys Leu Gly Asp Asp Asp Asp Pro Glu His Thr Leu	
90 95 100	
atc gtg tgg ttc tgt atg ctt ttt gct ggc ggt gtc ggt gca gtc tta	451
Ile Val Trp Phe Cys Met Leu Phe Ala Gly Gly Val Gly Ala Val Leu	
105 110 115	
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Met Phe Trp Gly Val Ala Glu Pro Ile Asn His Ala Phe Asn Val Pro	
120 125 130	
atg gct aat gaa gaa tcc atg agt gaa gcc gca att gtg cag gct ttt	547
Met Ala Asn Glu Glu Ser Met Ser Glu Ala Ala Ile Val Gln Ala Phe	
135 140 145	
gct tat act ttc tat cac ttc ggt att cac atg tgg gta atc atg gca	595
Ala Tyr Thr Phe Tyr His Phe Gly Ile His Met Trp Val Ile Met Ala	
150 155 160 165	
ctc cca gga tta tca ttg gga tac ttt att tac aaa cgt aag cta cct	643
Leu Pro Gly Leu Ser Leu Gly Tyr Phe Ile Tyr Lys Arg Lys Leu Pro	
170 175 180	
ccc cgt cta tcc tct gtg ttt tct ccg atc ttg ggt aag cac att tat	691
Pro Arg Leu Ser Ser Val Phe Ser Pro Ile Leu Gly Lys His Ile Tyr	
185 190 195	
tcc aca ccc ggc aag ctc atc gat gta ctg gcc atc gta ggc acc acg	739
Ser Thr Pro Gly Lys Leu Ile Asp Val Leu Ala Ile Val Gly Thr Thr	
200 205 210	
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Phe Gly Ile Ala Val Ser Val Gly Leu Gly Val Leu Gln Ile Asn Ala	
215 220 225	
ggc atg aac aaa cta tgg agc acc ccg caa gta tgc tgg gtt cag ctt	835
Gly Met Asn Lys Leu Trp Ser Thr Pro Gln Val Ser Trp Val Gln Leu	
230 235 240 245	
ttg atc atc ttg atc atc acc gcg gtt gca tgt att tcc gtt gct tcc	883
Leu Ile Ile Leu Ile Ile Thr Ala Val Ala Cys Ile Ser Val Ala Ser	
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ggc ttg gat aag ggc att aag tta ctg tcc aac att aat att gca atg	931
Gly Leu Asp Lys Gly Ile Lys Leu Leu Ser Asn Ile Asn Ile Ala Met	
265 270 275	
gcc gtt gcg ttg atg ttc ttc atc ttg ttc act ggt cca acc ctc aca	979
Ala Val Ala Leu Met Phe Phe Ile Leu Phe Thr Gly Pro Thr Leu Thr	
280 285 290	
ttg ctg cgc ttt ctc gta gaa tcc ttc gga atc tat gca tcc tgg atg	1027
Leu Leu Arg Phe Leu Val Glu Ser Phe Gly Ile Tyr Ala Ser Trp Met	
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cct aat ctg atg ttt tgg act gac tct ttc caa gat aac cca ggc tgg	1075

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Gln	Gly	Lys	Trp	Thr	Val	Phe	Tyr	Trp	Ala	Trp	Thr	Ile	Cys	Trp	Ser	
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cca	tat	gtc	ggc	atg	ttc	gtg	gcg	cgt	att	tcg	cgt	gga	cgt	acc	gtc	1171
Pro	Tyr	Val	Gly	Met	Phe	Val	Ala	Arg	Ile	Ser	Arg	Gly	Arg	Thr	Val	
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cgt	gaa	ttt	atc	ggg	ggg	gtt	cta	gct	ctg	cca	gcg	atc	ttt	ggc	gta	1219
Arg	Glu	Phe	Ile	Gly	Gly	Val	Leu	Ala	Leu	Pro	Ala	Ile	Phe	Gly	Val	
		360					365					370				
gtt	tgg	ttc	tct	atc	ttt	ggg	cgt	gca	ggc	atc	gaa	gtg	gaa	ctg	agt	1267
Val	Trp	Phe	Ser	Ile	Phe	Gly	Arg	Ala	Gly	Ile	Glu	Val	Glu	Leu	Ser	
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aac	cca	ggg	ttc	ttg	acc	cag	cca	act	gtt	gtt	gaa	ggg	gac	gtg	cca	1315
Asn	Pro	Gly	Phe	Leu	Thr	Gln	Pro	Thr	Val	Val	Glu	Gly	Asp	Val	Pro	
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Ala	Ala	Leu	Phe	Asn	Val	Leu	Gln	Glu	Tyr	Pro	Leu	Thr	Gly	Ile	Val	
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tcc	gcg	ttt	gca	ctt	gta	att	att	gtg	att	ttc	ttt	atc	acc	tcc	atc	1411
Ser	Ala	Phe	Ala	Leu	Val	Ile	Ile	Val	Ile	Phe	Phe	Ile	Thr	Ser	Ile	
			425					430					435			
gat	tcc	gca	gcg	cta	gtt	aac	gat	atg	ttc	gct	acc	ggg	gca	gaa	aat	1459
Asp	Ser	Ala	Ala	Leu	Val	Asn	Asp	Met	Phe	Ala	Thr	Gly	Ala	Glu	Asn	
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caa	aca	ccg	act	agt	tac	cgc	gtg	atg	tgg	gcc	tgc	acc	att	ggg	gcg	1507
Gln	Thr	Pro	Thr	Ser	Tyr	Arg	Val	Met	Trp	Ala	Cys	Thr	Ile	Gly	Ala	
	455					460					465					
gtc	gca	ggg	tcc	ttg	ctg	atc	att	tcc	cca	tcc	tct	ggg	att	gcc	acg	1555
Val	Ala	Gly	Ser	Leu	Leu	Ile	Ile	Ser	Pro	Ser	Ser	Gly	Ile	Ala	Thr	
470					475				480					485		
ctg	caa	gaa	gtg	gtt	atc	atc	gtg	gct	ttc	cca	ttc	ttc	ctc	gtg	caa	1603
Leu	Gln	Glu	Val	Val	Ile	Ile	Val	Ala	Phe	Pro	Phe	Phe	Leu	Val	Gln	
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ttt	gtc	atg	atg	ttt	tct	ttg	ctt	aaa	ggc	atg	agt	gaa	gat	gct	gct	1651
Phe	Val	Met	Met	Phe	Ser	Leu	Leu	Lys	Gly	Met	Ser	Glu	Asp	Ala	Ala	
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Ala	Val	Arg	Arg	Val	Gln	Thr	Arg	Gln	Trp	Glu	Lys	Thr	Asp	Thr	Pro	
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gaa	aaa	ctt	gaa	gag	cat	tcg	tcc	caa	cca	gcc	ccg	ggc	tat	gat	gac	1747
Glu	Lys	Leu	Glu	Glu	His	Ser	Ser	Gln	Pro	Ala	Pro	Gly	Tyr	Asp	Asp	
	535					540					545					
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Ile Val Val Phe Val Ile Ala Thr Ile Ala Leu Gly Glu Lys Ala Arg
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Thr Thr Phe Ser Ala Ile Ala Gly Trp Leu Leu Glu Asn Leu Gly Trp
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Met Tyr Ile Gly Gly Val Ser Leu Val Phe Ile Phe Leu Met Gly Ile
65 70 75 80

Phe Ala Ser Arg Tyr Gly Arg Val Lys Leu Gly Asp Asp Asp Asp Asp
85 90 95

Pro Glu His Thr Leu Ile Val Trp Phe Cys Met Leu Phe Ala Gly Gly
100 105 110

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Val Gly Ala Val Leu Met Phe Trp Gly Val Ala Glu Pro Ile Asn His  
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Ile Val Gln Ala Phe Ala Tyr Thr Phe Tyr His Phe Gly Ile His Met
145 150 155 160

Trp Val Ile Met Ala Leu Pro Gly Leu Ser Leu Gly Tyr Phe Ile Tyr
165 170 175

Lys Arg Lys Leu Pro Pro Arg Leu Ser Ser Val Phe Ser Pro Ile Leu
180 185 190

Gly Lys His Ile Tyr Ser Thr Pro Gly Lys Leu Ile Asp Val Leu Ala
 195 200 205
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 210 215 220
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 225 230 235 240
 Ser Trp Val Gln Leu Leu Ile Ile Leu Ile Ile Thr Ala Val Ala Cys
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 275 280 285
 Gly Pro Thr Leu Thr Leu Leu Arg Phe Leu Val Glu Ser Phe Gly Ile
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 Tyr Ala Ser Trp Met Pro Asn Leu Met Phe Trp Thr Asp Ser Phe Gln
 305 310 315 320
 Asp Asn Pro Gly Trp Gln Gly Lys Trp Thr Val Phe Tyr Trp Ala Trp
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 Thr Ile Cys Trp Ser Pro Tyr Val Gly Met Phe Val Ala Arg Ile Ser
 340 345 350
 Arg Gly Arg Thr Val Arg Glu Phe Ile Gly Gly Val Leu Ala Leu Pro
 355 360 365
 Ala Ile Phe Gly Val Val Trp Phe Ser Ile Phe Gly Arg Ala Gly Ile
 370 375 380
 Glu Val Glu Leu Ser Asn Pro Gly Phe Leu Thr Gln Pro Thr Val Val
 385 390 395 400
 Glu Gly Asp Val Pro Ala Ala Leu Phe Asn Val Leu Gln Glu Tyr Pro
 405 410 415
 Leu Thr Gly Ile Val Ser Ala Phe Ala Leu Val Ile Ile Val Ile Phe
 420 425 430
 Phe Ile Thr Ser Ile Asp Ser Ala Ala Leu Val Asn Asp Met Phe Ala
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 Thr Gly Ala Glu Asn Gln Thr Pro Thr Ser Tyr Arg Val Met Trp Ala
 450 455 460
 Cys Thr Ile Gly Ala Val Ala Gly Ser Leu Leu Ile Ile Ser Pro Ser
 465 470 475 480
 Ser Gly Ile Ala Thr Leu Gln Glu Val Val Ile Ile Val Ala Phe Pro
 485 490 495
 Phe Phe Leu Val Gln Phe Val Met Met Phe Ser Leu Leu Lys Gly Met
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 Ser Glu Asp Ala Ala Ala Val Arg Arg Val Gln Thr Arg Gln Trp Glu

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Lys Thr Asp Thr Pro Glu	Lys Leu Glu Glu His	Ser Ser Gln Pro Ala
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Pro Gly Tyr Asp Asp Glu	Gly Asn Pro Leu Pro	Met Pro Ala Leu Glu
545	550	555
His Asp Glu Asp Gly	Asn Ile Val Ile Pro	Gly Asn Val Val Ile Glu
565	570	575
Gly Asp Leu Gly Val Val	Gly Asp Val Val Asp	Asp Pro Glu Glu Ala
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Gln Glu Met Gly Ser Arg	Phe Lys Ile Val Glu	Gln Thr Arg Pro Gln
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Ser Arg Asp Glu Tyr Asp	Ile	
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 Met Leu Asn Ala Leu
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 Lys Phe Ile Pro Trp Leu Ile Gly Gln Ile Phe Leu Ser Gly Phe Ser
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 Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly Phe Asn Pro Val Val
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 atc cgc tac cca ctt cga gtg acc acg gac ttc cag atc gca gcc ctg 259
 Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe Gln Ile Ala Ala Leu
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 Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu Ser Leu Gly Leu Arg
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 gaa ccc cgc aag ccc ggc gac ccc acc att ttg ctg atc caa gca gtg 355
 Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu Leu Ile Gln Ala Val
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 Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser Ile Ala Asp Met Glu
 90 95 100

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 Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp His Gly Val Pro Gly
 105 110 115

caa ggc cct tac aag gag atc cgc ccc agc gat gct gag tgg cca agt 499
 Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp Ala Glu Trp Pro Ser
 120 125 130

cgc gag atc gct gac acc gcc caa aac acc gtc agc caa gac aag agg 547
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<213> Corynebacterium glutamicum

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 35 40 45

Gln Ile Ala Ala Leu Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu
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Ser Leu Gly Leu Arg Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu
 65 70 75 80

Leu Ile Gln Ala Val Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser
 85 90 95

Ile Ala Asp Met Glu Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp
 100 105 110

His Gly Val Pro Gly Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp
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                                         Met Glu Pro Leu Phe
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Gln Gly Thr Arg Asn Leu Tyr Thr Thr Asp Ala Pro Val Lys Arg Pro
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Ala Asp Leu Ala Gly Lys Lys Ile Arg Val Gln Glu Ser Ala Met His
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Ile Arg Met Ile Glu Leu Met Gly Gly Ser Ala Thr Pro Leu Thr Tyr
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Gly Glu Val Tyr Thr Ala Met Gln Ser Gly Val Leu Asp Gly Ala Glu
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Tyr Asn Ser Asn Thr Asn His Leu Val Gly Leu Asp Tyr Met Val Met
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cga cac gat ctg ctt gac gcc atg agc gag cca gac cgt gaa ttg ttc 499
Arg His Asp Leu Leu Asp Ala Met Ser Glu Pro Asp Arg Glu Leu Phe
                        120                        125                        130

ctg gaa gaa tgg gac gcc gcg atg act gag cac acg gat ctg tgg aac 547
Leu Glu Glu Trp Asp Ala Ala Met Thr Glu His Thr Asp Leu Trp Asn
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Thr Glu Thr Asp Ala Val Ile Glu Lys Ala Lys Ala Gly Gly Ala Glu
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Phe Val Glu Val Asp Ala Gln Ala Phe Thr Asp Ala Leu Ala Pro Ile
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Lys Asp Glu Phe Leu Thr Ser Glu Phe Gln Arg Glu Leu Tyr Glu Ala
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Leu	Asp	Gly	Ala	Glu	Asn	Asn	Glu	Ile	Ser	Tyr	Val	Thr	Gln	Asn	His
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Phe	Glu	Val	Ala	Arg	Tyr	Asn	Ser	Asn	Thr	Asn	His	Leu	Val	Gly	Leu
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Thr	Asp	Leu	Trp	Asn	Thr	Glu	Thr	Asp	Ala	Val	Ile	Glu	Lys	Ala	Lys
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Ser

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                                         1           5

tgg cgc att cca ttc ctg atg gcc gtg cca cta ggg ctt atc ggc tgg 163
Trp Arg Ile Pro Phe Leu Met Ala Val Pro Leu Gly Leu Ile Gly Trp
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Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr Glu Trp Lys Met Met
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                        105                        110                        115

aac atc atg gct ttc gct acc tta agc aca gta att atg gcg atc ccg 499
Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val Ile Met Ala Ile Pro
                        120                        125                        130

gcc tac atc att gca ggt caa ggt act ttg act gct tct ttg att gcg 547
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                        135                        140                        145

cag gta atg ctt gga atc ggc gcg gtt acc gct aac tgc gtt acc tca 595
Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys Val Thr Ser
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                        170                        175                        180

ggc att acc tac aac gtc act tac gca atc ttc ggc ggc tcg gct cca 691
Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly Ser Ala Pro
                        185                        190                        195

ttt atc tcc acc gca ttg gtc tcc tgg acc ggc agc ccg ctg gcc cct 739
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Pro Ala Ser Glu Arg Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr
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Glu Trp Lys Met Met Leu Arg Val Gly Gly Phe Ile Ser Cys Thr Gly
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Leu Ser Phe Tyr Ile Phe Thr Thr Tyr Met Thr Thr Phe Leu Arg Ser
 65 70 75 80

Thr Val Gly Leu Glu Gly Thr Leu Val Leu Ala Gly Asn Ile Ile Ala
 85 90 95

Leu Ser Met Ala Ala Ile Val Ala Pro Phe Val Gly Arg Ala Ile Asp
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Lys Phe Pro Arg Arg Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val
 115 120 125

Ile Met Ala Ile Pro Ala Tyr Ile Ile Ala Gly Gln Gly Thr Leu Thr
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Ala Ser Leu Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala
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Asn Cys Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr
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Arg Gly Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe
 180 185 190

Gly Gly Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly
 195 200 205

Ser Pro Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala
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 Ser Asp Thr Leu Phe Lys Val Thr Arg Glu Leu Glu Arg Val Val Met
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 aag acc atc acc gcc ttt gtc atc cca ctg ctg cca ctc ttc atc ttc 336
 Lys Thr Ile Thr Ala Phe Val Ile Pro Leu Leu Pro Leu Phe Ile Phe
 100 105 110
 ggc atc ttc ctc ggc atg ggc atg aac ggt ggc ctc ctg gag atc atg 384
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 115 120 125
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 Ser Ala Phe Gly Lys Val Leu Ile Leu Ala Val Val Gly Thr Leu Leu
 130 135 140
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 Phe Leu Ala Ile Gln Phe Ile Ile Ala Gly Ala Val Ser Lys Lys Asn
 145 150 155 160

cca tgg aaa ctg ttc aaa aac atg ctc cct gca tac ttc act gca ctg 528
 Pro Trp Lys Leu Phe Lys Asn Met Leu Pro Ala Tyr Phe Thr Ala Leu
 165 170 175

ggc act tcc tct tca gcg gca acc atc cca gtg acc tac cag cag acc 576
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 180 185 190

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 195 200 205

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 210 215 220

acc ttc gct gtt gtc ttc atg tac gac atg gaa gta ggc gtc ggc ctc 720
 Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu
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 Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
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 Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp
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 Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
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 Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
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 Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
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 Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
 180 185 190

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 195 200 205
 ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc 672
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 atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg atc gca gct 720
 Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala
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 245 250 255
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 ttc tcc ttc ctt atc ttc gca gtc gtc gga gtc att gcc ctg gcg ttc 1008
 Phe Ser Phe Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe
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 Val Thr Lys Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu
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<213> Corynebacterium glutamicum

<400> 546

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Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
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 Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp
 65 70 75 80
 Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
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 Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
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 Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
 115 120 125
 Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
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 Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
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 Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
 165 170 175
 Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
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 Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
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 Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
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 Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala
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 Ala Gly Thr Leu Leu Pro Glu Gly Asn Ser Ile Arg Pro Phe Ala Ile
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 Phe Ser Phe Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe
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 Val Thr Lys Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu
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ggc	aat	aac	ttg	cct	gaa	tcc	caa	gag	tca	ccc	gag	gaa	cct	cat	tat	163
Gly	Asn	Asn	Leu	Pro	Glu	Ser	Gln	Glu	Ser	Pro	Glu	Glu	Pro	His	Tyr	
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Tyr	Ile	Ala	Phe	Ser	Arg	Tyr	Gly	Arg	Ile	Lys	Leu	Gly	Thr	Asp	Glu	
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Asp	Glu	Pro	Glu	Phe	Ser	Arg	Phe	Ser	Trp	Ile	Ala	Met	Met	Phe	Gly	
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Ala	Gly	Ile	Gly	Val	Gly	Ile	Phe	Phe	Phe	Gly	Pro	Ser	Glu	Pro	Leu	
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tgg	cat	tat	ctc	agt	ccc	cca	cct	cac	acc	gtg	gaa	gga	tct	aca	cct	595
Trp	His	Tyr	Leu	Ser	Pro	Pro	Pro	His	Thr	Val	Glu	Gly	Ser	Thr	Pro	
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gag	tcc	ttg	cac	caa	gca	ctt	gcg	cag	tcc	cac	ttc	cac	tgg	ggc	tta	643
Glu	Ser	Leu	His	Gln	Ala	Leu	Ala	Gln	Ser	His	Phe	His	Trp	Gly	Leu	
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 Leu Ser Ile Glu Pro Ala Glu Glu Gly Arg Gly Ala Gly Ala Thr Phe
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 Asp Ser Thr Ala Asp His Ile Thr Asp Trp Tyr Gln Arg Thr Asp Glu
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 Glu Gly Ser Thr Pro Glu Ser Leu His Gln Ala Leu Ala Gln Ser His
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 Phe His Trp Gly Leu Ser Ala Trp Gly Leu Tyr Ala Leu Val Gly Gly
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 Ser Thr Phe Arg Ser Leu Phe Gly Glu Lys Thr Glu Gly Ile Ala Gly
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 Arg Leu Ile Asp Met Met Ala Ile Ile Ala Thr Leu Phe Gly Thr Ala
 225 230 235 240
 Ala Thr Leu Gly Leu Ser Ala Ile Gln Val Gly Gln Gly Val Gln Ile
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 Ala Ile Leu Thr Ile Gly Phe Ile Ile Ser Ser Val Ser Gly Val Ser
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 Lys Gly Ile Arg Tyr Leu Ser Asn Leu Asn Ile Ser Leu Thr Leu Gly
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Leu Ile Pro Ser Ser Val Leu Glu Tyr Gly Ser Glu Phe Leu Ser Met
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 <223> RXN02348

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Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly Asp Ile Gly Thr Ser
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Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met Gln His Asn Lys Val
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gct gac aac caa gga caa ggt ggc atc ctg gcg ctc gtt gct ttg ctg 403
Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala Leu Val Ala Leu Leu
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Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala Val Ala Gly Met Leu
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ggc gcc gca ttg ttt tat ggc gat gtg gtg atc acc ccg gcg atc tct 499
Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile Thr Pro Ala Ile Ser
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gtt ctc agc gca aca gaa ggc ttg acg gtt atc tcc cca agc ttt gag 547
Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile Ser Pro Ser Phe Glu
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Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu Ile Ala Ile Phe Ala
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Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser Pro His Trp Ala Leu	
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Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe Val Leu Leu Gly Ala	
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Val Val Leu Thr Val Thr Gly Ala Glu Ala Leu Tyr Ala Asp Met Gly	
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His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp Phe Cys Val Val Met	
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Ser Ala Tyr Gly Leu Ala Val Thr Gly Thr Leu Val Leu Val Ser Val	
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Thr Lys Ile His Asp Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val	
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Gln Glu Arg Ala Glu Leu Leu Pro Met Asp Lys Phe Leu Glu Lys	
455 460 465	
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Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg	
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Met Glu Val Leu His His Ala Pro Ile Arg Val Val Arg Val Asp Leu	
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His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro Glu His Leu His Ala	
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<212> PRT

<213> Corynebacterium glutamicum

<400> 550

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 Gln His Asn Lys Val Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile
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 Ser Met Val Leu Trp Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val
 65 70 75 80
 Met Leu Val Thr Arg Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala
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 Leu Val Ala Leu Leu Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala
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 Val Ala Gly Met Leu Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile
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 Ser Pro Ser Phe Glu Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu
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 Ile Ala Ile Phe Ala Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys
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 Ala Phe Gly Pro Ile Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu
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 Gly Ile Pro Gln Ile Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser
 195 200 205
 Pro His Trp Ala Leu Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe
 210 215 220
 Val Leu Leu Gly Ala Val Val Leu Thr Val Thr Gly Ala Glu Ala Leu
 225 230 235 240
 Tyr Ala Asp Met Gly His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp
 245 250 255
 Phe Cys Val Val Met Pro Ala Leu Ile Leu Thr Tyr Leu Gly Gln Gly
 260 265 270
 Ala Leu Val Ile Asn Gln Pro Glu Ala Val Arg Asn Pro Met Phe Tyr
 275 280 285
 Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu Val Ile Leu Ala Thr Ile
 290 295 300
 Ala Thr Val Ile Ala Ser Gln Ala Val Ile Ser Gly Ala Tyr Ser Leu
 305 310 315 320
 Thr Lys Gln Ala Val Asn Leu Lys Leu Leu Pro Arg Met Val Ile Arg

[illegible]

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<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(1012)  
<223> RXN00297
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<400> 551

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aaaacaacat	ggcacaataa	cgatcatgca	acagggtgctc	atg ggt ttc acg gtg	115	
				Met Gly Phe Thr Val	5	
				1		
gtg ttc atc gtc atc gga ata ggt tgg att ctc ggt aga aga gac acc	163					
Val Phe Ile Val Ile Gly Ile Gly Trp Ile Leu Gly Arg Arg Asp Thr						
	10			15	20	
ttg ggc aca cat gcc cag aaa cct ttg agc ctg ttt gtc tat tac gtg	211					
Leu Gly Thr His Ala Gln Lys Pro Leu Ser Leu Phe Val Tyr Tyr Val						
	25			30	35	
gcc acc cca gcg ttg ttg ttt gat cgg gtc acc aag tca gat acc tcg	259					
Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr Lys Ser Asp Thr Ser						
	40			45	50	
acg att ttc tct ctg aac ttc gtg gtc att gca ctc tct gcg ttg atc	307					
Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala Leu Ser Ala Leu Ile						
	55			60	65	
gta ggt ttc ctg ttt ttc cta ctc atg cgg ttc gtg atc aaa aga act	355					
Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe Val Ile Lys Arg Thr						
	70			75	80	
					85	
gcc gca gta tcg gtg atc ggc atg cta gct gcg tcc tac gcc aac gcc	403					
Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala Ser Tyr Ala Asn Ala						
	90			95	100	
ggg aac ctg ggt atc cct ttg gca gcc tat att ttg gat gat ttc acc	451					
Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile Leu Asp Asp Phe Thr						
	105			110	115	
gtg gtg att ccc gtg att ttg ttc cag gtg gcg ttc tac gca ccg atc	499					
Val Val Ile Pro Val Ile Leu Phe Gln Val Ala Phe Tyr Ala Pro Ile						
	120			125	130	
acc atg acc atc atg gag atg ctg acc aac aag aaa tcc acc aac ttg	547					
Thr Met Thr Ile Met Glu Met Leu Thr Asn Lys Lys Ser Thr Asn Leu						
	135			140	145	
gtg cgc aac ctc ctg gtc acg cca cta acc aac acc atg gtg ctc gca	595					
Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn Thr Met Val Leu Ala						
	150			155	160	
					165	
gcg att gcc ggt att gct gtg tct ttg act tcg atg agc gtg ccc gtg	643					
Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser Met Ser Val Pro Val						
	170			175	180	
gtg att gct cag cca gtg gaa atg ttg gcg aat gct tca gtg cca ctg	691					

Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn Ala Ser Val Pro Leu
 185 190 195

gct ttg gtg gtg ttc gga ctg tcc ttg tcc aag agc aag atc ctg gaa 739
 Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys Ser Lys Ile Leu Glu
 200 205 210

aag ggg cag gta tcc agg cgc gat gtg ttt acg gcg gca ctg ttc aag 787
 Lys Gly Gln Val Ser Arg Arg Asp Val Phe Thr Ala Ala Leu Phe Lys
 215 220 225

aat gtt ctg cac cca att gtt gcg gga ctt tta gcc tta gcc ttt ggt 835
 Asn Val Leu His Pro Ile Val Ala Gly Leu Leu Ala Leu Ala Phe Gly
 230 235 240 245

atg gaa ggt act gcc ttg ttg tcg gcg gtg att ctc ggt gca ctg cca 883
 Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile Leu Gly Ala Leu Pro
 250 255 260

aca gcg cag aat gtc tac acc tac gcg ttg cga ttt aga aca gct gaa 931
 Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg Phe Arg Thr Ala Glu
 265 270 275

tcg atg gcg aga gac aca ggg gtg gtc acc aca ctc att tcc ttc ccc 979
 Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr Leu Ile Ser Phe Pro
 280 285 290

gta ttg gtg gcg gtc tcc att atc ttt gga tct tagggtagc attagtggtc 1032
 Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser
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atg 1035

<210> 552

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<212> PRT

<213> Corynebacterium glutamicum

<400> 552

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Phe Val Tyr Tyr Val Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr
 35 40 45

Lys Ser Asp Thr Ser Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala
 50 55 60

Leu Ser Ala Leu Ile Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe
 65 70 75 80

Val Ile Lys Arg Thr Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala
 85 90 95

Ser Tyr Ala Asn Ala Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile
 100 105 110

Leu Asp Asp Phe Thr Val Val Ile Pro Val Ile Leu Phe Gln Val Ala
 115 120 125
 Phe Tyr Ala Pro Ile Thr Met Thr Ile Met Glu Met Leu Thr Asn Lys
 130 135 140
 Lys Ser Thr Asn Leu Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn
 145 150 155 160
 Thr Met Val Leu Ala Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser
 165 170 175
 Met Ser Val Pro Val Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn
 180 185 190
 Ala Ser Val Pro Leu Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys
 195 200 205
 Ser Lys Ile Leu Glu Lys Gly Gln Val Ser Arg Arg Asp Val Phe Thr
 210 215 220
 Ala Ala Leu Phe Lys Asn Val Leu His Pro Ile Val Ala Gly Leu Leu
 225 230 235 240
 Ala Leu Ala Phe Gly Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile
 245 250 255
 Leu Gly Ala Leu Pro Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg
 260 265 270
 Phe Arg Thr Ala Glu Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr
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 Leu Ile Ser Phe Pro Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser
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 <213> Corynebacterium glutamicum

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 <223> RXN03103

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 aatcagcga tgcaaccttt tagatatata aggagacaac atg tct gca aag cgt 115
 Met Ser Ala Lys Arg
 1 5
 act ttt acc cgt atc ggt gcg att ctt gga gca act gca ctt gcc gga 163
 Thr Phe Thr Arg Ile Gly Ala Ile Leu Gly Ala Thr Ala Leu Ala Gly
 10 15 20

ggt acc ctc acc gcc tgt ggt gat tca agc ggt ggc gac gga ttc ctc 211
 Val Thr Leu Thr Ala Cys Gly Asp Ser Ser Gly Gly Asp Gly Phe Leu
 25 30 35

gca gcc att gaa aat ggt tct gtc aat gtc ggc acc aaa tac gat cag 259
 Ala Ala Ile Glu Asn Gly Ser Val Asn Val Gly Thr Lys Tyr Asp Gln
 40 45 50

cct ggt ctt ggc ctc cgc aac cca gac aac tcc atg agc ggt ctc gac 307
 Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser Met Ser Gly Leu Asp
 55 60 65

gtg gat gtt gct gaa tac gta att caa ctc cat cgc tgatgacaag 353
 Val Asp Val Ala Glu Tyr Val Ile Gln Leu His Arg
 70 75 80

<210> 554

<211> 81

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 554

Met Ser Ala Lys Arg Thr Phe Thr Arg Ile Gly Ala Ile Leu Gly Ala
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Thr Ala Leu Ala Gly Val Thr Leu Thr Ala Cys Gly Asp Ser Ser Gly
 20 25 30

Gly Asp Gly Phe Leu Ala Ala Ile Glu Asn Gly Ser Val Asn Val Gly
 35 40 45

Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser
 50 55 60

Met Ser Gly Leu Asp Val Asp Val Ala Glu Tyr Val Ile Gln Leu His
 65 70 75 80

Arg

<210> 555

<211> 695

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (1)..(672)

<223> RXN02993

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 Val Ala Glu Tyr Val Val Asn Ser Ile Ala Asp Asp Lys Gly Trp Asp
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cac ccc acc atc gaa tgg cgt gaa tcc cct tct gcg cag cgt gaa acc 96
 His Pro Thr Ile Glu Trp Arg Glu Ser Pro Ser Ala Gln Arg Glu Thr
 20 25 30

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ctc att caa aac ggt gag gta gac atg atc gca gca acc tac tcc atc 144
Leu Ile Gln Asn Gly Glu Val Asp Met Ile Ala Ala Thr Tyr Ser Ile
      35                      40                      45

aac gct ggc cgt tca gag tcc gtc aac ttc ggt ggc cca tac ctg ctt 192
Asn Ala Gly Arg Ser Glu Ser Val Asn Phe Gly Gly Pro Tyr Leu Leu
      50                      55                      60

acc cac cag gct ctg ctt gtt cgc caa gat gac gat cgc att gaa acc 240
Thr His Gln Ala Leu Leu Val Arg Gln Asp Asp Asp Arg Ile Glu Thr
      65                      70                      75                      80

ctc gag gac ttg gat aac ggt ttg atc ctg tgc tcc gtt tcc gga tcc 288
Leu Glu Asp Leu Asp Asn Gly Leu Ile Leu Cys Ser Val Ser Gly Ser
      85                      90                      95

act cca gct cag aag gtc aag gat gtc ctc cca ggc gtt cag ctc caa 336
Thr Pro Ala Gln Lys Val Lys Asp Val Leu Pro Gly Val Gln Leu Gln
      100                     105                     110

gaa tac gac acc tac tct tcc tgt gtt gag gca ctg tcc cag ggc aac 384
Glu Tyr Asp Thr Tyr Ser Ser Cys Val Glu Ala Leu Ser Gln Gly Asn
      115                     120                     125

gtt gac gcc ctg acc act gac gcc acc atc ctc ttc ggc tac tcc cag 432
Val Asp Ala Leu Thr Thr Asp Ala Thr Ile Leu Phe Gly Tyr Ser Gln
      130                     135                     140

cag tac gaa ggc gac ttc cgc gtt gtg gaa atg gaa aag gac ggc gag 480
Gln Tyr Glu Gly Asp Phe Arg Val Val Glu Met Glu Lys Asp Gly Glu
      145                     150                     155                     160

cca ttc acc gac gag tac tac ggc att ggc ctg aag aag gat gac cag 528
Pro Phe Thr Asp Glu Tyr Tyr Gly Ile Gly Leu Lys Lys Asp Asp Gln
      165                     170                     175

gaa ggc acc gac gct atc aac gcc gca ctt gag cgc atg tac gct gac 576
Glu Gly Thr Asp Ala Ile Asn Ala Ala Leu Glu Arg Met Tyr Ala Asp
      180                     185                     190

ggc acc ttc cag cga ctg ctc acc gag aac ctc ggt gaa gac tcc gtg 624
Gly Thr Phe Gln Arg Leu Leu Thr Glu Asn Leu Gly Glu Asp Ser Val
      195                     200                     205

gtt gtt gaa gaa ggc acc cca ggt gac ctc tcc ttc ctc gac gca agc 672
Val Val Glu Glu Gly Thr Pro Gly Asp Leu Ser Phe Leu Asp Ala Ser
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tagtgtgacg gcttttaaaa gcc 695

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<210> 556

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 556

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Val Ala Glu Tyr Val Val Asn Ser Ile Ala Asp Asp Lys Gly Trp Asp
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His Pro Thr Ile Glu Trp Arg Glu Ser Pro Ser Ala Gln Arg Glu Thr

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Asn	Ala	Gly	Arg	Ser	Glu	Ser	Val	Asn	Phe	Gly	Gly	Pro	Tyr	Leu	Leu				
	50					55					60								
Thr	His	Gln	Ala	Leu	Leu	Val	Arg	Gln	Asp	Asp	Asp	Arg	Ile	Glu	Thr				
65					70					75					80				
Leu	Glu	Asp	Leu	Asp	Asn	Gly	Leu	Ile	Leu	Cys	Ser	Val	Ser	Gly	Ser				
			85						90					95					
Thr	Pro	Ala	Gln	Lys	Val	Lys	Asp	Val	Leu	Pro	Gly	Val	Gln	Leu	Gln				
		100						105					110						
Glu	Tyr	Asp	Thr	Tyr	Ser	Ser	Cys	Val	Glu	Ala	Leu	Ser	Gln	Gly	Asn				
		115					120					125							
Val	Asp	Ala	Leu	Thr	Thr	Asp	Ala	Thr	Ile	Leu	Phe	Gly	Tyr	Ser	Gln				
	130					135					140								
Gln	Tyr	Glu	Gly	Asp	Phe	Arg	Val	Val	Glu	Met	Glu	Lys	Asp	Gly	Glu				
145					150					155					160				
Pro	Phe	Thr	Asp	Glu	Tyr	Tyr	Gly	Ile	Gly	Leu	Lys	Lys	Asp	Asp	Gln				
			165						170					175					
Glu	Gly	Thr	Asp	Ala	Ile	Asn	Ala	Ala	Leu	Glu	Arg	Met	Tyr	Ala	Asp				
		180						185					190						
Gly	Thr	Phe	Gln	Arg	Leu	Leu	Thr	Glu	Asn	Leu	Gly	Glu	Asp	Ser	Val				
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Val	Val	Glu	Glu	Gly	Thr	Pro	Gly	Asp	Leu	Ser	Phe	Leu	Asp	Ala	Ser				
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 <212> DNA
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 <223> RXN00349

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 Met Leu Ser Phe Ala
 1 5
 acc ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct 163
 Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro

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ccg	cca	tcg	cca	cta	gcc	ccg	att	gat	ctc	act	gac	cat	agt	caa	gtg	211				
Pro	Pro	Ser	Pro	Leu	Ala	Pro	Ile	Asp	Leu	Thr	Asp	His	Ser	Gln	Val					
25					30					35										
gcc	ggt	gtg	atg	aat	ttg	gct	gcg	aga	att	ggc	gat	att	ttg	ctt	tct	259				
Ala	Gly	Val	Met	Asn	Leu	Ala	Ala	Arg	Ile	Gly	Asp	Ile	Leu	Leu	Ser					
40					45					50										
tca	ggt	acg	tca	aat	agt	gac	acc	aag	gta	caa	ggt	cga	gca	gtg	acc	307				
Ser	Gly	Thr	Ser	Asn	Ser	Asp	Thr	Lys	Val	Gln	Val	Arg	Ala	Val	Thr					
55					60					65										
tct	gcg	tac	ggt	ttg	tac	tac	acg	cac	gtg	gat	atc	acg	ttg	aat	acg	355				
Ser	Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp	Ile	Thr	Leu	Asn	Thr					
70					75					80					85					
atc	acc	atc	ttc	acc	aac	atc	ggt	gtg	gag	agg	aag	atg	ccg	gtc	aac	403				
Ile	Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg	Lys	Met	Pro	Val	Asn					
90					95					100										
gtg	ttt	cat	gtt	gta	ggc	aag	ttg	gac	acc	aac	ttc	tcc	aaa	ctg	tct	451				
Val	Phe	His	Val	Val	Gly	Lys	Leu	Asp	Thr	Asn	Phe	Ser	Lys	Leu	Ser					
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gag	gtt	gac	cgt	ttg	atc	cgt	tcc	att	cag	gct	ggt	gcg	acc	ccg	cct	499				
Glu	Val	Asp	Arg	Leu	Ile	Arg	Ser	Ile	Gln	Ala	Gly	Ala	Thr	Pro	Pro					
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gag	gtt	gcc	gag	aaa	atc	ctg	gac	gag	ttg	gag	caa	tcc	cct	gcg	tct	547				
Glu	Val	Ala	Glu	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Gln	Ser	Pro	Ala	Ser					
135					140					145										
tat	ggt	ttc	cct	gtt	gcg	ttg	ctt	ggc	tgg	gca	atg	atg	ggt	ggt	gct	595				
Tyr	Gly	Phe	Pro	Val	Ala	Leu	Leu	Gly	Trp	Ala	Met	Met	Gly	Gly	Ala					
150					155					160					165					
gtt	gct	gtg	ctg	ttg	ggt	ggt	gga	tgg	cag	gtt	tcc	cta	att	gct	ttt	643				
Val	Ala	Val	Leu	Leu	Gly	Gly	Gly	Trp	Gln	Val	Ser	Leu	Ile	Ala	Phe					
170					175					180										
att	acc	gcg	ttc	acg	atc	att	gcc	acg	acg	tca	ttt	ttg	gga	aag	aag	691				
Ile	Thr	Ala	Phe	Thr	Ile	Ile	Ala	Thr	Thr	Ser	Phe	Leu	Gly	Lys	Lys					
185					190					195										
ggt	ttg	cct	act	ttc	ttc	caa	aat	gtt	gtt	ggt	ggt	ttt	att	gcc	acg	739				
Gly	Leu	Pro	Thr	Phe	Phe	Gln	Asn	Val	Val	Gly	Gly	Phe	Ile	Ala	Thr					
200					205					210										
ctg	cct	gca	tcg	att	gct	tat	tct	ttg	gcg	ttg	caa	ttt	ggt	ctt	gag	787				
Leu	Pro	Ala	Ser	Ile	Ala	Tyr	Ser	Leu	Ala	Leu	Gln	Phe	Gly	Leu	Glu					
215					220					225										
atc	aaa	ccg	agc	cag	atc	atc	gca	tct	gga	att	gtt	gtg	ctg	ttg	gca	835				
Ile	Lys	Pro	Ser	Gln	Ile	Ile	Ala	Ser	Gly	Ile	Val	Val	Leu	Leu	Ala					
230					235					240					245					
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Gly	Leu	Thr	Leu	Val	Gln	Ser	Leu	Gln	Asp	Gly	Ile	Thr	Gly	Ala	Pro					
250					255					260										

gtg	aca	gca	agt	gca	cga	ttt	ttc	gaa	aca	ctc	ctg	ttt	acc	ggc	ggc	931
Val	Thr	Ala	Ser	Ala	Arg	Phe	Phe	Glu	Thr	Leu	Leu	Phe	Thr	Gly	Gly	
			265					270					275			
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Ile	Val	Ala	Gly	Val	Gly	Leu	Gly	Ile	Gln	Leu	Ser	Glu	Ile	Leu	His	
		280					285					290				
gtc	atg	ttg	cct	gcc	atg	gag	tcc	gct	gca	gca	cct	aat	tat	tcg	tct	1027
Val	Met	Leu	Pro	Ala	Met	Glu	Ser	Ala	Ala	Ala	Pro	Asn	Tyr	Ser	Ser	
	295					300					305					
aca	ttc	gcc	cgc	att	atc	gct	ggg	ggc	gtc	acc	gca	gcg	gcc	ttc	gca	1075
Thr	Phe	Ala	Arg	Ile	Ile	Ala	Gly	Gly	Val	Thr	Ala	Ala	Ala	Phe	Ala	
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Val	Gly	Cys	Tyr	Ala	Glu	Trp	Ser	Ser	Val	Ile	Ile	Ala	Gly	Leu	Thr	
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gcg	ctg	atg	ggg	tct	gcg	ttt	tat	tac	ctc	ttc	gtt	gtt	tat	tta	ggc	1171
Ala	Leu	Met	Gly	Ser	Ala	Phe	Tyr	Tyr	Leu	Phe	Val	Val	Tyr	Leu	Gly	
			345				350						355			
ccc	gtc	tct	gcc	gct	gcg	att	gct	gca	aca	gca	gtt	ggg	ttc	act	ggg	1219
Pro	Val	Ser	Ala	Ala	Ala	Ile	Ala	Ala	Thr	Ala	Val	Gly	Phe	Thr	Gly	
		360					365					370				
ggg	ttg	ctt	gcc	cgt	cga	ttc	ttg	att	cca	ccg	ttg	att	gtg	gcg	att	1267
Gly	Leu	Leu	Ala	Arg	Arg	Phe	Leu	Ile	Pro	Pro	Leu	Ile	Val	Ala	Ile	
	375					380					385					
gcc	ggc	atc	aca	cca	atg	ctt	cca	ggg	cta	gca	att	tac	cgc	gga	atg	1315
Ala	Gly	Ile	Thr	Pro	Met	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Arg	Gly	Met	
390					395				400						405	
tac	gcc	acc	ctg	aat	gat	caa	aca	ctc	atg	ggg	ttc	acc	aac	att	gcg	1363
Tyr	Ala	Thr	Leu	Asn	Asp	Gln	Thr	Leu	Met	Gly	Phe	Thr	Asn	Ile	Ala	
				410					415					420		
gtt	gct	tta	gcc	act	gct	tca	tca	ctt	gcc	gct	ggc	gtg	gtt	ttg	ggg	1411
Val	Ala	Leu	Ala	Thr	Ala	Ser	Ser	Leu	Ala	Ala	Gly	Val	Val	Leu	Gly	
			425					430					435			
gag	tgg	att	gcc	cgc	agg	cta	cgt	cgt	cca	cca	cgc	ttc	aac	cca	tac	1459
Glu	Trp	Ile	Ala	Arg	Arg	Leu	Arg	Arg	Pro	Pro	Arg	Phe	Asn	Pro	Tyr	
		440					445					450				
cgt	gca	ttt	acc	aag	gcg	aat	gag	ttc	tcc	ttc	cag	gag	gaa	gct	gag	1507
Arg	Ala	Phe	Thr	Lys	Ala	Asn	Glu	Phe	Ser	Phe	Gln	Glu	Glu	Ala	Glu	
	455					460					465					
cag	aat	cag	cgc	cgg	cag	aga	aaa	cgt	cca	aag	act	aat	cag	aga	ttc	1555
Gln	Asn	Gln	Arg	Arg	Gln	Arg	Lys	Arg	Pro	Lys	Thr	Asn	Gln	Arg	Phe	
470					475				480						485	
ggg	aat	aaa	agg	taaaaaatcaa	cctgcttagg	cgt										1590
Gly	Asn	Lys	Arg													

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 558

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Ala Lys Ala Ala Pro Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr
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Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly
          35           40           45

Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln
          50           55           60

Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp
          65           70           75           80

Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg
          85           90           95

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn
          100          105          110

Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala
          115          120          125

Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu
          130          135          140

Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala
          145          150          155          160

Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val
          165          170          175

Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser
          180          185          190

Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly
          195          200          205

Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu
          210          215          220

Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile
          225          230          235          240

Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly
          245          250          255

Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu
          260          265          270

Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu
          275          280          285
  
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Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala
 290 295 300
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr
 305 310 315 320
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile
 325 330 335
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe
 340 345 350
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala
 355 360 365
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro
 370 375 380
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala
 385 390 395 400
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly
 405 410 415
 Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala
 420 425 430
 Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro
 435 440 445
 Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe
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 <223> RXN03095

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 Met Asn Ala Asp Lys
 1 5
 aaa atg tgc gga atg aac ccg gat agc caa tac gtc gaa ctt gcc gtc 163
 Lys Met Cys Gly Met Asn Pro Asp Ser Gln Tyr Val Glu Leu Ala Val
 10 15 20

gaa gtt ttc gga ctc ctc gcg gac gcc act cga gtt cgc atc atc ttg 211
 Glu Val Phe Gly Leu Leu Ala Asp Ala Thr Arg Val Arg Ile Ile Leu
 25 30 35

gca ctt cga aac agt ggt gaa ctt tcc gta aac cac ctc gcg gac atc 259
 Ala Leu Arg Asn Ser Gly Glu Leu Ser Val Asn His Leu Ala Asp Ile
 40 45 50

gtc gat aaa tcc ccc gca gca gtt tcc caa cac ctc gcc cgg ctg cgc 307
 Val Asp Lys Ser Pro Ala Ala Val Ser Gln His Leu Ala Arg Leu Arg
 55 60 65

atg gcc cga atc gtg tcc acc cgt caa gaa ggt caa cga gtt ttc tac 355
 Met Ala Arg Ile Val Ser Thr Arg Gln Glu Gly Gln Arg Val Phe Tyr
 70 75 80 85

aaa ctc acc aat gaa cac gca tca cag cta gtc tcc gac gct att ttt 403
 Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val Ser Asp Ala Ile Phe
 90 95 100

cag gcg gaa cac acc att gcg gac ggc cag act ccc cca cac cac cac 451
 Gln Ala Glu His Thr Ile Ala Asp Gly Gln Thr Pro Pro His His His
 105 110 115

cga gaa cga gaa caa tca tgaccaccca cagtcaccaa gaa 492
 Arg Glu Arg Glu Gln Ser
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<211> 123

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

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 20 25 30

Val Arg Ile Ile Leu Ala Leu Arg Asn Ser Gly Glu Leu Ser Val Asn
 35 40 45

His Leu Ala Asp Ile Val Asp Lys Ser Pro Ala Ala Val Ser Gln His
 50 55 60

Leu Ala Arg Leu Arg Met Ala Arg Ile Val Ser Thr Arg Gln Glu Gly
 65 70 75 80

Gln Arg Val Phe Tyr Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val
 85 90 95

Ser Asp Ala Ile Phe Gln Ala Glu His Thr Ile Ala Asp Gly Gln Thr
 100 105 110

Pro Pro His His His Arg Glu Arg Glu Gln Ser
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<210> 561


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<213> Corynebacterium glutamicum
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<400> 562

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Ser Ala Phe Gly Gly Pro Thr Ala His Leu Gly Tyr Phe Arg Thr Glu
 20 25 30

Phe Val Glu Arg Arg Arg Trp Leu Asp Asp Arg Gln Tyr Ser Glu Ile
 35 40 45

Val Ala Leu Ser Gln Leu Leu Pro Gly Pro Gly Ser Ser Gln Val Gly
 50 55 60

Met Met Leu Gly Tyr His Arg Ala Gly Phe Ser Gly Met Ala Ile Ala
 65 70 75 80

Trp Leu Met Phe Thr Trp Pro Ser Leu Ala Leu Met Ala Ala Phe Ala
 85 90 95

Leu Leu Phe Asp Ala Thr Ser Ala Ser Trp Thr Leu Gly Leu Leu Ala
 100 105 110

Ala Ala Val Ala Val Val Phe Lys Arg Ser His Arg Ala Trp Arg Gly
 115 120 125

Ser Met Ala Ser Thr Pro Gly Arg Arg Pro Pro Ser Gly Val Gly Leu
 130 135 140

Gly Ala Ser Arg Val Leu Gly Pro Pro Gln Arg Gly
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<212> DNA

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aagcagtgcg cgccgctgat acttcaggag gtgcggcatc atg atg aat ttt aag 115
 Met Met Asn Phe Lys
 1 5

tcc atc gtg tgc gtc act gcc tgg cag gtg ttt agc cgc cag gtg ctg 163
 Ser Ile Val Cys Val Thr Ala Trp Gln Val Phe Ser Arg Gln Val Leu
 10 15 20

cac agc cca tca acg tgg tct gaa gaa cta tcc aag ctg ttg ttc gtg 211
 His Ser Pro Ser Thr Trp Ser Glu Glu Leu Ser Lys Leu Leu Phe Val
 25 30 35

tgg cta tct ttc gca ggt agt gcg ttc ctc ttt gga gag cgt gga cat 259
 Trp Leu Ser Phe Ala Gly Ser Ala Phe Leu Phe Gly Glu Arg Gly His
 40 45 50

att gcg gtt gat ttc atc gcg cgc aaa ctg cct gtt tct gcg cag cgg 307
 Ile Ala Val Asp Phe Ile Ala Arg Lys Leu Pro Val Ser Ala Gln Arg
 55 60 65

gtc ctg cag gtc att gtt cag ttg ttg att gtt gtt ttt gcg atc ctc 355
 Val Leu Gln Val Ile Val Gln Leu Leu Ile Val Val Phe Ala Ile Leu
 70 75 80 85

ggc atg atc tgg ggt ggc tac ttg gct gca tca atc gcg tgg aat cag 403
 Gly Met Ile Trp Gly Gly Tyr Leu Ala Ala Ser Ile Ala Trp Asn Gln
 90 95 100

cag ctc act gcg ctg cca ctt acc ttg gga tgg gtg tat gtt gtc atc 451
 Gln Leu Thr Ala Leu Pro Leu Thr Leu Gly Trp Val Tyr Val Val Ile
 105 110 115

ccg atc gcg ggt gtg ttc atc gcg ttg ttc gcg atc atc gat ctc atc 499
 Pro Ile Ala Gly Val Phe Ile Ala Leu Phe Ala Ile Ile Asp Leu Ile
 120 125 130

gaa gtg gcc aca ggc aag gaa gag cct tac ccc ctt gtt gat gaa tca 547
 Glu Val Ala Thr Gly Lys Glu Glu Pro Tyr Pro Leu Val Asp Glu Ser
 135 140 145

gaa gaa cct cga gat ttg gac gag cta gag gcc caa agc gct ata gat 595
 Glu Glu Pro Arg Asp Leu Asp Glu Leu Glu Ala Gln Ser Ala Ile Asp
 150 155 160 165

tct gca agt tca gcg gaa ggt agg aac taatatgttg tcgccagcag 642
 Ser Ala Ser Ser Ala Glu Gly Arg Asn
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ctg 645

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Lys Leu Leu Phe Val Trp Leu Ser Phe Ala Gly Ser Ala Phe Leu Phe
 35 40 45

Gly Glu Arg Gly His Ile Ala Val Asp Phe Ile Ala Arg Lys Leu Pro
 50 55 60

Val Ser Ala Gln Arg Val Leu Gln Val Ile Val Gln Leu Leu Ile Val
 65 70 75 80

Val Phe Ala Ile Leu Gly Met Ile Trp Gly Gly Tyr Leu Ala Ala Ser
 85 90 95

Ile Ala Trp Asn Gln Gln Leu Thr Ala Leu Pro Leu Thr Leu Gly Trp

100 105 110
 Val Tyr Val Val Ile Pro Ile Ala Gly Val Phe Ile Ala Leu Phe Ala
 115 120 125
 Ile Ile Asp Leu Ile Glu Val Ala Thr Gly Lys Glu Glu Pro Tyr Pro
 130 135 140
 Leu Val Asp Glu Ser Glu Glu Pro Arg Asp Leu Asp Glu Leu Glu Ala
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 Gln Ser Ala Ile Asp Ser Ala Ser Ser Ala Glu Gly Arg Asn
 165 170

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 Met Val Val Lys Glu
 1 5
 gtt gac gtc gaa aag caa aaa gct ggc cgg gtg cct ggt gct ata gct 163
 Val Asp Val Glu Lys Gln Lys Ala Gly Arg Val Pro Gly Ala Ile Ala
 10 15 20
 aag cgt cgg acc gtg cgg att gtg ctg ttt gtc gcg ctg ggc gcg atc 211
 Lys Arg Arg Thr Val Arg Ile Val Leu Phe Val Ala Leu Gly Ala Ile
 25 30 35
 gtg att gcg gcg tcg ctg tgg tcg att ctg gtc ggc caa tac acc atc 259
 Val Ile Ala Ala Ser Leu Trp Ser Ile Leu Val Gly Gln Tyr Thr Ile
 40 45 50
 ccg att cgc gat cta cct gcg att tta gcc tcc ggt ccg acc ggt gcg 307
 Pro Ile Arg Asp Leu Pro Ala Ile Leu Ala Ser Gly Pro Thr Gly Ala
 55 60 65
 cag acg atg gcg gaa caa gtc gtg tgg caa atc cgc atg ccg cgc atc 355
 Gln Thr Met Ala Glu Gln Val Val Trp Gln Ile Arg Met Pro Arg Ile
 70 75 80 85
 gtg ctg gga ctg ctc gtg ggt gcc gct ttg ggc gtg gcc ggc gcg ctg 403
 Val Leu Gly Leu Leu Val Gly Ala Ala Leu Gly Val Ala Gly Ala Leu
 90 95 100
 ttg cag gcg gtg ttt tcc aac ccg ctg gcg gaa ccg tcg atc atc ggc 451
 Leu Gln Ala Val Phe Ser Asn Pro Leu Ala Glu Pro Ser Ile Ile Gly
 105 110 115
 gtg acc tcc ggc gcg ggc gtg ggt gct gct gcg gtg atc gtg ttt aac 499

Val	Thr	Ser	Gly	Ala	Gly	Val	Gly	Ala	Ala	Ala	Val	Ile	Val	Phe	Asn	
		120					125					130				
ctg	aca	ttt	ttg	ggc	aca	tcc	acc	gtc	gca	gtc	ggc	gcg	ttt	att	acc	547
Leu	Thr	Phe	Leu	Gly	Thr	Ser	Thr	Val	Ala	Val	Gly	Ala	Phe	Ile	Thr	
	135					140					145					
gcg	gtg	atc	acc	acg	att	ttg	gta	tat	cag	ctg	gcc	aga	agc	cgt	gga	595
Ala	Val	Ile	Thr	Thr	Ile	Leu	Val	Tyr	Gln	Leu	Ala	Arg	Ser	Arg	Gly	
150					155					160					165	
cgt	gtg	caa	gtg	atc	aac	ctg	atc	ctg	aca	ggc	ata	gcc	att	aat	gca	643
Arg	Val	Gln	Val	Ile	Asn	Leu	Ile	Leu	Thr	Gly	Ile	Ala	Ile	Asn	Ala	
				170					175					180		
gta	tcc	ggc	gcg	ctg	acc	tca	gtt	ctt	gat	cta	cat	cgc	gcc	gac	gag	691
Val	Ser	Gly	Ala	Leu	Thr	Ser	Val	Leu	Asp	Leu	His	Arg	Ala	Asp	Glu	
			185					190						195		
ctc	ccg	cga	aga	aat	att	ttc	tgc	aga	tgg	gtt	cct	cac	ggc	tcg	cat	739
Leu	Pro	Arg	Arg	Asn	Ile	Phe	Cys	Arg	Trp	Val	Pro	His	Gly	Ser	His	
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ggc	gca	cgt	caa	cgt												754
Gly	Ala	Arg	Gln	Arg												
				215												

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<212> PRT

<213> Corynebacterium glutamicum

<400> 566

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Pro	Gly	Ala	Ile	Ala	Lys	Arg	Arg	Thr	Val	Arg	Ile	Val	Leu	Phe	Val	
			20					25					30			
Ala	Leu	Gly	Ala	Ile	Val	Ile	Ala	Ala	Ser	Leu	Trp	Ser	Ile	Leu	Val	
		35					40					45				
Gly	Gln	Tyr	Thr	Ile	Pro	Ile	Arg	Asp	Leu	Pro	Ala	Ile	Leu	Ala	Ser	
	50					55					60					
Gly	Pro	Thr	Gly	Ala	Gln	Thr	Met	Ala	Glu	Gln	Val	Val	Trp	Gln	Ile	
65					70					75					80	
Arg	Met	Pro	Arg	Ile	Val	Leu	Gly	Leu	Leu	Val	Gly	Ala	Ala	Leu	Gly	
				85					90					95		
Val	Ala	Gly	Ala	Leu	Leu	Gln	Ala	Val	Phe	Ser	Asn	Pro	Leu	Ala	Glu	
			100					105					110			
Pro	Ser	Ile	Ile	Gly	Val	Thr	Ser	Gly	Ala	Gly	Val	Gly	Ala	Ala	Ala	
		115					120					125				
Val	Ile	Val	Phe	Asn	Leu	Thr	Phe	Leu	Gly	Thr	Ser	Thr	Val	Ala	Val	
	130					135						140				

Gly Ala Phe Ile Thr Ala Val Ile Thr Thr Ile Leu Val Tyr Gln Leu
 145 150 155 160
 Ala Arg Ser Arg Gly Arg Val Gln Val Ile Asn Leu Ile Leu Thr Gly
 165 170 175
 Ile Ala Ile Asn Ala Val Ser Gly Ala Leu Thr Ser Val Leu Asp Leu
 180 185 190
 His Arg Ala Asp Glu Leu Pro Arg Arg Asn Ile Phe Cys Arg Trp Val
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 Pro His Gly Ser His Gly Ala Arg Gln Arg
 210 215

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 <223> RXN02979

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 Met Thr Ala Pro Asn
 1 5
 act ctc aag caa aca act ctt cgc tct gat gag ttc tct tgc cca tcc 163
 Thr Leu Lys Gln Thr Thr Leu Arg Ser Asp Glu Phe Ser Cys Pro Ser
 10 15 20
 tgt gtc tcc aag att gaa aac aaa ttg aat gga ttg gat ggc gtc gac 211
 Cys Val Ser Lys Ile Glu Asn Lys Leu Asn Gly Leu Asp Gly Val Asp
 25 30 35
 aat gca gag gtg aag ttc tcc tcc gga aga atc ctt gtt gat cac gac 259
 Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile Leu Val Asp His Asp
 40 45 50
 ccc agc aag gtc tct atc aag gat cta gtc gct gca gtc gca gag gtt 307
 Pro Ser Lys Val Ser Ile Lys Asp Leu Val Ala Ala Val Ala Glu Val
 55 60 65
 ggc tac acc gca aag cca tca gca atc taaaactctc agttagacca 354
 Gly Tyr Thr Ala Lys Pro Ser Ala Ile
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<210> 568
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 568

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 20 25 30

Leu Asp Gly Val Asp Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile
 35 40 45

Leu Val Asp His Asp Pro Ser Lys Val Ser Ile Lys Asp Leu Val Ala
 50 55 60

Ala Val Ala Glu Val Gly Tyr Thr Ala Lys Pro Ser Ala Ile
 65 70 75

<210> 569

<211> 357

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXN02987

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 Met Thr Ala Pro Ala
 1 5

acg ctg aag aac acc acc ttg cgc tct gat gag ttc acc tgt ccg agc 163
 Thr Leu Lys Asn Thr Thr Leu Arg Ser Asp Glu Phe Thr Cys Pro Ser
 10 15 20

tgt gtc gcc aag atc gaa aac aag ctg aat ggt ttg gac ggc gtg gag 211
 Cys Val Ala Lys Ile Glu Asn Lys Leu Asn Gly Leu Asp Gly Val Glu
 25 30 35

aat gcg gag gtg aag ttc tcc tcc gga cgc atc ctg atc acc cac gac 259
 Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile Leu Ile Thr His Asp
 40 45 50

cca cag aag gtc tcc gta cgt gac ctg gtc acc gcg gta gcc gag gtc 307
 Pro Gln Lys Val Ser Val Arg Asp Leu Val Thr Ala Val Ala Glu Val
 55 60 65

ggg tac acc gcc aag ccg tcg gcg atc tgacgcactc ccgacccac 354
 Gly Tyr Thr Ala Lys Pro Ser Ala Ile
 70 75

aag 357

<210> 570

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 570

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 20 25 30
 Leu Asp Gly Val Glu Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile
 35 40 45
 Leu Ile Thr His Asp Pro Gln Lys Val Ser Val Arg Asp Leu Val Thr
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<212> DNA

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<222> (101)..(1018)

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 Met Ser Ser Arg Arg
 1 5
 aaa ctg tcc tcc gca ctg atc gtg ctt ctg gca gca gca cta cct ctt 163
 Lys Leu Ser Ser Ala Leu Ile Val Leu Leu Ala Ala Ala Leu Pro Leu
 10 15 20
 act gct tgt tcc tcc agc tca gaa gag gaa gca tcc acc agc tct gcg 211
 Thr Ala Cys Ser Ser Ser Ser Glu Glu Glu Ala Ser Thr Ser Ser Ala
 25 30 35
 act cgc gaa ttc aca gac gct cac gga aca acc gaa gtt ccc gaa aat 259
 Thr Arg Glu Phe Thr Asp Ala His Gly Thr Thr Glu Val Pro Glu Asn
 40 45 50
 cct cag cgc gtc gtt gtc ctg gag cca ctt gag cta gac acc gca atc 307
 Pro Gln Arg Val Val Val Leu Glu Pro Leu Glu Leu Asp Thr Ala Ile
 55 60 65
 gcc ctg gga atc acc cca gtg ggt gca gct gtc gcc aac aac gtc act 355
 Ala Leu Gly Ile Thr Pro Val Gly Ala Ala Val Ala Asn Asn Val Thr
 70 75 80 85
 ggt att cct gca tat ctg ggc gtc gat gga atc gag cct gtc ggc acc 403
 Gly Ile Pro Ala Tyr Leu Gly Val Asp Gly Ile Glu Pro Val Gly Thr
 90 95 100
 gtt tct gag cca aat atc gaa gcg atc gct gct ctg gag ccc gac ctg 451
 Val Ser Glu Pro Asn Ile Glu Ala Ile Ala Ala Leu Glu Pro Asp Leu

105					110					115						
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Ile	Leu	Gly	Thr	Asp	Ser	Arg	His	Ala	Glu	Ile	Tyr	Asp	Arg	Leu	Glu	
120					125					130						
tcc	atc	gcc	cca	acc	gtg	ttc	atg	aca	acc	cat	gtt	gat	ccg	tgg	aaa	547
Ser	Ile	Ala	Pro	Thr	Val	Phe	Met	Thr	Thr	His	Val	Asp	Pro	Trp	Lys	
135					140					145						
gac	aat	gtc	gtc	ttc	atc	ggc	gat	gca	ttg	ggc	aag	aag	cag	gaa	tcc	595
Asp	Asn	Val	Val	Phe	Ile	Gly	Asp	Ala	Leu	Gly	Lys	Lys	Gln	Glu	Ser	
150					155					160					165	
gag	gat	ctc	atc	caa	ggc	ttt	aat	gac	aag	tgc	gaa	gag	atc	aag	tcc	643
Glu	Asp	Leu	Ile	Gln	Gly	Phe	Asn	Asp	Lys	Cys	Glu	Glu	Ile	Lys	Ser	
170					175					180						
gag	cat	gat	gtc	gaa	ggc	aag	acc	gtc	aac	atg	att	cgt	ccc	cgc	gac	691
Glu	His	Asp	Val	Glu	Gly	Lys	Thr	Val	Asn	Met	Ile	Arg	Pro	Arg	Asp	
185					190					195						
gag	caa	acc	atg	agc	cta	tac	ggc	ccg	acc	tca	ttt	gcc	ggc	agc	tct	739
Glu	Gln	Thr	Met	Ser	Leu	Tyr	Gly	Pro	Thr	Ser	Phe	Ala	Gly	Ser	Ser	
200					205					210						
ttg	gag	tgc	gca	gga	ctc	acc	att	cct	gat	cag	gaa	tgg	aag	gat	gac	787
Leu	Glu	Cys	Ala	Gly	Leu	Thr	Ile	Pro	Asp	Gln	Glu	Trp	Lys	Asp	Asp	
215					220					225						
ctc	cag	gcc	gac	atc	gct	cct	gag	aac	ttc	atg	ctc	gcc	acc	gcc	gac	835
Leu	Gln	Ala	Asp	Ile	Ala	Pro	Glu	Asn	Phe	Met	Leu	Ala	Thr	Ala	Asp	
230					235					240					245	
tac	gtc	ttt	gtc	acc	gca	act	gat	gtc	acc	gat	gaa	aat	gag	ctc	ccc	883
Tyr	Val	Phe	Val	Thr	Ala	Thr	Asp	Val	Thr	Asp	Glu	Asn	Glu	Leu	Pro	
250					255					260						
gaa	gta	atc	cga	gaa	aac	cgc	gaa	cag	ttc	cca	tca	ctc	acc	ctt	gtc	931
Glu	Val	Ile	Arg	Glu	Asn	Arg	Glu	Gln	Phe	Pro	Ser	Leu	Thr	Leu	Val	
265					270					275						
gat	acc	agc	tac	tgg	gta	tct	ggc	gtc	ggc	cca	ctt	ggc	ggc	agc	aaa	979
Asp	Thr	Ser	Tyr	Trp	Val	Ser	Gly	Val	Gly	Pro	Leu	Gly	Gly	Ser	Lys	
280					285					290						
gtc	ttg	gaa	gac	atc	gat	gcc	ttc	ctc	gac	gca	cag	caa	taatgtccac			1028
Val	Leu	Glu	Asp	Ile	Asp	Ala	Phe	Leu	Asp	Ala	Gln	Gln				
295					300					305						
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<210> 572

<211> 306

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

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 20 25 30
 Ser Thr Ser Ser Ala Thr Arg Glu Phe Thr Asp Ala His Gly Thr Thr
 35 40 45
 Glu Val Pro Glu Asn Pro Gln Arg Val Val Val Leu Glu Pro Leu Glu
 50 55 60
 Leu Asp Thr Ala Ile Ala Leu Gly Ile Thr Pro Val Gly Ala Ala Val
 65 70 75 80
 Ala Asn Asn Val Thr Gly Ile Pro Ala Tyr Leu Gly Val Asp Gly Ile
 85 90 95
 Glu Pro Val Gly Thr Val Ser Glu Pro Asn Ile Glu Ala Ile Ala Ala
 100 105 110
 Leu Glu Pro Asp Leu Ile Leu Gly Thr Asp Ser Arg His Ala Glu Ile
 115 120 125
 Tyr Asp Arg Leu Glu Ser Ile Ala Pro Thr Val Phe Met Thr Thr His
 130 135 140
 Val Asp Pro Trp Lys Asp Asn Val Val Phe Ile Gly Asp Ala Leu Gly
 145 150 155 160
 Lys Lys Gln Glu Ser Glu Asp Leu Ile Gln Gly Phe Asn Asp Lys Cys
 165 170 175
 Glu Glu Ile Lys Ser Glu His Asp Val Glu Gly Lys Thr Val Asn Met
 180 185 190
 Ile Arg Pro Arg Asp Glu Gln Thr Met Ser Leu Tyr Gly Pro Thr Ser
 195 200 205
 Phe Ala Gly Ser Ser Leu Glu Cys Ala Gly Leu Thr Ile Pro Asp Gln
 210 215 220
 Glu Trp Lys Asp Asp Leu Gln Ala Asp Ile Ala Pro Glu Asn Phe Met
 225 230 235 240
 Leu Ala Thr Ala Asp Tyr Val Phe Val Thr Ala Thr Asp Val Thr Asp
 245 250 255
 Glu Asn Glu Leu Pro Glu Val Ile Arg Glu Asn Arg Glu Gln Phe Pro
 260 265 270
 Ser Leu Thr Leu Val Asp Thr Ser Tyr Trp Val Ser Gly Val Gly Pro
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<212> DNA

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<223> RXN03183

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aaa gac ggc gtc ggc gta tcc acc ctt ggt ggc tac aac aac ggc atc 96
Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile
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aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc 144
Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe
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atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca 192
Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro
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cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240
Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr
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cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288
Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg
          85             90             95

cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336
Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn
          100             105             110

gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384
Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr
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gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca 437
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<213> Corynebacterium glutamicum

<400> 574

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Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe

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Met Glu Ser His Asp																
1 5																
ctt cag cag cgc agt tat gcg cac aat ccc gat ggc cac gac cac agc																163
Leu Gln Gln Arg Ser Tyr Ala His Asn Pro Asp Gly His Asp His Ser																
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cat gac gga ctc gga cac tca cat gct ccc agc tcc ctc aag gct ctt																211
His Asp Gly Leu Gly His Ser His Ala Pro Ser Ser Leu Lys Ala Leu																
25 30 35																
ttt gcg gtc atc att ttc acc tcg atc atc ttc cta gcg gaa cta atc																259
Phe Ala Val Ile Ile Phe Thr Ser Ile Ile Phe Leu Ala Glu Leu Ile																
40 45 50																
gcc gcc ctt att tcc gga tct ttg gca ctg ctg gct gac gcc atg cac																307
Ala Gly Leu Ile Ser Gly Ser Leu Ala Leu Leu Ala Asp Ala Met His																
55 60 65																
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Met Leu Ser Asp Ser Thr Gly Leu Ile Ile Ala Ala Val Ala Met Leu																
70 75 80 85																
att gcc cgt cgg gca cgc act tct cgt gcg acc tac gga tac aag cgt																403
Ile Gly Arg Arg Ala Arg Thr Ser Arg Ala Thr Tyr Gly Tyr Lys Arg																
90 95 100																

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 Ala Glu Val Leu Ala Ala Met Val Asn Ala Thr Val Val Thr Ala Leu
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 tct gtg tgg atc gtc gtt gag gcc atc atg cgt ctg ggc aag gac ctg 499
 Ser Val Trp Ile Val Val Glu Ala Ile Met Arg Leu Gly Lys Asp Leu
 120 125 130
 gaa atc cag acc aac ctg atg ctc atc gtc gcg gtc att ggt ttt gtc 547
 Glu Ile Gln Thr Asn Leu Met Leu Ile Val Ala Val Ile Gly Phe Val
 135 140 145
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 Thr Asn Gly Ile Ser Ala Leu Val Leu Met Arg His Gln Asp Gly Asn
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 atc aat atg cgt gga gca ttc ctt cac gtt ctc agt gac atg ctg ggt 643
 Ile Asn Met Arg Gly Ala Phe Leu His Val Leu Ser Asp Met Leu Gly
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 tcc gtt gcc gtc att att gcg ggc ctg gtg att cgc tac acg gga tgg 691
 Ser Val Ala Val Ile Ile Ala Gly Leu Val Ile Arg Tyr Thr Gly Trp
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 Met Pro Ala Asp Thr Ile Ala Ser Ile Ala Ile Ala Ala Ile Ile Ile
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 Pro Arg Ala Phe Ser Leu Leu Lys Glu Ala Leu Asn Ile Leu Leu Glu
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 cgt gtt cct aca ggt gcg gag cct gca gag gtc gac gca gcc ctt cgt 835
 Arg Val Pro Thr Gly Glu Glu Pro Ala Glu Val Asp Ala Ala Leu Arg
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 aaa gtc cca ggt gtc agc gat gtg cat gat ctt cac att tgg agc att 883
 Lys Val Pro Gly Val Ser Asp Val His Asp Leu His Ile Trp Ser Ile
 250 255 260
 gac ggc aag gaa atc ctg gcc acg gtg cat ttg gtg gtg gat tcg tct 931
 Asp Gly Lys Glu Ile Leu Ala Thr Val His Leu Val Val Asp Ser Ser
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 Thr Asn Gln Leu His Ser Cys Gly Val Leu Asp Arg Ala Glu Ala Glu
 280 285 290
 cta tcc aaa ctt ggg atc ttg cac tca aca att cag ctg gaa agc gca 1027
 Leu Ser Lys Leu Gly Ile Leu His Ser Thr Ile Gln Leu Glu Ser Ala
 295 300 305
 gat cac agt gat cat gaa agt gtg tgc tgatatagag tatgtcccat 1074
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<210> 576

<211> 318

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

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Ser Leu Lys Ala Leu Phe Ala Val Ile Ile Phe Thr Ser Ile Ile Phe
          35           40           45
Leu Ala Glu Leu Ile Ala Gly Leu Ile Ser Gly Ser Leu Ala Leu Leu
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Ala Asp Ala Met His Met Leu Ser Asp Ser Thr Gly Leu Ile Ile Ala
          65           70           75           80
Ala Val Ala Met Leu Ile Gly Arg Arg Ala Arg Thr Ser Arg Ala Thr
          85           90           95
Tyr Gly Tyr Lys Arg Ala Glu Val Leu Ala Ala Met Val Asn Ala Thr
          100           105           110
Val Val Thr Ala Leu Ser Val Trp Ile Val Val Glu Ala Ile Met Arg
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Leu Gly Lys Asp Leu Glu Ile Gln Thr Asn Leu Met Leu Ile Val Ala
          130           135           140
Val Ile Gly Phe Val Thr Asn Gly Ile Ser Ala Leu Val Leu Met Arg
          145           150           155           160
His Gln Asp Gly Asn Ile Asn Met Arg Gly Ala Phe Leu His Val Leu
          165           170           175
Ser Asp Met Leu Gly Ser Val Ala Val Ile Ile Ala Gly Leu Val Ile
          180           185           190
Arg Tyr Thr Gly Trp Met Pro Ala Asp Thr Ile Ala Ser Ile Ala Ile
          195           200           205
Ala Ala Ile Ile Ile Pro Arg Ala Phe Ser Leu Leu Lys Glu Ala Leu
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Asn Ile Leu Leu Glu Arg Val Pro Thr Gly Ala Glu Pro Ala Glu Val
          225           230           235           240
Asp Ala Ala Leu Arg Lys Val Pro Gly Val Ser Asp Val His Asp Leu
          245           250           255
His Ile Trp Ser Ile Asp Gly Lys Glu Ile Leu Ala Thr Val His Leu
          260           265           270
Val Val Asp Ser Ser Thr Asn Gln Leu His Ser Cys Gly Val Leu Asp
          275           280           285
Arg Ala Glu Ala Glu Leu Ser Lys Leu Gly Ile Leu His Ser Thr Ile
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 <213> Corynebacterium glutamicum

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 <223> RXN00378

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 Val Asp Lys Ala Val
 1 5
 aac act gct atc tct gac gcc aaa aca gcg gcg ctc aag gca ggt gtt 163
 Asn Thr Ala Ile Ser Asp Ala Lys Thr Ala Ala Leu Lys Ala Gly Val
 10 15 20
 gga ttg aac cga gcc acc gcc tca gaa gaa gag gaa gat tta agc tca 211
 Gly Leu Asn Arg Ala Thr Ala Ser Glu Glu Glu Glu Asp Leu Ser Ser
 25 30 35
 agc att aag gtt tct ttg gcc ttt gag ctc gag ggg tta agc aat gca 259
 Ser Ile Lys Val Ser Leu Ala Phe Glu Leu Glu Gly Leu Ser Asn Ala
 40 45 50
 cca tcg ttg atg gtg gtg gaa aaa gcc cta gag aag atc ccc ggt gta 307
 Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu Lys Ile Pro Gly Val
 55 60 65
 tcc gcg gat ctg att tac cct tca caa act gca tgg att aca gca act 355
 Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala Trp Ile Thr Ala Thr
 70 75 80 85
 gat cgg gta cat ccc gaa acc ctc att gag gtg ttt gag cag ttc ggc 403
 Asp Arg Val His Pro Glu Thr Leu Ile Glu Val Phe Glu Gln Phe Gly
 90 95 100
 atc aaa gca cac ctt tct aat tca tcg ctg ctg cgc agg cat caa cag 451
 Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu Arg Arg His Gln Gln
 105 110 115
 ctc agc gcg gaa gta aat agg gaa gca cgc ctt gat cgt tac cgc tcc 499
 Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu Asp Arg Tyr Arg Ser
 120 125 130
 cga atg gat gcc aag cga atc tcg cct cgt gtg cga agg cat aac cga 547
 Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val Arg Arg His Asn Arg
 135 140 145
 caa gaa atg gta cat gcg gta cgc gct cgt gaa agt ggt tgg att aaa 595
 Gln Glu Met Val His Ala Val Arg Ala Arg Glu Ser Gly Trp Ile Lys
 150 155 160 165

cgc agg aat cac acc acc tcg cag cat gaa gac cca atg tcg ggc gat	643
Arg Arg Asn His Thr Thr Ser Gln His Glu Asp Pro Met Ser Gly Asp	
170 175 180	
gtg ctg ttc acc gcc cgc gca ctg att aca cct aag cgt ttg tgg gtg	691
Val Leu Phe Thr Ala Arg Ala Leu Ile Thr Pro Lys Arg Leu Trp Val	
185 190 195	
tcg ttg ccg ttt gcg ctc atc gta ttg gcg tta tcg ttg aat cct tcg	739
Ser Leu Pro Phe Ala Leu Ile Val Leu Ala Leu Ser Leu Asn Pro Ser	
200 205 210	
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Trp Gln Phe Asp Tyr Trp Gln Trp Leu Ser Ala Val Leu Ala Ile Pro	
215 220 225	
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Val Val Val Trp Gly Ala Trp Pro Phe His Arg Ala Ala Ala Gly Gly	
230 235 240 245	
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Ile Arg Arg Gly Ile Ser Ala Leu Asp Ala Thr Ser Ser Ile Ala Ile	
250 255 260	
gct gct gca tac gcg tgg tct atc gcc atg ctg ttg ttt gaa acc cca	931
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265 270 275	
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Thr Val Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln	
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Ser Ser Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg	
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Ile Val Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu	
345 350 355	
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Leu Asn Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val	
360 365 370	
cca cct aat acc acg atc cct gtg gat ggc act gtc atc ggt ggc ggt	1267
Pro Pro Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly	
375 380 385	
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390 395 400 405	

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Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu	
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425 430 435	
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Val His Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn	
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Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu	
615 620 625	
cca ctg atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca	2035
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Glu	Thr	Met	Met	Leu	Ser	Arg	Asp	Thr	Tyr	Pro	Val	Ala	Arg	Arg	Tyr		
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gtg	ggg	gta	ctg	atg	ggc	gtc	gat	cgt	ccc	tca	gat	ctg	cgt	gat	gat	2467	
Val	Gly	Val	Leu	Met	Gly	Val	Asp	Arg	Pro	Ser	Asp	Leu	Arg	Asp	Asp		
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Ser	Val	Pro	Thr	Leu	Phe	Lys	Leu	Ala	Arg	Arg	Tyr	Ala	Lys	Leu	Val		
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Leu	Ala	Ser	Ser	Leu	Leu	Ile	Glu	Trp	Arg	Ser	Gly	Arg	Ala	Arg	Lys		
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Tyr																	
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<211> 870

<212> PRT

<213> Corynebacterium glutamicum

<400> 578

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 35 40 45
 Gly Leu Ser Asn Ala Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu
 50 55 60
 Lys Ile Pro Gly Val Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala
 65 70 75 80
 Trp Ile Thr Ala Thr Asp Arg Val His Pro Glu Thr Leu Ile Glu Val
 85 90 95
 Phe Glu Gln Phe Gly Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu
 100 105 110
 Arg Arg His Gln Gln Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu
 115 120 125
 Asp Arg Tyr Arg Ser Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val
 130 135 140
 Arg Arg His Asn Arg Gln Glu Met Val His Ala Val Arg Ala Arg Glu
 145 150 155 160
 Ser Gly Trp Ile Lys Arg Arg Asn His Thr Thr Ser Gln His Glu Asp
 165 170 175
 Pro Met Ser Gly Asp Val Leu Phe Thr Ala Arg Ala Leu Ile Thr Pro
 180 185 190
 Lys Arg Leu Trp Val Ser Leu Pro Phe Ala Leu Ile Val Leu Ala Leu
 195 200 205
 Ser Leu Asn Pro Ser Trp Gln Phe Asp Tyr Trp Gln Trp Leu Ser Ala
 210 215 220
 Val Leu Ala Ile Pro Val Val Val Trp Gly Ala Trp Pro Phe His Arg
 225 230 235 240
 Ala Ala Ala Gly Gly Ile Arg Arg Gly Ile Ser Ala Leu Asp Ala Thr
 245 250 255
 Ser Ser Ile Ala Ile Ala Ala Ala Tyr Ala Trp Ser Ile Ala Met Leu
 260 265 270
 Leu Phe Glu Thr Pro Gly Gly Lys Ser Trp Arg Ser Tyr Pro Ser Trp
 275 280 285
 Phe Ala Phe Asp His Gly Thr Leu Thr Gln Asn Glu Ile Tyr Phe Asp
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Val Ala Cys Gly Ile Thr Val Leu Leu Leu Ala Gly Arg Leu Leu Thr
 305 310 315 320
 Arg Arg Arg Ser Gln Ser Ser Leu Leu Ala Glu Leu Gly Arg Leu Gln
 325 330 335
 Ile Asp Pro Gln Arg Ile Val Thr Val Val Arg Lys His Arg Leu Lys
 340 345 350
 Arg Val Val Gln Glu Leu Asn Ile Pro Val Gln Glu Val Arg Val Asn
 355 360 365
 Asp Asp Val Lys Val Pro Pro Asn Thr Thr Ile Pro Val Asp Gly Thr
 370 375 380
 Val Ile Gly Gly Gly Ser Arg Ile Ala Ala Ser Ile Ile Met Gly Gln
 385 390 395 400
 Asp Gln Arg Asp Val Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu
 405 410 415
 Asn Leu Glu Ser Glu Ile Lys Val Arg Val Ile Arg Thr Gly His Arg
 420 425 430
 Thr Arg Ile Ala Ala Val His Arg Trp Val Lys Glu Ala Thr Leu Lys
 435 440 445
 Glu Asn Arg His Asn Arg Ala Ala Ile Arg Ser Ala Gly Asn Leu Val
 450 455 460
 Pro Ile Thr Phe Thr Leu Ala Val Val Asp Phe Cys Leu Trp Ala Leu
 465 470 475 480
 Ile Ser Gly Asn Ile Asn Ala Ala Phe Thr Thr Thr Leu Ala Val Leu
 485 490 495
 Ala Cys Val Ala Pro Val Ala Leu Ala Leu Ser Ala Pro Leu Ala Thr
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 Arg Asn Ser Ile Glu Ala Ala Ala Arg His Gly Ile Leu Val Arg Ser
 515 520 525
 Gly Glu Ile Phe Arg Val Leu Asp Asp Val Asp Thr Ala Val Phe Asn
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 545 550 555 560
 Ala Asp Lys Gly Glu Asp Pro Glu Leu Val Leu Arg Val Ala Gly Ala
 565 570 575
 Leu Ala Met Glu Ser His His Ala Ile Ser Lys Ala Leu Val Lys Ala
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 Ser Arg Glu Ala Arg Asp Thr Gly Ala Gly Gly Glu Asp Val Pro His
 595 600 605
 Trp Ile Glu Val Gly Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln
 610 615 620

Ala Thr Ile Glu Leu Pro Leu Ile Lys Pro Ser Gly Glu Lys Ile Met
625 630 635 640

Arg Thr Thr Glu Ala Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val
645 650 655

Arg Glu His Leu Ser Pro Arg Leu Val Ala Ala Ala Thr Ser Gly Gly
660 665 670

Ala Pro Leu Ile Val Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr
675 680 685

Leu Ser Asp His Val Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile
690 695 700

Glu Glu Gln Gly Ile Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro
705 710 715 720

Val Ala Arg Arg Tyr Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala
725 730 735

Gly Ile Ala Pro Gly Lys Lys Ala Gln Val Val Arg Ala Val His Thr
740 745 750

Arg Gly Ser Thr Val Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys
755 760 765

Leu Lys Val Ala Asp Val Gly Val Leu Met Gly Val Asp Arg Pro Ser
770 775 780

Asp Leu Arg Asp Asp Ser Asp Asp Pro Ala Ala Asp Val Val Val Met
785 790 795 800

Arg Glu Glu Val Met Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg
805 810 815

Tyr Ala Lys Leu Val Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn
820 825 830

Gly Val Ala Met Val Leu Ala Val Ser Gly Leu Leu His Pro Met Ala
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Gly Arg Ala Arg Lys Tyr
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<210> 579

<211> 1925

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1902)

<223> RXN01338

<400> 579

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Gly	Ile	Ile	Thr	Val	Ala	Ala	Leu	Val	Ala	Ile	Ala	Ile	His	Leu	Ile	
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tta	tgg	ctg	gct	cta	gat	cta	gat	ggc	ctt	gct	aaa	aac	tgg	cct	tta	144
Leu	Trp	Leu	Ala	Leu	Asp	Leu	Asp	Gly	Leu	Ala	Lys	Asn	Trp	Pro	Leu	
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ata	gcc	atc	gtt	atc	gta	ggt	ggc	att	ccg	ttg	atg	tgg	gat	gtg	ctg	192
Ile	Ala	Ile	Val	Ile	Val	Gly	Gly	Ile	Pro	Leu	Met	Trp	Asp	Val	Leu	
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aaa	tca	gcc	att	aaa	act	cgc	ggt	ggc	gcg	gat	act	tta	gca	gca	gtc	240
Lys	Ser	Ala	Ile	Lys	Thr	Arg	Gly	Gly	Ala	Asp	Thr	Leu	Ala	Ala	Val	
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tcc	atc	att	act	tct	gtg	ttg	tta	ggg	gag	tgg	ttg	gtt	gcc	gcg	atc	288
Ser	Ile	Ile	Thr	Ser	Val	Leu	Leu	Gly	Glu	Trp	Leu	Val	Ala	Ala	Ile	
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atc	gtg	ctc	atg	ctc	tct	ggt	ggt	gaa	gcg	cta	gaa	gag	gca	gca	tca	336
Ile	Val	Leu	Met	Leu	Ser	Gly	Gly	Glu	Ala	Leu	Glu	Glu	Ala	Ala	Ser	
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Arg	Arg	Ala	Ser	Gly	Thr	Leu	Asp	Ala	Leu	Ala	Arg	Arg	Ala	Pro	Ser	
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Thr	Ala	His	Arg	Leu	Leu	Gly	Ala	Thr	Ile	Leu	Asp	Gly	Thr	Glu	Glu	
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Ile	Ala	Val	Glu	Glu	Ile	Thr	Val	Gly	Asp	Leu	Val	Ala	Val	Leu	Pro	
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cat	gaa	ctt	tgt	ccc	gtg	gat	ggt	gaa	atc	gtg	gca	ggc	cac	ggc	acc	528
His	Glu	Leu	Cys	Pro	Val	Asp	Gly	Glu	Ile	Val	Ala	Gly	His	Gly	Thr	
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Met	Asp	Glu	Ser	Tyr	Leu	Thr	Gly	Glu	Pro	Tyr	Val	Val	Ser	Lys	Ser	
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Lys	Gly	Ser	Gln	Ala	Met	Ser	Gly	Ala	Val	Asn	Gly	Asp	Thr	Pro	Leu	
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Thr	Ile	Val	Ala	Thr	Lys	Leu	Ala	His	Asp	Ser	Arg	Tyr	Ala	Gln	Ile	
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Val	Gly	Val	Leu	His	Glu	Ala	Glu	Asn	Asn	Arg	Prc	Glu	Met	Arg	Arg	
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Met	Ala	Asp	Arg	Leu	Gly	Ala	Trp	Tyr	Thr	Val	Ile	Ala	Leu	Ala	Leu	

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Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala Val Pro Val																				
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Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val Ile Thr Asp																				
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Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu Ala Leu Ala																				
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Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg																				
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Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser																				
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Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu																				
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Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg																				
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Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val																				
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465 470 475 480																				
ctt gcg gac aag gtt ggc att gat gag gta cac gca gag gcc tca ccg	1488																			
Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro																				
485 490 495																				

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 Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr
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 atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg gcc gtt gcc 1584
 Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala
 515 520 525
 acc gtt ggt gtc gcg atg gga gca gac tcc gat gtc acg tcc gaa gca 1632
 Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala
 530 535 540
 gca gat gct gtg att ttg gat tct tcc ctg gaa cgt ctc gac gat ctg 1680
 Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu
 545 550 555 560
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 Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly
 565 570 575
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 Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly
 580 585 590
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 Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val Ile Asp Val
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 ctg gct atc ctc aat tcc gct cgg gtc gca ctg cca cgc gga gcg att 1872
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 625 630
 cgt 1925

<210> 580
 <211> 634
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 580
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 Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu
 35 40 45
 Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu
 50 55 60
 Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val
 65 70 75 80

Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile
 85 90 95
 Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser
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 Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser
 115 120 125
 Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly Thr Glu Glu
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 Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala Val Leu Pro
 145 150 155 160
 His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr
 165 170 175
 Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val Ser Lys Ser
 180 185 190
 Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp Thr Pro Leu
 195 200 205
 Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile
 210 215 220
 Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg
 225 230 235 240
 Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala Leu Ala Leu
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 Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg Phe Leu Ala
 260 265 270
 Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala Val Pro Val
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 Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly Ile Ile Val
 290 295 300
 Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys Thr Val Met
 305 310 315 320
 Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val Ile Thr Asp
 325 330 335
 Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu Ala Leu Ala
 340 345 350
 Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg
 355 360 365
 Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val Val Glu Val
 370 375 380
 Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu
 385 390 395 400
 Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser

405 410 415
 Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu
 420 425 430
 Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg
 435 440 445
 Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val
 450 455 460
 Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr
 465 470 475 480
 Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro
 485 490 495
 Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr
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 Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala
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 Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala
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 Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu
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 Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly
 565 570 575
 Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly
 580 585 590
 Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val Ile Asp Val
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 Ser Asp Phe Asp Thr Gln Glu Lys Val Ser
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<210> 581
 <211> 1917
 <212> DNA
 <213> Corynebacterium glutamicum

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 <221> CDS
 <222> (101)..(1894)
 <223> RXN00980

<400> 581
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 Met Leu Ala Asp Ala
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ttc atg atc gcg gct gca att gtt gca ggt tgg ccg atc gcg cag tct	163
Phe Met Ile Ala Ala Ala Ile Val Ala Gly Trp Pro Ile Ala Gln Ser	
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gca tat caa gca ctt cgc att cga atg gtg tgc att gac tta ctg gtc	211
Ala Tyr Gln Ala Leu Arg Ile Arg Met Val Ser Ile Asp Leu Leu Val	
25 30 35	
gtt gtg gct gcc gtt ggt gcc atg ttc atc aac aac tat tgg gag tct	259
Val Val Ala Ala Val Gly Ala Met Phe Ile Asn Asn Tyr Trp Glu Ser	
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gcg gcg gtg acg ttc ctc ttt gcc ctt ggc aag gca ctg gaa cgc gcg	307
Ala Ala Val Thr Phe Leu Phe Ala Leu Gly Lys Ala Leu Glu Arg Ala	
55 60 65	
aca atg aac cgc aca cga aaa gca cta tgc gat ctg gtg gat gca gct	355
Thr Met Asn Arg Thr Arg Lys Ala Leu Ser Asp Leu Val Asp Ala Ala	
70 75 80 85	
cca gaa act gca aca agg ctc aac gcg gat gac tca aca gag gta gtt	403
Pro Glu Thr Ala Thr Arg Leu Asn Ala Asp Asp Ser Thr Glu Val Val	
90 95 100	
gag ctg tgg gag ctt gag ccc ggt gac atc gtc ttg gta cgc aat ggc	451
Glu Leu Trp Glu Leu Glu Pro Gly Asp Ile Val Leu Val Arg Asn Gly	
105 110 115	
gaa caa att ccc gtc gat gga aac gtg att gcg ggt gtc ggt gga att	499
Glu Gln Ile Pro Val Asp Gly Asn Val Ile Ala Gly Val Gly Gly Ile	
120 125 130	
gat gaa tcc aac atc acg ggt gaa tca atg ccg gct gaa aag ggt caa	547
Asp Glu Ser Asn Ile Thr Gly Glu Ser Met Pro Ala Glu Lys Gly Gln	
135 140 145	
ggc tct gat gtg tat gca gga acc tgg ctg cga tct ggt gtt ttg aga	595
Gly Ser Asp Val Tyr Ala Gly Thr Trp Leu Arg Ser Gly Val Leu Arg	
150 155 160 165	
gtc gag gca aca gga att ggt tca gac tca act ttg gca aaa atc att	643
Val Glu Ala Thr Gly Ile Gly Ser Asp Ser Thr Leu Ala Lys Ile Ile	
170 175 180	
cac cgc gtt gaa gac gcc cag gat gac aaa gcc cgc aca caa aca ttc	691
His Arg Val Glu Asp Ala Gln Asp Asp Lys Ala Arg Thr Gln Thr Phe	
185 190 195	
tta gag aaa ttc tct aag tgg tac acc ccg ggc gtc atg atc gcc gcc	739
Leu Glu Lys Phe Ser Lys Trp Tyr Thr Pro Gly Val Met Ile Ala Ala	
200 205 210	
gca gtg gtg gga ctt atc acc tgg gac gta gaa cta gca ctg acg ctc	787
Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu Leu Ala Leu Thr Leu	
215 220 225	
tta gtg atc ggc tgc ccc ggc gcg ttg gtt atc tcc atc ccg gtg tcc	835
Leu Val Ile Gly Cys Pro Gly Ala Leu Val Ile Ser Ile Pro Val Ser	
230 235 240 245	

atc gtc gca ggc atc ggc cgt gct gca cgc gat ggc gtg ctg atc aag	883
Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp Gly Val Leu Ile Lys	
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ggt gga gaa tac cta gaa acc gcc gcg aaa gtc gac gtc gtt gtc gtg	931
Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val Asp Val Val Val Val	
265 270 275	
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Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro Glu Leu Thr Asp Val	
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gaa gtc atc gag ccc gcc tac agc cag ggc gag gtg ctg gag ctc gcc	1027
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Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu Ala Asp Ala Ile Ile	
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Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr Leu Val Glu Ala Ala	
330 335 340	
gaa aac atc acc ggc cga ggc att atc gca aat gtt gat gga cag gca	1171
Glu Asn Ile Thr Gly Arg Gly Ile Ile Ala Asn Val Asp Gly Gln Ala	
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Val Ala Val Gly Ser Ala Glu Leu Leu Asp His Glu Pro Asp Ser Thr	
360 365 370	
agg atc ctg gag cta aat gcc gaa gga aag acc gcg atg ttt gtc gga	1267
Arg Ile Leu Glu Leu Asn Ala Glu Gly Lys Thr Ala Met Phe Val Gly	
375 380 385	
gtg aac gga cac gcc att gga atc gtg gcc gtc gcc gac gcc gtt cgt	1315
Val Asn Gly His Ala Ile Gly Ile Val Ala Val Ala Asp Ala Val Arg	
390 395 400 405	
tca gat tct gcc tca gca atc gaa tcg ctg cat aag gcg ggc att caa	1363
Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys Ala Gly Ile Gln	
410 415 420	
gtt gtc atg gcg act ggc gac gct cac cgc gtt gca caa aac gtg gcc	1411
Val Val Met Ala Thr Gly Asp Ala His Arg Val Ala Gln Asn Val Ala	
425 430 435	
tcc aag ctg gga gtg gat gaa gtc tac tca gag cta ctc cct gaa cag	1459
Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu Leu Pro Glu Gln	
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aaa tta gaa ctg gtg cgt gat ctg caa gct gcc ggc aaa acg gtc gcg	1507
Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly Lys Thr Val Ala	
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atg gtg ggt gac gga gtc aac gac acc cca gca ttg gca gct gct gat	1555
Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu Ala Ala Ala Asp	
470 475 480 485	
atc gga gta gcg atg ggc gtg gca ggt tcc cct gca gcc att gaa acc	1603

Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala Ala Ile Glu Thr
490 495 500

gct gat atc gca ctc atg gcg gat cgt ctc cca cgg ctg gca cat gca 1651
Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg Leu Ala His Ala
505 510 515

gtg acc ttg gca aaa cgc acc gta aga acc atg cgc atc aat att ctg 1699
Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg Ile Asn Ile Leu
520 525 530

att gcg ttg gct acc gtg atg gtg tta cta gct ggc gtc cta ttt ggc 1747
Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly Val Leu Phe Gly
535 540 545

gga gtt acc atg tcg gtt ggc atg ctc gtt cac gaa gca agc gtg ctg 1795
Gly Val Thr Met Ser Val Gly Met Leu Val His Glu Ala Ser Val Leu
550 555 560 565

ctt gtt atc agc atc gcc atg ctg ttg ctg cgt cca aca ctt aaa gaa 1843
Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro Thr Leu Lys Glu
570 575 580

gat gct gcg caa gca agt gat att aaa cgc tcg gaa ata caa cag atc 1891
Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser Glu Ile Gln Gln Ile
585 590 595

gca taaccaatgg ctgggtactg atg 1917
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<210> 582

<211> 598

<212> PRT

<213> Corynebacterium glutamicum

<400> 582

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Ile Asp Leu Leu Val Val Val Ala Ala Val Gly Ala Met Phe Ile Asn
35 40 45

Asn Tyr Trp Glu Ser Ala Ala Val Thr Phe Leu Phe Ala Leu Gly Lys
50 55 60

Ala Leu Glu Arg Ala Thr Met Asn Arg Thr Arg Lys Ala Leu Ser Asp
65 70 75 80

Leu Val Asp Ala Ala Pro Glu Thr Ala Thr Arg Leu Asn Ala Asp Asp
85 90 95

Ser Thr Glu Val Val Glu Leu Trp Glu Leu Glu Pro Gly Asp Ile Val
100 105 110

Leu Val Arg Asn Gly Glu Gln Ile Pro Val Asp Gly Asn Val Ile Ala
115 120 125

Gly Val Gly Gly Ile Asp Glu Ser Asn Ile Thr Gly Glu Ser Met Pro
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 Ala Glu Lys Gly Gln Gly Ser Asp Val Tyr Ala Gly Thr Trp Leu Arg
 145 150 155 160
 Ser Gly Val Leu Arg Val Glu Ala Thr Gly Ile Gly Ser Asp Ser Thr
 165 170 175
 Leu Ala Lys Ile Ile His Arg Val Glu Asp Ala Gln Asp Asp Lys Ala
 180 185 190
 Arg Thr Gln Thr Phe Leu Glu Lys Phe Ser Lys Trp Tyr Thr Pro Gly
 195 200 205
 Val Met Ile Ala Ala Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu
 210 215 220
 Leu Ala Leu Thr Leu Leu Val Ile Gly Cys Pro Gly Ala Leu Val Ile
 225 230 235 240
 Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp
 245 250 255
 Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val
 260 265 270
 Asp Val Val Val Val Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro
 275 280 285
 Glu Leu Thr Asp Val Glu Val Ile Glu Pro Ala Tyr Ser Gln Gly Glu
 290 295 300
 Val Leu Glu Leu Ala Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu
 305 310 315 320
 Ala Asp Ala Ile Ile Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr
 325 330 335
 Leu Val Glu Ala Ala Glu Asn Ile Thr Gly Arg Gly Ile Ile Ala Asn
 340 345 350
 Val Asp Gly Gln Ala Val Ala Val Gly Ser Ala Glu Leu Leu Asp His
 355 360 365
 Glu Pro Asp Ser Thr Arg Ile Leu Glu Leu Asn Ala Glu Gly Lys Thr
 370 375 380
 Ala Met Phe Val Gly Val Asn Gly His Ala Ile Gly Ile Val Ala Val
 385 390 395 400
 Ala Asp Ala Val Arg Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His
 405 410 415
 Lys Ala Gly Ile Gln Val Val Met Ala Thr Gly Asp Ala His Arg Val
 420 425 430
 Ala Gln Asn Val Ala Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu
 435 440 445

Leu Leu Pro Glu Gln Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala
 450 455 460
 Gly Lys Thr Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala
 465 470 475 480
 Leu Ala Ala Ala Asp Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro
 485 490 495
 Ala Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro
 500 505 510
 Arg Leu Ala His Ala Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met
 515 520 525
 Arg Ile Asn Ile Leu Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala
 530 535 540
 Gly Val Leu Phe Gly Gly Val Thr Met Ser Val Gly Met Leu Val His
 545 550 555 560
 Glu Ala Ser Val Leu Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg
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 Pro Thr Leu Lys Glu Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser
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 Glu Ile Gln Gln Ile Ala
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 Val Lys Asn Pro Arg 5
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 ctc ata gca ctg gcc gct atc atc ctg acc tcg ttc aat ctg cga aca 163
 Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser Phe Asn Leu Arg Thr 20
 10 15
 gct att act gct tta gct ccg ctg gtt tct gag att cgg gat gat tta 211
 Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu Ile Arg Asp Asp Leu 35
 25 30
 ggg gtt agt gct tct ctt att ggt gtg ttg ggc atg atc ccg act gct 259
 Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly Met Ile Pro Thr Ala 50
 40 45
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Met	Phe	Ala	Asp	Ala	Ala	Phe	Ala	Leu	Pro	Ser	Leu	Lys	Arg	Lys	Phe		
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act	act	tcc	caa	ctg	ttg	atg	ttt	gcc	atg	ctg	ttg	act	gct	gcc	ggc	355	
Thr	Thr	Ser	Gln	Leu	Leu	Met	Phe	Ala	Met	Leu	Leu	Thr	Ala	Ala	Gly	85	
70					75				80								
cag	att	att	cgt	gtc	gct	gga	cct	gct	tgc	ctg	ttg	atg	gtc	ggc	act	403	
Gln	Ile	Ile	Arg	Val	Ala	Gly	Pro	Ala	Ser	Leu	Leu	Met	Val	Gly	Thr	100	
				90				95									
gtg	ttc	gcg	atg	ttt	gcg	atc	gga	gtt	acc	aat	gtg	ttg	ctt	ccg	att	451	
Val	Phe	Ala	Met	Phe	Ala	Ile	Gly	Val	Thr	Asn	Val	Leu	Leu	Pro	Ile	115	
			105				110						115				
gct	gtt	agg	gag	tat	ttt	ccg	cgt	cac	gtc	ggc	gga	atg	tgc	aca	act	499	
Ala	Val	Arg	Glu	Tyr	Phe	Pro	Arg	His	Val	Gly	Gly	Met	Ser	Thr	Thr	130	
		120					125										
tat	ctg	gtg	tgc	ttc	cag	att	gtt	cag	gca	ctt	gct	ccg	acg	ctt	gcc	547	
Tyr	Leu	Val	Ser	Phe	Gln	Ile	Val	Gln	Ala	Leu	Ala	Pro	Thr	Leu	Ala	145	
	135					140											
gtg	ccg	att	tct	cag	tgg	gct	aca	cat	gtg	ggc	ttg	acc	ggc	tgg	agg	595	
Val	Pro	Ile	Ser	Gln	Trp	Ala	Thr	His	Val	Gly	Leu	Thr	Gly	Trp	Arg	165	
150					155					160							
gtg	tgc	ctc	ggc	tgc	tgg	gcg	ctg	ctg	ggc	ttg	gtt	gcg	gcg	att	tgc	643	
Val	Ser	Leu	Gly	Ser	Trp	Ala	Leu	Leu	Gly	Leu	Val	Ala	Ala	Ile	Ser	180	
				170					175								
tgg	att	ccg	ctg	ttg	agt	ttg	cag	ggc	agg	gtt	gtt	gcg	gcg	ccg		691	
Trp	Ile	Pro	Leu	Leu	Ser	Leu	Gln	Gly	Ala	Arg	Val	Val	Ala	Ala	Pro	195	
			185					190									
tgc	aag	gtt	tct	ctt	cct	gtg	tgg	aag	tct	tgc	gtt	ggc	gtg	ggc	ctc	739	
Ser	Lys	Val	Ser	Leu	Pro	Val	Trp	Lys	Ser	Ser	Val	Gly	Val	Gly	Leu	210	
		200					205										
ggc	ttg	atg	ttt	ggc	ttt	act	tgc	ttt	gcg	acg	tat	atc	ctc	atg	ggc	787	
Gly	Leu	Met	Phe	Gly	Phe	Thr	Ser	Phe	Ala	Thr	Tyr	Ile	Leu	Met	Gly	225	
	215					220											
ttt	atg	ccg	cag	atg	gta	ggc	gat	cct	cag	ctc	ggc	gcg	gtg	ttg	tta	835	
Phe	Met	Pro	Gln	Met	Val	Gly	Asp	Pro	Gln	Leu	Gly	Ala	Val	Leu	Leu	245	
230					235					240							
ggc	tgg	tgg	tca	att	ttg	gga	ttg	ccg	ctg	aac	att	ctg	gga	ccg	tgg	883	
Gly	Trp	Trp	Ser	Ile	Leu	Gly	Leu	Pro	Leu	Asn	Ile	Leu	Gly	Pro	Trp	260	
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ttg	gtg	acg	cgt	ttc	act	aac	tgc	ttc	ccg	atg	gtt	gtt	atc	gcc	agt	931	
Leu	Val	Thr	Arg	Phe	Thr	Asn	Cys	Phe	Pro	Met	Val	Val	Ile	Ala	Ser	275	
			265					270									
gtc	atg	ttt	ctc	atc	ggc	aat	ggc	ggc	ttt	tgt	ttg	gct	ccg	gat	gtt	979	
Val	Met	Phe	Leu	Ile	Gly	Asn	Gly	Gly	Phe	Cys	Leu	Ala	Pro	Asp	Val	290	
		280					285										
gcg	ccg	tgg	ttg	tgg	gcg	acg	ttg	tct	ggc	ctt	ggc	ccc	ctt	gcg	ttc	1027	
Ala	Pro	Trp	Leu	Trp	Ala	Thr	Leu	Ser	Gly	Leu	Gly	Pro	Leu	Ala	Phe		

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ccg atg gcg ttg acg ctc att aat att cgt gct gaa act agt gct ggt			1075
Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala Glu Thr Ser Ala Gly			
310	315	320	325
gct tct gcg ttg agt tcc ttc ggg cag ggt ttg ggt tat acg att gcg			1123
Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu Gly Tyr Thr Ile Ala			
	330	335	340
tgt ttc ggt ccc ttg ttg act ggt ttc att gtc gat gcg aca ggc agc			1171
Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val Asp Ala Thr Gly Ser			
	345	350	355
ttc cga aca atc ttt gtg ctt ttt gcg gtt gca aca ctc ttc gtt att			1219
Phe Arg Thr Ile Phe Val Leu Phe Ala Val Ala Thr Leu Phe Val Ile			
	360	365	370
aga ggc ggt tac ttt gcg aca agg cag gtt tac gtc gaa aag ctt tta			1267
Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr Val Glu Lys Leu Leu			
	375	380	385
aat cgc taggatggcg ctatgccgca aag			1296
Asn Arg			
390			

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Phe Asn Leu Arg Thr Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu
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Ile Arg Asp Asp Leu Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly
35 40 45

Met Ile Pro Thr Ala Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser
50 55 60

Leu Lys Arg Lys Phe Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu
65 70 75 80

Leu Thr Ala Ala Gly Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu
85 90 95

Leu Met Val Gly Thr Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn
100 105 110

Val Leu Leu Pro Ile Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly
115 120 125

Gly Met Ser Thr Thr Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu
130 135 140

Ala Pro Thr Leu Ala Val Pro Ile Ser Gln Trp Ala Thr His Val Gly

145		150		155		160
Leu Thr Gly Trp Arg Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu						
		165		170		175
Val Ala Ala Ile Ser Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg						
		180		185		190
Val Val Ala Ala Pro Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser						
		195		200		205
Val Gly Val Gly Leu Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr						
		210		215		220
Tyr Ile Leu Met Gly Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu						
		225		230		235
						240
Gly Ala Val Leu Leu Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn						
		245		250		255
Ile Leu Gly Pro Trp Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met						
		260		265		270
Val Val Ile Ala Ser Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys						
		275		280		285
Leu Ala Pro Asp Val Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu						
		290		295		300
Gly Pro Leu Ala Phe Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala						
		305		310		315
						320
Glu Thr Ser Ala Gly Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu						
		325		330		335
Gly Tyr Thr Ile Ala Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val						
		340		345		350
Asp Ala Thr Gly Ser Phe Arg Thr Ile Phe Val Leu Phe Ala Val Ala						
		355		360		365
Thr Leu Phe Val Ile Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr						
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Val Glu Lys Leu Leu Asn Arg						
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Met Arg Arg Lys Leu
1 5

acc acc aca tta gaa aac aag ccc ggt gca cga ctt ggt ggc ttc cgc 163
Thr Thr Thr Leu Glu Asn Lys Pro Gly Ala Arg Leu Gly Gly Phe Arg
10 15 20

gca ctt gca cca act tca aaa atc gcg ctg gtt ttc ctt ctc ctg atc 211
Ala Leu Ala Pro Thr Ser Lys Ile Ala Leu Val Phe Leu Leu Leu Ile
25 30 35

ttc ctc ctc gcg atc ttt gcc cca ctg att gct aaa tac gat cca ctg 259
Phe Leu Leu Ala Ile Phe Ala Pro Leu Ile Ala Lys Tyr Asp Pro Leu
40 45 50

gcc tcc gga act cca gtc cag cct cca agc ggt gag cac tgg ttt ggt 307
Ala Ser Gly Thr Pro Val Gln Pro Pro Ser Gly Glu His Trp Phe Gly
55 60 65

acc gac gcc atc ggc cgc gat att ttc tcc cgc gta gcc acg gcg cca 355
Thr Asp Ala Ile Gly Arg Asp Ile Phe Ser Arg Val Ala Thr Ala Pro
70 75 80 85

gag cct ccc tgatcattgg tcttttcgct acg 387
Glu Pro Pro

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20 25 30

Phe Leu Leu Leu Ile Phe Leu Leu Ala Ile Phe Ala Pro Leu Ile Ala
35 40 45

Lys Tyr Asp Pro Leu Ala Ser Gly Thr Pro Val Gln Pro Pro Ser Gly
50 55 60

Glu His Trp Phe Gly Thr Asp Ala Ile Gly Arg Asp Ile Phe Ser Arg
65 70 75 80

Val Ala Thr Ala Pro Glu Pro Pro
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